

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1788	100.0	1788	6	AR078244	Sequence
2	1788	100.0	1788	6	AR195308	Sequence
3	1788	100.0	1788	6	AR222273	Sequence
4	1788	100.0	1788	9	CGU11453	U11453 Cricetus
5	1786	99.9	1825	6	AR091980	Sequence
6	1786	99.9	1825	6	AR112115	Sequence
7	1786	99.9	1825	6	AR149157	Sequence
8	1441.2	80.6	2496	9	CQ868666	Sequence
9	1441.2	80.6	2512	9	BC004656	Mus muscu
10	1413	79.0	2497	9	AB002151	Rattus no
11	1390.6	77.8	2392	9	D89655	Rattus norv
12	1390.6	77.8	2408	9	BC076504	Rattus no
13	1381	77.2	2401	9	AY451993	Rattus no
14	1369.8	76.6	1785	6	AR078245	Sequence
15	1369.8	76.6	1785	6	AR195310	Sequence
16	1369.8	76.6	1785	6	AX305450	Sequence
17	1369.8	76.6	1785	9	MMU37799	Mus musculu
18	1363.2	76.2	1674	9	U76205	Rattus norv

[illegible]

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Db	1441	CGTTTCTACAGCAGCTGGTGTCTGATGCCCCAGGTAATTTGAGTATGTGCAGTATGTGTCTGC	1500
Qy	1501	TGGGGCTGGGCGGCTCTCTGCTGCTGGTGGCCGTCTACTACCAAGTTTCGCGAGCCAGGAGA	1560
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Db	1681	TGTAGGTTCCCAAGACACCAACGAGCCCCCCCCAACCTGATAGCTTGGTCAGACCGCCAT	1740
Qy	1741	CCAGCCCTTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGTGC	1788
Db	1741	CCAGCCCTTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGTGC	1788
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LOCUS	AR195308	1788 bp	DNA linear PAT 20-APR-2002
DEFINITION	Sequence 3 from patent US 6350859.		
ACCESSION	AR195308		
VERSION	AR195308.1	GI:20244745	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1788)		
TITLE	Krieger,M., Acton,S.L. and Rigotti,A.		
JOURNAL	Class BI and CI scavenger receptors		
FEATURES	Patent: US 6350859-A 3 26-FEB-2002;		
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Best Local Similarity	100.0%;	Preid. No. 0;	Length 1788;
Matches 1788;	Conservative	0;	Mismatches 0;
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Db	1	GCCACCTGCAGGGCTACTGCTGTCTCCGGCCACTGCTCAGACTCACCTTGTCTGGAACGTG	60
Qy	61	AGCTCGGCTTCTGTATCTCTGTGGCCTCTGTGGCTTCTGTGCTGTCCCCCTTCAGTC	120
Db	61	AGCTCGGCTTCTGTATCTCTGTGGCCTCTGTGGCTTCTGTGCTGTCCCCCTTCAGTC	120
Qy	121	CCTGAGCCCGCGAGCCCGGGCCGACACCGGACATGGGGCGCAGCGCCAGGGCGCGCT	180
Db	121	CCTGAGCCCGCGAGCCCGGGCCGACACCGGACATGGGGCGCAGCGCCAGGGCGCGCT	180
Qy	181	GGGTGGCGGTGGGGCTGGGGCTGGTGGGGCTGTGTGGCTGTGTGCTCGGTGTGTTATGA	240
Db	181	GGGTGGCGGTGGGGCTGGGGCTGGTGGGGCTGTGTGGCTGTGTGCTCGGTGTGTTATGA	240
Qy	241	TCCTCGTATGCTCCCTCGCTCATCAACACAGAGGTACTGAAGAAATGTCCGCATAGACCCCA	300

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Db 301 GCAGCCTGCTCTTTGCAATGTGAAGAGATCCCTGTACCTCTACTTGTCCGTCTACT 360
Qy 361 TCCTCGAGGTGGTCAATCCAGCGAGATCCTTAAGGCTGAGACCCAGTGTGCGGAGC 420
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Qy 421 GTGACCCCTATGTCTACAGGGAATTCAGACATTAAGGCCAATCATCACCCTTCAATGACAATG 480
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Db 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
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RESULT 3
AR222273
LOCUS 1788 bp mRNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6429289.
ACCESSION AR222273
VERSION AR222273.1 GI:23329756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1788)
AUTHORS Krieger,M., Acton,S.L. and Pearson,A.M.
TITLE Class BI and CI scavenger receptors
JOURNAL Patent: US 6429289-A 3 06-AUG-2002;
Massachusetts Institute of Technology; Cambridge, MA;
WOX;
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1. .1788
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Query Match 100.0%; Score 1788; DB 6; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
CGU11453 1788 bp mRNA linear ROD 26-JAN-1995
LOCUS Cricetulus griseus CD36-related class B scavenger receptor hasR-Bi
(hasR-bi) mRNA, complete cds.
ACCESSION U11453
VERSION U11453.1 GI:562021
KEYWORDS modified lipoprotein receptor; oxidized low density lipoprotein; adipocytes.
SOURCE Cricetulus griseus (Chinese hamster)
ORGANISM Cricetulus griseus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Cricetidae; Cricetinae; Cricetulus.
REFERENCE 1 (bases 1 to 1788)
AUTHORS Acton, S.L., Scherer, P.E., Lodish, H.F. and Krieger, M.
TITLE Expression cloning of SR-BI, a CD36-related class B scavenger receptor
JOURNAL J. Biol. Chem. 269 (33), 21003-21009 (1994)
PUBMED 7520436
REFERENCE 2 (bases 1 to 1788)
AUTHORS Acton, S.L.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Susan L. Acton, Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA

FEATURES
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	Unclassified.
REFERENCE	1 (bases 1 to 1825)
AUTHORS	Acton, S. Laurene.
TITLE	Human intronic and polymorphic SR-BI nucleic acids and uses

ORIGIN

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Query Match          99.9%; Score 1786; DB 6; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0
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Qy	121	CTTGAGCCCCCGAGACCCCGGCCGCGCACACGCGGACATGGGCGGACGCGCCAGGGCGCGCT	180
Db	121	CTTGAGCCCCCGAGACCCCGGCCGCGCACACGCGGACATGGGCGGACGCGCCAGGGCGCGCT	180
Qy	181	GGGTGGGGTGGGGCTGGGCGTCTGTGGGGCTGCTGTGCGCTGCTGCTCGGTGGTATTGA	240
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Qy	241	TCCTCTGTGATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAAATGTCGCGATAGACCCCA	300
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RESULT 7	
AR149157	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	

Qy	841	GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCATTCAG	900
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Qy	901	AGCAGTGCACATGATCAATGGGCACATTCGGGGCAGATGTGGGCACCACTCATGACACCCC	960
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Qy	1081	CCAATGGGTCTGTTTAAACCCACCAATGAAGGTTTCTGCCGCTGCTTGAATCCGGCAATTC	1140
Db	1081	CCAATGGGTCTGTTTAAACCCACCAATGAAGGTTTCTGCCGCTGCTTGAATCCGGCAATTC	1140
Qy	1141	AAAATGTCAACACTTGCAGGTTTGGTGCAACCCCTGTTTCTGTCAACCCCTCACTTCTACA	1200
Db	1141	AAAATGTCAACACTTGCAGGTTTGGTGCAACCCCTGTTTCTGTCAACCCCTCACTTCTACA	1200
Qy	1201	ATGCAGACCCCTGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACCCCAAGGAGCATTT	1260
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Qy	1261	CTTTGTTCTCTTGACATCCATCCGCTCACTGGGATCCCCATGAATGTTCTGTGAAGTTGC	1320
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Qy	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCAATTTGGGCAAAACAGGGAAGATCGAGCCCG	1380
Db	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCAATTTGGGCAAAACAGGGAAGATCGAGCCCG	1380
Qy	1381	TGGTCTCTCCATTTGCTGTGTTTTGACAGAGCGGTGTCATGGGGGGGCGGCCCTCTGAACA	1440
Db	1381	TGGTCTCTCCATTTGCTGTGTTTTGACAGAGCGGTGTCATGGGGGGGCGGCCCTCTGAACA	1440
Qy	1441	CGTTCTACACGCACTGGTGTCTGATGCCCCAGGTACTTTCAGTATGTGCAGTATGTGCTGC	1500
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
MORRIS, D.W. and MALANDRO, M.S.
Novel therapeutic gpcr targets in cancer
Patent: WO 2004/074321-A 78 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
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ORIGIN

Query Match 80.6%; Score 1441.2; DB 6; Length 2496;
Best Local Similarity 88.3%; Pred. No. 1.5e-301;
Matches 1577; Conservative 0; Mismatches 208; Indels 1; Gaps 1;

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Qy 481 ATACTGTGCTTGTGGAGCAGCGAGCTTCCATTTCCAGCGGAGAGTCCCAAGGCT 540
Db 518 ACACCGGTGCTTGTGGAGAACCGAGCTTCCATTTCCAGCGTGAAGTCCGATGGCT 577

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Qy 601 AGACAAAGTCTGACAGGCTGAAGCTGATGATGACCTTGGGGGCTGGCCACCTTGGGGCAGC 660
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RESULT 9
BC004656
LOCUS
DEFINITION

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Mus musculus scavenger receptor class B, member 1, mRNA (cDNA clone
MGC:5988 IMAGE:3498018), complete cds.

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RESULT 10 AB002151 LOCUS

DEFINITION Rattus norvegicus mRNA for scavenger receptor class B type I, complete cds.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AB002151.1 GI:4210541
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Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;

REFERENCE AUTHORS TITLE

1 (sites)
Shiratsuchi, A., Kawasaki, Y., Ikemoto, M., Arai, H. and Nakanishi, Y.
Role of class B scavenger receptor type I in phagocytosis of apoptotic rat spermatogenic cells by sertoli cells
J. Biol. Chem. 274, 5888-5894 (1999)
2 (bases 1 to 2497)
Nakanishi, Y.

JOURNAL AUTHORS TITLE

Direct Submission
Submitted (26-MAR-1997) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@db.p.kanazawa-u.ac.jp, Tel:076-234-4424, Fax:076-234-4480)

FEATURES source

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CDS

ORIGIN

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[illegible]

BC076504

LOCUS	BC076504	2408 bp	mRNA	linear	ROD 07-JUL-2004
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DEFINITION *Rattus norvegicus* scavenger receptor class B, member 1, mRNA (cDNA

ACCESSION BC076504
CLONE MGC:91637 IMAGE:7099863), complete cds.

ACCESSION	BC076504
VERSION	BC076504.1 GT:49904284

KEYWORDS
MGC.

SOURCE *Rattus norvegicus* (Norway rat)

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Chlamydia	Adult
Staphylococcus aureus	Adult
Pseudomonas aeruginosa	Adult
Escherichia coli	Adult
Salmonella enteritidis	Adult
Shigella flexneri	Adult
Yersinia enterocolitica	Adult
Legionella pneumophila	Adult
Brucella abortus	Adult
Mycobacterium tuberculosis	Adult
Streptococcus pneumoniae	Adult
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Plasmodium falciparum	Adult
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QY 965 TACTCTGTTTGGCAACGGGTCCGTCTACCCCAACGAAGGCTTCTGCCCATGSCCGAGA 1024
DB |||||
QY 1130 ATCCGGCATTCAAAATGTACAGACTTGCAGGTTTGGTGACCCCTGTTCTGTCTCACACCC 1189
DB |||||
QY 1025 GTCTGGCATTCAGAAATGTCAGACCTGCAAGTTTGGTGCGCTCTGTGTTCTCTCCACCC 1084
DB |||||
QY 1190 TCACCTTCTACAATGCAGACCTGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACCC 1249
DB |||||
QY 1085 CCACCTTTACAACGCCGACCTGTGTTGTGTCAGAACTGTTCTTGGTCTGAACCTTAACCC 1144
DB |||||
QY 1250 AAGGGAGCATCTTTGTTCTTGACATCCATCCGGTCACTGGGATCCCAATGAACCTGTTTC 1309
DB |||||
QY 1145 AAAGGAGCATCTCTGTTCTTAGACATCCATCCGGTCACTGGGATCCCAATGAACCTGTTTC 1204
DB |||||
QY 1310 TGTGAAGTTCAGATAGCCTCTACATCAAGCTGTCAAGGCAATGGGCAACAGGAA 1369
DB |||||
QY 1205 TGTGAAGATGCACTGAGCTCTACATCAAACTGTCAAGGCAATGGGCAACAGGAA 1264
DB |||||
QY 1370 GATCGAGCCCGTGTCTCCCATTTGCTGTGTTGAGCAGAGGGGTGCCATGGGCGGCGGA 1429
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QY 1265 GATCGAGCAGTAGTTCTGCGGTGCTGTGTTGCGAACAGAGCGAATGGTGGCAA 1324
DB |||||
QY 1430 GCCCTGAAACAGGTTCTACAGGAGCTGTGCTGATGCCCCAGGTACTTCAGTATGTGCA 1489
DB |||||
QY 1325 GCCCTTGAGCACGTTCTACACGAGCTGTGCTGATGCCCCAGGTTCTTCACTACGCGCA 1384
DB |||||

QY 1490 GTATGTGCTGTGGGGCTGGGGGCTCCTGTGCTGTGCTGCTCATCTACCACTTGGC 1549
DB |||||
QY 1385 GTATGTGCTGTGGGGCTGGAGGCTCCTGTGCTGTGCTGCCATCATCTGCCAAGTGGC 1444
DB |||||
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DB |||||
QY 1445 CAGCCAGGAGAAATGCTTTTCTTTTGGAGTGGTAGTAAAAAGGGCTCCAGGATAAGGA 1504
DB |||||
QY 1610 GGCCATTCAAGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCACGGTGTGCA 1669
DB |||||
QY 1505 GGCCATTCAAGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCACGGTGTGCA 1564
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DB |||||
QY 1565 AGAAGCCAAAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCAACCTCATAGCTTGGTC 1624
DB |||||
QY 1730 AGACCAAGCCATCCAGCCCCCTACACCCCGTCTTTGAGGACTCTCTCAGCGGACAGTC 1786
DB |||||
QY 1625 AGACCAAGCCACCAAGTCCCTACACCCCGTCTTTGAGGACTCTCTCAGCGGACAGCC 1681
DB |||||

Search completed: February 23, 2006, 22:46:12
Job time : 9019.06 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:34:57 ; Search time 1079.41 Seconds
(without alignments)
11039.845 Million cell updates/sec

Title: US-08-765-108-3

Perfect score: 1788
Sequence: 1 GCCACTGCGGGCTACTGC.....CTCTCAGCGGACAGTCGC 1788

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1788	100.0	1788	2 AAT10116	Aat10116 Hamster s
2	1788	100.0	1788	2 AAX23403	Aax23403 Hamster s
3	1788	100.0	1788	6 AAZ30615	Aaz30615 Hamster S
4	1788	100.0	1788	6 ABS53744	AbS53744 CDNA enco
5	1788	100.0	1788	6 AAD33915	Aad33915 Hamster S
6	1788	100.0	1788	12 ADJ53334	Adj53334 Hamster S
7	1786	99.9	1825	9 ACD44926	Acd44926 Human cdn
8	1786	99.9	1825	12 ADJ46120	Adj46120 Human var
9	1718	96.1	1788	14 AEB03191	Aeb03191 Hamster S
10	1441.2	80.6	2496	13 ABD33431	Abd33431 Murine ca
11	1441.2	80.6	2496	13 ADR67032	Adr67032 Mouse can
12	1441.2	80.6	2513	14 ADZ13454	Adz13454 Murine ca
13	1413	79.0	2497	10 ADB58616	Adb58616 Toxicity-
14	1413	79.0	2497	10 ADB53264	Adb53264 Primary r
15	1413	79.0	2497	10 ABT42207	Abt42207 Toxicity
16	1413	79.0	2497	13 ADV41414	Adv41414 Rat cardl
17	1369.8	76.6	1785	2 AAX23404	Aax23404 Mouse sca
18	1369.8	76.6	1785	2 AAZ30616	Aaz30616 Mouse sca
19	1369.8	76.6	1785	6 ABI99330	Abi99330 Mouse isc

20	1369.8	76.6	1785	6 AAD33917	Aad33917 Murine sc
21	1369.8	76.6	1785	12 ADJ53336	Adj53336 Murine SR
22	1359.8	76.1	1785	14 AEB03942	Aeb03942 Murine Sc
23	1358	76.0	1718	14 AEB03937	Aeb03937 Hamster S
24	1255.8	70.2	1531	13 ADS73684	AdS73684 Rat SRB-I
25	1247.8	69.8	1546	14 AEA33429	Aea33429 SR-BI CDN
26	1243.8	69.6	1607	6 ABL46318	AbL46318 Mouse sca
27	1233	69.0	2382	14 ADZ13452	Adz13452 Murine ca
28	1201.8	67.2	1761	14 AEB03939	Aeb03939 Murine Sc
29	1153.4	64.5	2637	14 ADZ13457	Adz13457 Human can
30	1153.4	64.5	3116	14 ADZ13463	Adz13463 Human can
31	1139.4	63.7	2630	9 ACD44925	Acd44925 Human CDN
32	1139.4	63.7	2630	12 ADJ46118	Adj46118 Human CDN
33	1137.8	63.6	2558	4 ABA09256	AbA09256 Human SR-
34	1136.2	63.5	2565	2 AAZ32194	Aaz32194 Human CLA
35	1136.2	63.5	2566	3 AAA40750	Aaa40750 Wild type
36	1136.2	63.5	2566	9 AAL62623	Aal62623 Human CD3
37	1136.2	63.5	2566	12 ADL61166	AdL61166 Human tyr
38	1135.4	63.5	3143	14 ADZ13465	Adz13465 Human can
39	1135.4	63.5	3144	13 ABD33433	Abd33433 Human can
40	1135.4	63.5	3144	13 ADR67035	Adr67035 Human can
41	1129.8	63.2	2628	10 ADE40209	Ade40209 Human NOV
42	1129.8	63.2	2630	2 AAX24497	Aax24497 Human SR-
43	1129.8	63.2	2630	2 AAX24589	Aax24589 Human SR-
44	1120.4	62.7	2604	10 ADE09617	Ade09617 Novel DNA
45	1066	59.6	3185	14 ADZ13461	Adz13461 Human can

ALIGNMENTS

RESULT 1	
AAT10116	
ID	AAT10116 standard; cDNA; 1788 BP.
XX	
AC	AAT10116;
XX	
DT	29-MAR-1996 (first entry)
XX	
DE	Hamster scavenger receptor class B-I CDNA.
XX	
KW	Scavenger receptor class BI; HaSR-BI; low density lipoprotein;
KW	atherosclerosis; CHO; Chinese hamster ovary; lipoprotein receptor;
KW	cholesterol; ds.
XX	
OS	Cricetulus sp.
XX	
FH	Key
CDS	Location/Qualifiers
FT	156..1685
FT	/*tag= a
FT	/product= "scavenger receptor class B-I"
XX	
PN	WO9600288-A2.
XX	
PD	04-JAN-1996.
XX	
PF	19-JUN-1995; 95WO-US007721.
XX	
PR	23-JUN-1994; 94US-00265428.
XX	
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.
XX	
PI	Krieger M, Acton SL, Pearson AM, Rigotti A;
XX	
DR	WPI; 1996-068872/07.
DR	P-PSDB; AAR88465.
XX	
PT	Class BI and CI scavenger receptor proteins - used to develop products
PT	for treating or preventing atherosclerosis, fat uptake by adipocyte(s)
XX	
PS	Claim 14; Page 56-57; 84pp; English.
XX	

XX Scavenger receptor class B type I; hamster; steroid production; HDL;
KW cholesterol; cholesteryl ester transport; high-density lipoprotein;
KW lipoprotein; liver; steroidogenic tissue; SR-BI; contraception;
KW treatment; disorder; overproduction; underproduction; menopause;
KW breast cancer; prostate cancer; endometriosis; fibroid tumour; ss.
XX Cricetulus griseus.
XX WO9911288-A1.
XX 11-MAR-1999.
XX 04-SEP-1998; 98WO-US018463.
XX 05-SEP-1997; 97US-0057943P.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX Krieger M;
XX WPI; 1999-204984/17.
XX P-PSDB; AAW93574.
XX Modification of steroid production in mammals - by administering
XX modulator of SR-BI expression or activity.
XX Disclosure; Page 77; 86pp; English.
XX CC This invention describes a method for modifying steroid production in a
XX mammal which comprises administering a compound that alters cholesterol
XX or cholesteryl ester transport from high-density lipoprotein (HDL) or
XX other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger
XX receptor class B type I). This method is useful for female contraception,
XX for treating disorders characterised by overproduction of steroids, for
XX treating disorders characterised by underproduction of steroids, for
XX especially menopause, for treating disorders that can be treated by
XX decreasing steroid production, especially breast cancer, prostate cancer,
XX endometriosis or fibroid tumours
XX Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;
Query Match 100.0%; Score 1788; DB 2; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTTCTGGAACGTG 60
DB 1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTTCTGGAACGTG 60
QY 61 AGCTCGGCTTCTGTCATCTCTGCGGCTCTGTCGCTTCTGTCGCTGCTCCCTTCAGTC 120
DB 61 AGCTCGGCTTCTGTCATCTCTGCGGCTCTGTCGCTTCTGTCGCTGCTCCCTTCAGTC 120
QY 121 CCTGAGCCCCCGAGCCCGGCGCCACACCGGACATGCGCGGAGCGCGCGCGCT 180
DB 121 CCTGAGCCCCCGAGCCCGGCGCCACACCGGACATGCGCGGAGCGCGCGCGCT 180
QY 181 GGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT 240
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QY 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGAGTCTGGAAGATGTCGCGATAGACCCCA 300
DB 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGAGTCTGGAAGATGTCGCGATAGACCCCA 300
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DB 301 GCAGCCTGTCTTTGCAATGGAAGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACT 360
QY 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTTAAGGTGAGAGCCAGTAGTGGGGAGC 420
DB 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTTAAGGTGAGAGCCAGTAGTGGGGAGC 420

QY 421 GTGAGCCTTATGCTACAGGGAATTGACATTAAGGCCAAACATCACCTTCAATGACAATG 480
DB 421 GTGAGCCTTATGCTACAGGGAATTGACATTAAGGCCAAACATCACCTTCAATGACAATG 480
QY 481 ATACTGTGCTCTTTGTGGAGCACCGAGCCTCATTTCCAGCCGACAGTCCACGGCT 540
DB 481 ATACTGTGCTCTTTGTGGAGCACCGAGCCTCATTTCCAGCCGACAGTCCACGGCT 540
QY 541 CTGAGAGTGACTACTATATATCTGCTAAACATTTCTGGTCTTTGGGGGGCGAGTAATGATG 600
DB 541 CTGAGAGTGACTACTATATATCTGCTAAACATTTCTGGTCTTTGGGGGGCGAGTAATGATG 600
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QY 721 ATTTTATCAACAATACTTACAGAGATGTTCCCATCAAGGGCAAGTTTCGGCTGTTT 780
DB 721 ATTTTATCAACAATACTTACAGAGATGTTCCCATCAAGGGCAAGTTTCGGCTGTTT 780
QY 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
DB 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA 840
QY 841 GCAAGATCCACCTGGTGGAGATGGAATGGGCTCAGCAAGGTCAACTACTGGGATTCAG 900
DB 841 GCAAGATCCACCTGGTGGAGATGGAATGGGCTCAGCAAGGTCAACTACTGGGATTCAG 900
QY 901 AGCAGTGCAACATGATCAATGSCACTTCCGGGAGATGCGGACCATTCATGACACCCC 960
DB 901 AGCAGTGCAACATGATCAATGSCACTTCCGGGAGATGCGGACCATTCATGACACCCC 960
QY 961 AGTCTCGCTGGGAATTTCTTCACTGCGGAAAGCTTCAGAGTCTATGAAGCTCACCTACCATG 1020
DB 961 AGTCTCGCTGGGAATTTCTTCACTGCGGAAAGCTTCAGAGTCTATGAAGCTCACCTACCATG 1020
QY 1021 ATTGAGGGTGGTGAAGGATCCCACTATCGCTTTCAGCCCTTAAACCTTTGTTG 1080
DB 1021 ATTGAGGGTGGTGAAGGATCCCACTATCGCTTTCAGCCCTTAAACCTTTGTTG 1080
QY 1081 CCAATGGGCTGTTTACCCACCAATGAAGTTCCTGCGGCTGCTTGAATCCGGCATTC 1140
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QY 1141 AATAATGTCAGCACTGTCAGGTTGGTGCAACCTGTTTCTGTCAACCTTCACTTCTACA 1200
DB 1141 AATAATGTCAGCACTGTCAGGTTGGTGCAACCTGTTTCTGTCAACCTTCACTTCTACA 1200
QY 1201 ATGAGACCTGTGCTATCAGAACGCGTTCGGGTCTGAACCTGACCCAGGAGGACATT 1260
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DB 1441 CGTTCTTACAGCAGCTGGTGTGATGTCGCCAGGTACTTCAATGTCAGTATGTCAGTATGTCGTC 1500

601 AGAGCAAGTCTGAGGCTTCAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGGCCAGC 660
601 AGAGCAAGTCTGAGGCTTCAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGGCCAGC 660
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Db 1681 TGTAGGGTCCCAAGACACACAGAGCCCGCCCACTGATAGCTTGGTCAGACCGCCAT 1740
Qy 1741 CCAGGCCCTACACCCCGCTTCTTGGAGCTCTCTCAGCGGACAGTCGC 1788
Db 1741 CCAGGCCCTACACCCCGCTTCTTGGAGCTCTCTCAGCGGACAGTCGC 1788
RESULT 5
AAD33915
ID AAD33915 standard; cDNA; 1788 BP.
XX
AC AAD33915;
XX
DT 16-JUL-2002 (first entry)
XX
DE Hamster scavenger receptor type B-I (haSR-BI) cDNA.
XX
KW Scavenger receptor protein type BI; low density lipoprotein; LDL;
KW hamster; SR-BI; gene; ss.
XX
OS Cricetulus sp.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..155
FT /*tag= a
FT CDS 156..1685
FT /*tag= b
FT /*product= "haSR-BI protein"
FT 3'UTR 1686..1788
FT /*tag= c
XX
PN US6350859-BI.
XX
PD 26-FEB-2002.
XX
PF 02-FEB-1999; 99US-00241581.
XX
PR 23-JUN-1994; 94US-00265428.
PR 27-MAR-1997; 97US-00765108.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Krieger M, Acton SL, Rigotti A;
XX
DR WPI; 2002-314680/35.
DR P-PSDB; ABE21523.
XX
PT Antibody specific for scavenger receptor protein type BI useful for
PT detection, characterization or isolation of receptor proteins, as well
PT inhibiting scavenger protein binding to low density lipoprotein.
XX
PS Disclosure; Col 31-32; 41pp; English.
XX
CC The invention relates to an antibody specific for scavenger receptor
CC protein type B-I (SR-BI) derived from murine and hamster. Antibodies of
CC the invention are useful for detection, characterisation and isolation of
CC receptor proteins and for inhibiting scavenger protein binding to low
CC density lipoprotein (LDL). The present sequence is hamster (ha) SR-BI
CC cDNA
XX
SQ Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;
Query Match 100.0%; Score 1788; DB 6; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCACCTGACGGCTACTGCTCGGGCACCTGCTGAGACTCAGCTTGTGGAACGTG 60
Db 1 GCCACCTGACGGCTACTGCTCGGGCACCTGCTGAGACTCAGCTTGTGGAACGTG 60
Qy 61 AGCCTCGGCTTGTGTCATCTCTGTGGCCTCTGTGCTGTGTGCTGTGTGCTGTGCT 120

PA (KOZA/) KOZARSKY K.
 PA (RIGO/) RIGOTTI A.
 PA (KRIE/) KRIEGER M.
 XX
 PI Kozarsky K, Rigotti A, Krieger M;
 XX WPI; 2004-246237/23.
 DR P-PSDB; ADJ53335.
 DR
 XX
 PT Screening for agents that influence lipid transport, useful e.g. for
 PT treating or preventing atherosclerosis, based on modulation of the SR-BI
 PT scavenge receptor.
 PT
 XX
 PS Disclosure; SEQ ID NO 1; 22pp; English.
 XX
 CC The invention relates to a method for screening compounds that alter
 CC transport of lipids, cholesterol, lipoproteins or their components,
 CC mediated by the SR-BI scavenger receptor (SR-BI HDL receptor) or a
 CC homologue. The test compound is administered to an animal and cholesterol
 CC or bile acid levels, production levels of steroid hormones or alterations
 CC in chemical composition of lipids, lipoproteins, cholesterol, steroid
 CC hormones, bile acids and Vitamin A is measured. Agents that alter
 CC transport of lipids, cholesterol or lipoproteins are potentially useful
 CC for the treatment or prevention of atherosclerosis, fat uptake by
 CC adipocytes and some endocrine disorders. This sequence represents cDNA
 CC encoding the hamster SR-BI scavenger receptor of the invention.
 XX
 XX Sequence 1788 BP; 370 A; 511 C; 487 G; 420 T; 0 U; 0 Other;

Query Match 100.0%; Score 1788; DB 12; Length 1788;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 GCCACCTGACGGGTACTGCTGCTCCGGCCACTGCTGAGACTCACCTTCTGGACGGT 60
 61 AGCTCGGCTTCTGTCATCTCTGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCT 120
 61 AGCTCGGCTTCTGTCATCTCTGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCT 120
 121 CCTGAGCCCGCGAGCCCGGCGCGCACACGCGACATGCGCGGCGAGCGCGCGCGCT 180
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 241 TCCTCGTGATGCTCGCTCATCAACAGCAGGTACTGAGAAATGTCGCGCATAGACCCCA 300
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 541 CTGAGAGTGACTACATTTACTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGAG 600
 541 CTGAGAGTGACTACATTTACTGCTTAACATTTCTGGTCTTGGGGGGCGCAGTAAATGAG 600

601 AGAGCAAGTCTGCAGGCTGGAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGGCCAGC 660
 601 AGAGCAAGTCTGCAGGCTGGAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGGCCAGC 660
 661 GTGCCCTTTATGAACCGAACAGTTGGTGGATCCTGTGGGGCTATGAGGATCCCTTCTGTTGA 720
 661 GTGCCCTTTATGAACCGAACAGTTGGTGGATCCTGTGGGGCTATGAGGATCCCTTCTGTTGA 720
 721 ATTTTATCAACAATACTTTACAGACATGTTCCCATCAAGGGCAGTTTGGGCTCTTTTG 780
 721 ATTTTATCAACAATACTTTACAGACATGTTCCCATCAAGGGCAGTTTGGGCTCTTTTG 780
 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTTCAAGGGCTCCAGAACTTCA 840
 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTTCAAGGGCTCCAGAACTTCA 840
 841 GCAAGATCCACCTGTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCACTCAG 900
 841 GCAAGATCCACCTGTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCACTCAG 900
 901 AGCAGTGAACAATGATCAATGGCCTTCCGGCAGATGTGGGCACCATTCATGACACCCC 960
 901 AGCAGTGAACAATGATCAATGGCCTTCCGGCAGATGTGGGCACCATTCATGACACCCC 960
 961 AGTCCTCGCTGGAATTTCTTCAGTCCGGAAGCCTGCAAGTCTATGAGCTCACCTACCATG 1020
 961 AGTCCTCGCTGGAATTTCTTCAGTCCGGAAGCCTGCAAGTCTATGAGCTCACCTACCATG 1020
 1021 ATTGAGGGTGTGTTGAAGGCATCCCACTATCGCTTCAAGCCCTTAAACTTTGTTTG 1080
 1021 ATTGAGGGTGTGTTGAAGGCATCCCACTATCGCTTCAAGCCCTTAAACTTTGTTTG 1080
 1081 CCAATGGGCTGTGTTTACCCACCAATGAAGTTTTCGCCGCTGCTTGAATCCGGCATTC 1140
 1081 CCAATGGGCTGTGTTTACCCACCAATGAAGTTTTCGCCGCTGCTTGAATCCGGCATTC 1140
 1141 AAAATGTGACACTTGCAGGTTTGGTGACCCCTGTTTCTGTACACCTCTCACTTCTACA 1200
 1141 AAAATGTGACACTTGCAGGTTTGGTGACCCCTGTTTCTGTACACCTCTCACTTCTACA 1200
 1201 ATGCAGACCTGTGCTGCTATCAGAAAGCGTTTGGGCTGAAACCTGTGACCCAAAGGAGCAT 1260
 1201 ATGCAGACCTGTGCTGCTATCAGAAAGCGTTTGGGCTGAAACCTGTGACCCAAAGGAGCAT 1260
 1261 CTTTGTCTTGCACATCCATCCGTCACCTGGATCCCCATGAAGTCTTCTGTGAAGTTC 1320
 1261 CTTTGTCTTGCACATCCATCCGTCACCTGGATCCCCATGAAGTCTTCTGTGAAGTTC 1320
 1321 AGATAAGCCTCTACATCAAGGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
 1321 AGATAAGCCTCTACATCAAGGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
 1381 TGGTCTCTCCATTTGCTGTTGAGCAGAGCGGTGCCATGGGCGCGAGCCCTGAAACA 1440
 1381 TGGTCTCTCCATTTGCTGTTGAGCAGAGCGGTGCCATGGGCGCGAGCCCTGAAACA 1440
 1441 CGTTCTTACAGCAGCTGCTGCTGATGCCCGGATCCCCATGAAGTCTTCTGTGAAGTTC 1500
 1441 CGTTCTTACAGCAGCTGCTGCTGATGCCCGGATCCCCATGAAGTCTTCTGTGAAGTTC 1500
 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 1561 AATGCTTTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGGATTAAGGAGGCCATTCAGG 1620
 1561 AATGCTTTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGGATTAAGGAGGCCATTCAGG 1620
 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAGCGTGTGCAAGAGGCAAGC 1680
 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAGCGTGTGCAAGAGGCAAGC 1680
 1681 TGTAGGGTCCCAAGACACACGAGCCCCCCCCAACTGATAGCTTGTGTCAGACCGCAT 1740

Db 1681 TGTAGGTCCAAAGACACACAGAGCCCCCAACCTGATAGTGTGTGACACAGCCAT 1740
Qy 1741 CCAGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTCGC 1788
Db 1741 CCAGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTCGC 1788

RESULT 7

ACD44926
ID ACD44926 standard; cDNA; 1825 BP.
XX
AC ACD44926;
XX
DT 10-SEP-2003 (first entry)
XX
DE Human cDNA encoding scavenger receptor BI, splice variant.
XX
KW Human; ss; gene; scavenger receptor BI; SR-BI; cardiant; antilipemic;
KW high density lipoprotein; HDL; hormone replacement therapy;
KW postmenopausal female; cardiovascular disorder; coronary heart disease;
KW atherosclerosis; stroke; ischaemia; restenosis; congestive heart failure;
KW gangrene; SNP; single-nucleotide polymorphism.
XX

OS Homo sapiens.

XX US2003044782-A1.

XX 06-MAR-2003.

XX 08-FEB-2001; 2001US-00779152.

XX 10-JUL-1997; 97US-00890979.

XX 27-FEB-1998; 98US-00031626.

XX (ACTO/) ACTON S L.

PA (MCCA/) MCCARTHY J J.

XX Acton SL, McCarthy JJ;

XX WPI; 2003-503489/47.

DR P-PSDB; ABO27241.

XX
PT Determining if a subject has or is at risk of developing abnormally low
PT high density lipoprotein level, involves determining identity of allelic
PT variant of polymorphic region of SR-BI gene of the subject.

XX Example 1; Fig 3; 84pp; English.

XX The invention relates to determining whether a subject has, or is at risk
CC of developing, an abnormally low high density lipoprotein (HDL) level,
CC involves determining the identity of the allelic variant of a polymorphic
CC region of the SR-BI (scavenger receptor BI) gene of the subject, and
CC comparing the allelic variant of the subject with allelic variants
CC associated with abnormally low HDL levels. Also included are a kit for
CC determining whether a subject has, or is at risk of developing, a low HDL
CC level (comprises a probe or primer which is capable of hybridising to an
CC SR-BI gene, and thus identifying whether the SR-BI gene contains an
CC allelic variant of a polymorphic region which is associated with a low
CC HDL level) and predicting the effect of hormone replacement therapy on
CC the HDL level in a female subject (by identifying one or more allelic
CC variants of the SR-BI gene which are associated with abnormally low HDL
CC levels in females (especially postmenopausal females), thus predicting
CC the effect of hormone replacement therapy on the HDL level in the
CC subject). Also disclosed are methods of treating low HDL levels and
CC resulting cardiovascular disorders (e.g. coronary heart disease,
CC atherosclerosis, stroke, ischaemia, restenosis, congestive heart failure
CC and gangrene) by administering a compound that increases HDL levels, when
CC the subject has been identified as having the common allele at residue 41
CC of exon 8. The present sequence is a cDNA encoding a SR-BI protein

XX Sequence 1825 BP; 377 A; 525 C; 496 G; 427 T; 0 U; 0 Other;

Query Match 99.9%; Score 1786; DB 9; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCACCTGCAGGGCTACTGCTGCTCCGGCCACATGCTGAGACTCACCTTGTGGAGCGT 60
Db 1 GCACCTGCAGGGCTACTGCTGCTCCGGCCACATGCTGAGACTCACCTTGTGGAGCGT 60
Qy 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 CCTGAGCCCGGAGCCCGGCGCCGACACGCGACATGCGCGGCGAGCGCGCGCT 180
Db 121 CCTGAGCCCGGAGCCCGGCGCCGACACGCGACATGCGCGGCGAGCGCGCGCT 180
Qy 181 GCGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCT 240
Db 181 GCGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCT 240
Qy 241 TCCTCGTGTGCTGCTGCTGCTCATCAAAACAGCAGGTACTTGAAGAATGTCCGATAGACCCCA 300
Db 241 TCCTCGTGTGCTGCTGCTGCTCATCAAAACAGCAGGTACTTGAAGAATGTCCGATAGACCCCA 300
Qy 301 GCAGCCTGCTCTTTGCAATGTGAAGGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACT 360
Db 301 GCAGCCTGCTCTTTGCAATGTGAAGGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACT 360
Qy 361 TCTTCAGGTGTCAATCCAGCGAGATCCTTAAGGGTGAGAGCCAGTAGTGGGGAGC 420
Db 361 TCTTCAGGTGTGTCAATCCAGCGAGATCCTTAAGGGTGAGAGCCAGTAGTGGGGAGC 420
Qy 421 GTGGACCTATGTCTACAGGGAAATTCAGACATGAAGGCCAAATCACCTTCAATGACAATG 480
Db 421 GTGGACCTATGTCTACAGGGAAATTCAGACATGAAGGCCAAATCACCTTCAATGACAATG 480
Qy 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGAGCTCCACCGCT 540
Db 481 ATACTGTGCTCTTTGTGGAGCACCGCAGCTCCATTTCCAGCCGAGCTCCACCGCT 540
Qy 541 CTGAGAGTGTACATATATATCTGCTTAACATTTCTGCTTGGGGGGGGGAGTATGATGG 600
Db 541 CTGAGAGTGTACATATATATCTGCTTAACATTTCTGCTTGGGGGGGGGAGTATGATGG 600
Qy 601 AGAGCAAGTCTGAGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATG 660
Db 601 AGAGCAAGTCTGAGCGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 660
Qy 661 GTCCCTTTATGAACCGAAGAGTGTGGTGAAGATCCTGTGGGGCTATGAGGATCCCTTCTGA 720
Db 661 GTCCCTTTATGAACCGAAGAGTGTGGTGAAGATCCTGTGGGGCTATGAGGATCCCTTCTGA 720
Qy 721 ATTTTATCAAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTCGGGCTGTTTG 780
Db 721 ATTTTATCAAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTCGGGCTGTTTG 780
Qy 781 TTGAGATGAACAACTCAGACTCTGSGCTTCTACTGTGTTTTCAGGGCGTCCAGAACTTCA 840
Db 781 TTGAGATGAACAACTCAGACTCTGSGCTTCTACTGTGTTTTCAGGGCGTCCAGAACTTCA 840
Qy 841 GCAAGATCCACCTGGTGGAGCAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCATTCAG 900
Db 841 GCAAGATCCACCTGGTGGAGCAGATGGAATGGGCTCAGCAAGGTCAACTACTGGCATTCAG 900
Qy 901 AGCAGTGCACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACCATTCATGACACCCC 960
Db 901 AGCAGTGCACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACCATTCATGACACCCC 960
Qy 961 AGTCCTCGCTGGAAATTTCTTTCAGTCCGGAAGCCCTGAGGCTCTATGAAGCTCACCTCATG 1020
Db 961 AGTCCTCGCTGGAAATTTCTTTCAGTCCGGAAGCCCTGAGGCTCTATGAAGCTCACCTCATG 1020
Qy 1021 ATTTCAGGGGTGTTTGAAGGCAATCCCACTATCGCTTTCAGAGCCCTTAAATCTTTGTTG 1080

XX Kozarsky K, Rigotti A, Krieger M;
PI WPI; 2005-457475/46.
XX P-PSDB; AEB03938.
PT New genetically engineered mouse or derivative cells with inactivated SR-
PT BI gene expression or activity, useful as a model for designing drugs
XX that can modulate cholesterol transport.
PS Disclosure; SEQ ID NO 1; 21pp; English.
XX
CC The present invention relates to a novel genetically engineered mouse, or
CC cells derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene
CC expression or SR-BI activity has been inactivated. SR-BI is a high
CC density lipoprotein (HDL) receptor. It was found that estrogen
CC downregulates SR-BI under conditions of upregulation of the low density
CC lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
CC adrenal membranes and other non-placental steroidogenic tissues from
CC animals treated with estrogen, but not in other non-placental non-
CC steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
CC tissue causes a decrease in blood cholesterol levels. The animal is
CC useful as a model for designing drugs that can modulate cholesterol
CC transport or that can stimulate or inhibit the binding to and lipid
CC movements mediated by SR-BI and redirect uptake and metabolism of lipids
CC and cholesterol by cells. The present sequence is a coding sequence for
CC SR-BI, which was used to illustrate the invention. Note: The SEQ ID 1
CC given in the sequence listing (the sequence shown in AEB03937) is stated
CC to be 1788 nucleotides in length. However, there appears to be a 1 to 3
CC nucleotide deletion at the end of each line of the sequence shown in the
CC sequence listing, resulting in a sequence that is 1718 nucleotides in
CC length. Therefore a corrected version of the sequence has been produced
CC with Ns added to replace the missing nucleotides (the sequence shown in
CC AEB03941). SEQ ID 1 is stated to encode SEQ ID 2 (given in AEB03938).
XX
SQ Sequence 1788 BP; 354 A; 492 C; 468 G; 404 T; 0 U; 70 Other;

Query Match 96.1%; Score 1718; DB 14; Length 1788;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1718; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGCTACTGCTGCCGGCACTGCCTGAGACTCACCTTGCTGGAACTG 60
DB 1 GCCACCTGCAGGCTACTGCTGCCGGCACTGCCTGAGACTCACCTTGCTGGAACTG 60
QY 61 AGCCTCGGCTTCTGTCATCTCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 AGCCTCGGCTTCTGTCATCTCTGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCTGAGCCCCCGAGCCCCGGCGGCACACGCGGACATGGCGGCGAGCGCGCGCT 180
DB 121 CCTGAGCCCCCGAGCCCCGGCGGCACACGCGGACATGGCGGCGAGCGCGCGCGGNN 180
QY 181 GGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCT 240
DB 181 GGGTGGCGGTGGGGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCTGCTGGGGCT 240
QY 241 TCCTCGTGTATGCTCGCTCATCAACAGCAGGTACTGAAGAATGTCCGATAGACCCCA 300
DB 241 TCCTCGTGTATGCTCGCTCATCAACAGCAGGTACTGAAGAATGTCCGATAGACCCNN 300
QY 301 GCAGCTGTCTTGGCAATGTGAAGAGATCCCTGTACCCTTCTACTTGTCCGCTACT 360
DB 301 GCAGCTGTCTTGGCAATGTGAAGAGATCCCTGTACCCTTCTACTTGTCCGCTTANN 360
QY 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGGTGAGAGCCAGTAGTCGGGAGC 420
DB 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGGTGAGAGCCAGTAGTCGGGANN 420
QY 421 GTGACCCCTATGTCTACAGGGAATTGACATGAAGGCCAACATCACCTTCAATGACAATG 480
DB 421 GTGACCCCTATGTCTACAGGGAATTGACATGAAGGCCAACATCACCTTCAATGACAANN 480

QY 481 ATACTGTGTCCTTTGTGGAGCACCGCAGCCTCCATTTCCAGCCGCGACAGTCCACGGCT 540
DB 481 ATACTGTGTCCTTTGTGGAGCACCGCAGCCTCCATTTCCAGCCGCGACAGTCCACGGNN 540
QY 541 CTGAGAGTCACTACATTATATCTGCTTAAACATTCTGCTTTGGGGGGCGCAGTAAATG 600
DB 541 CTGAGAGTCACTACATTATATCTGCTTAAACATTCTGCTTTGGGGGGCGCAGTAAATG 600
QY 601 AGAGCAAGTCTGCGAGCCCTGAAGCTGATGATGATGATGATGATGATGATGATGATG 660
DB 601 AGAGCAAGTCTGCGAGCCCTGAAGCTGATGATGATGATGATGATGATGATGATGATG 660
QY 661 GTGCTCTTTATGAACCAAGCAAGTTGGTGAGATCTGCTGGGGCTATGAGGATCCCTTC 720
DB 661 GTGCTCTTTATGAACCAAGCAAGTTGGTGAGATCTGCTGGGGCTATGAGGATCCCTTC 720
QY 721 ATTTTATCAACAAATACTTACCAGACATGTTCCCATCAAGGGCAAGTTGGGCTGTTG 780
DB 721 ATTTTATCAACAAATACTTACCAGACATGTTCCCATCAAGGGCAAGTTGGGCTGTTNN 780
QY 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTACGGGGCTGCAGAACTTCA 840
DB 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTACGGGGCTGCAGAACTTNN 840
QY 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGTCATTG 900
DB 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGTCATTNN 900
QY 901 AGCAGTGAACAACCTGATCAATGGCACTTCCGGGCGAGATGGGGCACCATTATGACACCCC 960
DB 901 AGCAGTGAACAACCTGATCAATGGCACTTCCGGGCGAGATGGGGCACCATTATGACACCCNN 960
QY 961 AGTCTCGCTGGAATTTCTTCACTGCGGAAGCTGCAAGTCTATGAAGCTCACCTACATG 1020
DB 961 AGTCTCGCTGGAATTTCTTCACTGCGGAAGCTGCAAGTCTATGAAGCTCACCTACCCNN 1020
QY 1021 ATTGAGGGGTGTTGAAGGCATCCCGACCTATCGCTTACAGCCCTTAAACCTTTGTTG 1080
DB 1021 ATTGAGGGGTGTTGAAGGCATCCCGACCTATCGCTTACAGCCCTTAAACCTTTGTTNN 1080
QY 1081 CCAATGGGTCTGTTTACCCCAATGAAGTTTCTGCCCGTGCCTTGAATCCGGCATTC 1140
DB 1081 CCAATGGGTCTGTTTACCCCAATGAAGTTTCTGCCCGTGCCTTGAATCCGGCANNN 1140
QY 1141 AAAATGTGACACTTGCAGGTTTGGTGCAACCTGTTCTGTCTGCAACCTCATTCTACA 1200
DB 1141 AAAATGTGACACTTGCAGGTTTGGTGCAACCTGTTCTGTCTGCAACCTCATTCTNN 1200
QY 1201 ATGCAAGCCCTGCTGCTATCAGAAAGCGTTCTGGGTCTGAACCTGACCCAGGGAGCAT 1260
DB 1201 ATGCAAGCCCTGCTGCTATCAGAAAGCGTTCTGGGTCTGAACCTGACCCAGGGAGC 1260
QY 1261 CTTTGTCTTGCATCTCAATCCGGTCACTGGGATCCCATGAATGTTCTGTGAAAGTTGC 1320
DB 1261 CTTTGTCTTGCATCTCAATCCGGTCACTGGGATCCCATGAATGTTCTGTGAAAGTTNN 1320
QY 1321 AGATAAGCCCTTACATCAAGCTGTCAAGGCAATGGGCAACAGGGAAGATGAGACCCG 1380
DB 1321 AGATAAGCCCTTACATCAAGCTGTCAAGGCAATGGGCAACAGGGAAGATGAGACCCNN 1380
QY 1381 TGGTCTCTCCATTTGCTGTTTGAAGCAGAGCGGTGTCATGGGGCGAGCCCTCAACA 1440
DB 1381 TGGTCTCTCCATTTGCTGTTTGAAGCAGAGCGGTGTCATGGGGCGAGCCCTGANN 1440
QY 1441 CGTTCTTACACGAGCTGCTGATGCCCCAGGATCTTTCAGTATGTGCAAGTGTGCTGC 1500
DB 1441 CGTTCTTACACGAGCTGCTGATGCCCCAGGATCTTTCAGTATGTGCAAGTGTGNN 1500
QY 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 TGGGGCTGGGGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 AATGCTTTTTTTTGGAGTGGTAGTAAAAAGGGCTCGCAGGATAGAGGGCCATTTCAG 1620

Db	1561	AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAAAGAGGCCATTCCNN	1620
Qy	1621	CCTACTCTGAGTCTCTGATGTCACAGTCCCAAGGGCACGGTGTCTCAAGAAGCCCAAGC	1680
Db	1621	CCTACTCTGAGTCTCTGATGTCACAGTCCCAAGGGCACGGTGTCTCAAGAAGCCCANNN	1680
Qy	1681	TGTAGGTCCTCAAGAAGACACACAGAGGCCCCCCCACCTGATAGTGTGTGTGACAGCCAT	1740
Db	1681	TGTAGGTCCTCAAGAAGACACACAGAGGCCCCCCCACCTGATAGTGTGTGTGACAGCCANN	1740
Qy	1741	CCAGGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTGGC	1788
Db	1741	CCAGGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTGGC	1788
RESULT 10			
ABD33431			
ID	ABD33431	standard; cDNA; 2496 BP.	
XX	ABD33431;		
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE	Murine cancer-associated (CA) cDNA MR07-081.		
XX			
KW	Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;		
KW	ss; cancer; cytostatic.		
XX			
OS	Mus musculus.		
XX			
PN	W02004058146-A2.		
XX			
PD	15-JUL-2004.		
XX			
PF	15-DEC-2003; 2003WO-US040081.		
XX			
PR	17-DEC-2002; 2002US-00322281.		
XX	(SAGR-) SAGRES DISCOVERY INC.		
XX			
PA	Morris DW, Malandro MS;		
PI			
DR	WPI; 2004-499109/47.		
DR	P-PSDB; ABO84950.		
PT	Novel human cancer associated protein encoded within open reading frame		
PT	of cancer associated gene, useful as targets for diagnosing cancer.		
XX			
PS	Disclosure; SEQ ID NO 564; 182pp; English.		
XX			
CC	The invention relates to cancer-associated proteins (CAP) and the cancer-		
CC	associated (CA) nucleic acids encoding them. The invention also relates		
CC	to a method for treating cancers involving administering to a patient an		
CC	inhibitor of CAP, and a method of screening for anticancer activity in a		
CC	potential drug involving providing a cell that expresses a CA gene,		
CC	contacting a tissue sample derived from a cancer cell with an anticancer		
CC	drug candidate and monitoring the effect of the anticancer drug candidate		
CC	on expression of the CA gene. The CAP proteins are useful for detecting		
CC	cancer associated with expression of a CAP protein in a test cell sample		
CC	and for screening for a bioactive agent capable of modulating the		
CC	activity of a CAP protein. The CA nucleic acids are useful for diagnosing		
CC	cancer, involving determining the expression of a CA nucleic acid in a		
CC	tissue. This sequence represents murine CA cDNA of the invention. Note:		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences		
XX			
SQ	Sequence 2496 BP; 517 A; 741 C; 660 G; 578 T; 0 U; 0 Other;		
Query Match 80.6%; Score 1441.2; DB 13; Length 2496;			
Best Local Similarity 88.3%; Pred. No. 0;			
Matches 1577; Conservative 0; Mismatches 208; Indels 1; Gaps 1;			

Query Match 80.6%; Score 1441.2; DB 13; Length 2496;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 1577; Conservative 0; Mismatches 208; Indels 1; Gaps 1;

1	GCACCTGCAGGGCTACTGCTGCTCCGGCCATGCTCCCTGAGACTCACCTTGCTGCTGGAAGCTG	60
39	GCACCTGCAGGGCTACTGCTGCTCCGGCCACCGCCAGGACACACCTTGCTGCTGCTGAGGG	98
61	AGCCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCGCTTCTGTGCTGTGCTGCTCCCTTCAGTC	120
99	AGTCTCGGCTTCTGTCATCTCTGTGGCCTTCGGTCACCTCTGTCTCCGT-CTCTTTCAGGT	157
121	CTGTAGCCCCGGAGCCCCGGGGCGGCAACGCGGAGCATGGCGGCGAGCGCCAGCGCGCT	180
158	CTGTAGCCCCGAGAGCCCTTCGCGCAACGCGGACATGGCGGCGAGCTCCAGGGCGCGCT	217
181	GGGTGGCGGTGGGGCTGGGGGCTGTTGGGGCTGCTGTGCGCTGTGCTGCTGCTGCTGCTATGA	240
218	GGGTGGCCTTTGGGGTTGGGGCGCCCTGGGGCTGCTGTTTGTGCGCTCGCGGTGTCATGA	277
241	TCTCTGTGATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAATGTCCGATAGACCCCA	300
278	TCTCTATGTTGCCCTCCCTCTATCAACGACAGGTGCTCAAGAAATGTCCGATAGACCCGA	337
301	GCAGCCTGTCTTTGCAATGTGGAAGGAGATCCCTGTACCCCTTTCTACTTTGTCCGCTCTACT	360
338	GCAGCCTGTCTTTGGGATGTGGAAGGAGATCCCCGTCCCTTTCTACTTTGTCTGCTCTACT	397
361	TCTTCGAGTGTGTAATCCAGCGAGATCCTAAAGGTTGAGAAGCCAGTAGTGTGCGGAGC	420
398	TCTTCGAAGTGTCAACCCAAACGAGGTCCTCAACGCGCCAGAAGCCAGTAGTCCGGGAGC	457
421	GTGGACCTTATGTTACAGGGAATTCAGACATAAAGCCCAACATCACCTTCAATGACAAATG	480
458	GTGGACCTTATGTTACAGGGAATTCAGACAAAGGTCAACATCACCTTCAATGACAAACG	517
481	ATACTGTGTCTTTGTGGAGCACCGCAGGCTCCATTTCCAGCCGGCAGAGTCCCCACGGCT	540
518	ACACCGTGTCTTGTGGAGAACCGCAGGCTCCATTTCCAGCTGACAAAGTCCGATGGCT	577
541	CTGAGAGTGACTACATTAFACTGCTCTAAACATTTCTGTGCTTTGGGGGGCGCAGTAATGATGG	600
578	CAGAGAGTGACTACATTTGACTGCTTAAACATCTTGTCTCTGGGGGGCTCGATATTTGATGG	637
601	AGAGCAAGTCTCAGCGCTTGAGCTGATGATGACCTTTGGGGCTGGCCACCTTTGGGGCCAGC	660
638	AGAGCAAGCCTGTGAGCCTTGAAGCTGATGATGACCTTTGGCGCTGGTTCACATGGGGCCAGC	697
661	GTGCTCTTATGAACCGAACAGTTGTTGAGATCTGTGGGGCTATGAGGATCCCTTCGTGA	720
698	GTGCTTATTAAGAACCGACAGTTGTTGAGATCTGTGGGGCTATGACGATCCCTTCGTGC	757
721	ATTTATCAACAAATACTTACAGACATGTTCCCAATCAAGGGCAAGTTGCGGCTGTTTG	780
758	ATTTTCTCAACAGTACCTCCAGACATGCTTCCCAATAAAGGGCAAAATTTGGCCTGTGTTG	817
781	TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTCCAGAACTTCA	840
818	TTGGGATGAACAACTCGAAATCTGGGGGTCTTCACTGTCTTTCAGGGCGCTCCAGAAATTTCA	877
841	GCAAGATCACTCTGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCGCATTCAG	900
878	GCAAGATCCATCTGTGGGACAAATGNAACGGACTCAGCAAGATTCGATTAATTGGCATTCAG	937
901	AGCAGTGCACACTGATCAATGGCACTTCCGGGGCAGATGTGGGCACCAATTCATGACACCCC	960
938	AGCAGTGAACATGATCAATGGACTTTCGGGCAGATGTGGGCACCTTTTCATGACACCCG	997
961	AGTCTCTGTGGAAATCTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCTCACCTCAATG	1020
998	AATCTCTCGTGGAAATCTTTCAGCCCGGAGGCATGCAAGTCCATGAAGCTGACCTCAACAG	1057
1021	ATTCAGGGGTGTTTGAAGCATCCCACTATCGCTTTCAGGCCCTTAAAACTTTGTTTG	1080
1058	AATCAAGGGGTGTTTGAAGCATTTCCACGATATCGCTTTCAGGCCCTTAAAACTTTGTTTG	1117

nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents murine cancer-associated cDNA of the invention.

Query Match 80.6%; Score 1441.2; DB 14; Length 2513;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 1577; Conservative 0; Mismatches 208; Indels 1; Gaps 1

Qy	1	GCACCTGCAGGGCTACTGCTGCTCCGGCCTACTGCGCTGAGACTCACTTGTCTGGAAAGTGC	60
Db	56	GCACCTGCAGGGCTACTGCTGCTCCGGCCACCGCCAGGCACACACTTGTCTGCTGAGGG	115
Qy	61	AGCCTCGGGCTTCTGTCATCTCTGTGGCTCTGTGCGCTTCTGTGCGTGTCCCCCTTCAGTC	120
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DE	Txin; toxin; gene expression profile; hepatotoxicity; liver;
XX	drug screening; toxicity assay; ds.
KW	Unidentified.
XX	WO2003064624-A2.
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PR	30-DEC-2002; 2002US-0436643P.
XX	(GENE-) GENE LOGIC INC.
PA	Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
PI	WI; 2003-689530/65.
XX	
DR	Predicting a toxic effect of a compound, useful in identifying toxicity
PT	markers in liver tissues or cells for drug screening and toxicity assays,
PT	comprises preparing gene expression profile of tissue or cells exposed to
PT	the compound.
XX	Claim 1; SEQ ID NO 3642; 1156pp; English.
PS	
XX	The present invention relates to a method for predicting a toxic effect
CC	of a compound. The method comprises preparing a gene expression profile
CC	of a tissue or cell sample exposed to the compound, and comparing the
CC	gene expression profile to a database comprising SEQ ID 1-4925, where
CC	differential expression of the genes indicates at least one toxic effect.
CC	The method is useful for predicting at least one toxic effect of a
CC	compound, predicting hepatotoxicity or the progression of a toxic effect
CC	of a compound, identifying an agent that modulates the onset or
CC	progression of a toxic response, predicting the cellular pathways that a
CC	compound modulates in a cell, and identifying an agent that modulates at
CC	least one activity of a protein. The method and compositions of the
CC	present invention using a database of genes having liver toxin-induced
CC	differential expression, are useful in identifying toxicity markers in
CC	liver tissues or cells for drug screening and toxicity assays. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;
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	Best Local Similarity 87.9%; Pred. No. 0;
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DB	112 ---CTGGTTTCTGTGTCATCTGTGGCCTCGTGTGCTCTGTGGCCT---CCCCTTCAGGT 167
QY	121 CCTGAGCCCGGAGCCCGCGGCACAGCGGACATGGCGGACATGGCGGAGGCGGCGCT 180
DB	168 CCTGAGCCCGGAGCTCTCTGGCGCGGCACAGCGGACATGGCGGCTCAGCTCCAGGCGAGCT 227
QY	181 GGCTGGCGGTGGGGCTGGGCGCTGTGGGGCTGTGTGGCGCTGTGTGGGTGTGTGTGA 240
DB	228 GGGTGGCGCTGGGGCTGGGGCGTTTAGGGGCTCTGTGTGCTGTGGCGCTTATCATGA 287
QY	241 TCCTCGTGTATGCCCTCGCTCATCAAACAGCAGGTACTGAAGAATACTGGCCATAGACCCCA 300

toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property Organization

XX Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;

Query Match 79.0%; Score 1413; DB 10; Length 2497;
Best Local Similarity 87.9%; Pred. No. 0;
Matches 1567; Conservative 0; Mismatches 205; Indels 11; Gaps 2;

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Db 112 ---CTCGGTTCTGTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 167

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Db 168 CCTGAGCCCGAGGACTCTCGGCGGCGGACGCGGACATGGGCGGCTGAGCTCAGGGCAGCT 227

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Db 228 GGGTGGCGTGGGCTGGGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 287

Qy 241 TCCTCGTGATCCCTCGCTCATCAACAGCAGGTACTGAGAGATGTCGCGATAGACCCCA 300
Db 288 TTCTCATGGTGGCTCGCTCATCAAGCAGAGGTGCTCAAGAGATGTCGCGATAGACCCCA 347

Qy 301 GCAGCCTGTCCTTTGCAATGGAAGAGATCCTGTACCTCTTCTACTTCTCGTCTACT 360
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Qy 361 TCTTCGAGGTGGTCAATCCGAGGAGATCCTAAAGGTGAGAGCCAGTATGTCGGGAGC 420
Db 408 TCTTCGAGGTGGTCAATCCGAGGAGTCTCTAAATGGCCAGAGCCAGTATGTCGGGAGC 467

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Qy 1321 AGATAGACCTCTACATCAAGCTGTCAAGGGATTTGGGCAAAACAGGGAAGATCGAGCCCG 1380
Db 1368 AGCTGAGTCTGTACATCAAAATCCGTCAAGGGCTCGGGCAAAACAGGGAAGATCGAGCCAG 1427
Qy 1381 TGTCTCTCCCATTTGCTGTGTTTGAAGAGGGTGCATGGGCGGCGAGCCCTTGAACA 1440
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1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBLISHED 11042159
REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hatahara, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2441)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
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FEATURES
source
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DB	541	TACTGCC	TAAATCTTGGTCTGGGGGGCTCGAT	TATTTGATGGAGAGCAAGCTGTGAGCC		600	
QY	619	TGAAGCTGAT	GAACCTTGGGGCTGCACCTTTGGCC	CAGCGTGCCTTTATGAACCGAA		678	
DB	601	TGAAGCTGAT	GAATGACCTTGGCTGCACCAT	TGGCCAGCGTGTCTTTATGAACCGCA		660	
QY	679	CAGTTGGT	GAGATCCTGTGGGGCTATGAGAT	CCCTTCGTGAATTTTATCAACAAATACT		738	
DB	661	CAGTTGGT	GAGATCCTGTGGGGCTATGACAT	CCCTTCGTGCAATTTTCTCAACACGTACC		720	
QY	739	TACCAGACAT	GTGTTCCCCCATCAAGGGCAAGT	TGGCCCTGTTTGTGAGATGAACAACCTCAG		798	
DB	721	TCCAGACAT	GTCTCCCATAAAGGCAAAATTTGGCCTGTTTGTGGAGTGAACAACTCGA		780		
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LOCUS AY412682 1364 bp DNA linear GSS 16-DEC-2003
DEFINITION Mus musculus SCARB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY412682
VERSION AY412682.1 GI:39768647
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1364)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/locus_tag="HCM4638"
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Best Local Similarity 88.9%; Pred. No. 7.5e-287;
Matches 1212; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
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QY 498 GAGCACCGGAGCTCCATTTCCAGCCGAGCAGCTCCACGGCTCTCAGAGTGAATCACTT 557
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DB 361 ACAGTTGGTGGATCCTGTGGGCTATGAGATCCCTTCTGTCATTTTCTCAACACGTAC 420
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Qy 1158 AGGTTTGGTGCACCCCTGTTTCTGTCACACCCCTCACTTTCATGATGAGACCCCTGCTA 1217
Db 841 AGGTTTGGTGGCTTCTGTTTCTTCCACCCCTCACTTTCATGATGAGACCCCTGCTA 900
Qy 1218 TCAGAAGCGTTCTGGGTCTGAACCTTGACCAAGGAGGATTCCTTGTCTTGCATC 1277
Db 901 TCAGAAGCTGTTCTTGTGTTGAACCTTAAACCAAGGAGGATTCCTTGTCTTGCATC 960
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Qy 1578 AGTGGTAGTAAAGGCTCGCAGGATAAGGAGGCTTCAAGGCTTCTGAGTCTCTG 1637
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Db 1321 ATGTACAGCTGCAAGGCGACGGTGTGCAAGAGCCAGCT 1364
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LOCUS full-length cDNA clone CS0DN004YM24 of Adult brain of Homo sapiens
DEFINITION CR607701 2515 bp mRNA linear HTC 21-JUL-2004
(human)
ACCESSION CR607701
VERSION CR607701.1 GI:50488508
KEYWORDS HTC; CNSLUT_cDNA.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 2515)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
REFERENCE 2 (bases 1 to 2515)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Best Local Similarity 77.4%; Pred.No.5.7e-251;
Matches 1211; Conservative 0; Mismatches 346; Indels 7; Gaps 1;
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Qy 294 GACCCAGAGCGCTGCTTGGCAATGTTGCAAGTGAAGAGATCCCTGCTGCTGCTGCTG 353
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Qy 474 GACAATGATGCTGCTTGGTGGAGCAGCGCTTCCATTTCCAGCGCGGAGCAGTCC 533
Db 516 AACACGACACCGTGTCTTCTCGAGTACCGCACCTTCCAGTTCAGGCTCCAAAGTCC 575
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[illegible]

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Qy	1260	TCCTTTGTCCTTGACATCCATCCCGGTCACTGGGATCCCAATGAACCTGTGTTCTGTGAAGTTG	1319
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Qy	1320	CAGATTAAGCTCTACATCAAGCTGTCAAGGCGCATTTGGGCAGATTTGGCAGGAGATCGAGCCC	1379
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Qy	1380	GTGGTCTCTCCATTGCTGTGTTTTCAGACAGACGGGTGCCATGCGCGCGCAGCCCTCGAAC	1439
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RESULT 7

AY412680

LOCUS

DEFINITION

AY412680

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

ORIGIN

AY412680 1364 bp DNA linear GSS 16-DEC-2003

Homo sapiens SCARB1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY412680.1 GI:39768645

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1364)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1364)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

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/gene="SCARB1"

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Best Local Similarity 81.0%; Pred. No. 3e-241;

Matches 1105; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

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RESULT 8
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LOCUS Pan troglodytes SCAR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY412681
VERSION AY412681.1 GI:39768646
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 1364)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
Gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1364)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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1..1364
/organism="Pan troglodytes"
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gene

ORIGIN
Query Match 45.9%; Score 821.4; DB 10; Length 1364;
Best Local Similarity 70.4%; Pred. NO. 4.3e-207;
Matches 960; Conservative 0; Mismatches 404; Indels 0; Gaps 0;
QY 318 ATGTGGAAGAGATCCCTGTACCTTCTACTTGTCCGTCTACTTCTTTCGAGTGGTCAAT 377
Db 1 ATGTGGAAGAGATCCCTGTATCTCTCTCCGTCTACTTCTTTGAGGTGATGAAC 60
QY 378 CCCAGCAGATCTTAAGAGGTGAGAACCGAGTAGTGGCGGAGCGTGGAACCTTATGCTAC 437
Db 61 CCCAGCAGATCTTGAAGGCGGAGAACCGAGTAGTGGCGGAGCGTGGAACCTTACGTGTAC 120
QY 438 AGGGAATTCAGACATTAAGGCGCAACATCACCTTCAATGACAAATGATCTGTGCTTGTG 497
Db 121 AGGAGTTTCAGGCACAAAGCAACATCACCTTCAACAAACGACACCGGTGCTTCTTCC 180
QY 498 GAGCACCGCAGCTTCCATTTCCAGCCGGAAGAGTCCCAACGCTCTGAGAGTGACTACAT 557
Db 181 GAGTACCGCAGCTTCCAGTTTCCAGCTTCCAGTCCCAAGTCCCAAGCTCGAGAGCGACTAC 240
QY 558 ATACTGCTTAACATTTCTGGTCTTGGGGGCGCAGTAATGATGAGAGCAAGTCTGCAGGC 617
Db 241 GTCATGCCCAACATCTCTGGTCTTGGGTGCGCGGTGATGATGAGAAATAAGCCCATGACC 300
QY 618 CTGAAGCTGATGATGACCTTGGGGCTGGCCACCTTGGGCGAGCGTCTTTATGACCGGA 677
Db 301 CTGAAGCTCATCATGACCTTGGCAATCACCACTTGGGCAAGCGTCTTTCATGAACCGC 360
QY 678 ACAGTTGGTGAGATCTCTGGGCTATGAGGATCCCTTCTGTAATTTTATCAACAATAC 737
Db 361 ACTGTGGTGATCATGTGGGCTACAGGACCCCTTCTGTAATCTCATCAACAGTAC 420
QY 738 TTACGACATGTTCCCACTAAGGGCAAGTGTGGCTGTTTGTGTGATGAAACAATCA 797
Db 421 TTTCCAGGCATGTTCCCTTCAAGGACAAGTGTGGATTTATTTGTGAGCTCAACAATCC 480
QY 798 GACTCTGGCTTCTACTGTGTTCAAGGGGCTCCAGAACTTCAGCAAGATCCACCTGGTG 857
Db 481 GACTCTGGCTTCTCAGGGTGTTCACGGGGTCCAGAACTTCAGCAAGATCCACCTGGTG 540
QY 858 GACAGATGGAATGGGCTCAGCAAGGTCAAATCTAGCTGCAATTCAGAGCAGTGCACATGATC 917
Db 541 GACAAGTGAACGGGCTGAGCAAGTTGACTTCTGGCATTCGATCCAGTGCACATGATC 600
QY 918 AATGGCATCTTCGGGCGAGATGTGGGCAACATTCATGACACCCAGTCTCTCGTGGAAATC 977
Db 601 AATGGAATCTTCTGGGCAATGTGGCCGCTTCTATGACTCTGAGTCTCTCGTGGAGTTC 660
QY 978 TTCACTCCGAGAGCTCAGCTCTATCAAGCTCACTACCATGATTCAGGGGTGTTTGA 1037
Db 661 TACAGCCGAGAGGCTCCGATCCATGAAGCTAATGTACAGGAGTCAAGGGGTGTTTGA 720
QY 1038 GGCATCCCACTTCTGCTTCCAGCCCTTAAACTTTGTTGCAATGGGTCTGTTTAC 1097
Db 721 GGCATCCCACTTCTGCTTCCCAACCCCTGTTGCAAGGGTCCATCTAC 780
QY 1098 CCACCCAAATGAAGTTTCTGCGCTGCTTGAATCCGGCAATCAAAATGCAGCACTTGC 1157
Db 781 CCACCCAAAGAGGCTTCTGCGCTGCTTGAATCCGGCAATCAAAATGCAGCACTTGC 840
QY 1158 AGGTTTGTGACCCCTGTTTCTGTCACCCCTCACTTCTACATGAGAGCCCTGCTA 1217
Db 841 AGGTTTGTGACCCCTGTTTCTTCTCCATCTCTCACTTCTCAAGCCGACCCGTTCTG 900
QY 1218 TCAGAAGCCGTTCTGGGTCTGAAACCTTGACCCAGGAGGAGATCTTGTGTTCTTGACATC 1277
Db 901 GCAGAAGGGGTGACTGGCTTGACCTTAAACAGAGAGGCACTCTTGTGTTCTTGGACATC 960
QY 1278 CATCCGTTCACTGGGATCCCATGAATGTTTCTGTGAAGTTGCAAGTAAAGCTTCTACATC 1337
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QY 1338 AAAGCTGTCAAGGCAATGGGCAACAGGAGAGATCGAGCCGTTGCTCCCATGTTGCTG 1397
Db 1021 AAATCTGTGCGAGGCAATGGGCAACAGTGGGAGATGAGCGTGTGGTCTGCGCGCTGCTC 1080
QY 1398 TGGTTTGAGCAGAGCGGTGCTTGGGCGGCGAGCCCTGAAACGTTTCTACAGCAGCTG 1457
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QY 438 AGGAAATTCACACATAGGCCCAACATCACCTTCAATGACATGATGATCTGTCTCTTTGGT 497
Db 121 AGGAGATTTCAGGCAAAAGCAACATCACCTTCAACCAATGACACCGTGTCTCTTCTC 180
QY 498 GAGCACCGCAGCTTCCATTTCCAGCCGACAGGTCCCAAGGCTCTGAGAGTACATCATT 557
Db 181 GAGTACCGCAGCTTCCAGTTCAGGCTCCAGTCCCAAGTCCCAAGGCTCGAGAGGATCATC 240
QY 558 ATACTGCTTAAATCTTGGTCTTGGGGGCGCAGTAAATGATGAGAGCAAGTCTGCGAGC 617
Db 241 GTCATGCCCAACATCTGGTCTTGGGTGCGCGGTGATGATGAGAGATAAGCCCATGACC 300
QY 618 CTGAAGCTGATGATGATCTGGGGCTGGCCAGCTTGGGCCAGCGTGTCTTTATGAAACGA 677
Db 301 CTGAAGCTCATCATGACCTTGGCATTCACCAACCTCGCGCAACGTGCTTCAAGCCGC 360
QY 678 ACAGTGTGTGATGATCTTGGGGCTATGAGGATCCCTTCGTGAAATTTATCAACAATAC 737
Db 361 ACTGTGGGTGATGATCATGTGGGGCTTACAGGACCCCTTGTGAACCTCATCAAGATAC 420
QY 738 TTACCAGACATGTTCCCATCAAGCGCAAGTTTCGGCTGTTTGTGAGATGAACAACTCA 797
Db 421 TTTCCAGCATGTTCCCTTCAAGACAGATTCGATTTATGCTGAGCTCAACACTCC 480
QY 798 GACTCTGGGCTTTCATCTGTGTTTACGGGGTCCAGAACTTTCAGCAAGATCCACCTGGT 857
Db 481 GACNNNGGCTTTCACGNTGTTTACGGGGTCCAGAACATCATCAGAGATCCACCTGGT 540
QY 858 GACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 917
Db 541 GACAAAGGAAACCGGCTGAGCAAGGTTGACTTCTGGCATTCGATCATGATGATGATGAT 600
QY 918 AATGGCACTTCCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 977
Db 601 AATGGCACTTCCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 978 TTAGTCCGGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1037
Db 661 TACAGCCTCGAGGCTGCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720
QY 1038 GGCATCCCACTATCGCTTCAAGCCCTTAAACTTGTGTCATGATGATGATGATGATGAT 1097
Db 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
QY 1098 CACCCCAATGAAGGTTTCTGCCCGTCTTGAATCCGCGATTCAAAATGTGACGACTTGC 1157
Db 781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840
QY 1158 AGGTTTGTGACCCCTGTTTCTGTCACACCTCCTCACTTCTACAAATGACAGACCTTGT 1217
Db 841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900
QY 1218 TCAGAGCGGTTCTGGGTCTGAACCTTGAACCCAGAGGAGATTTCTTGTCTTGTGATC 1277
Db 901 GCAGAGCGGTGACTGGGCTGACCCCTTAAACAGAGGAGCAGACTCTTGTCTTGTGATC 960
QY 1278 CATCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1337
Db 961 CACCCGCTGACGGAAATCCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1338 AAAGCTGTCAAGGCGATTTGGGCAAAAGGGAAGATCGAGCGGTGCTTCCCATTTCTG 1397
Db 1021 AATCTGTGACGAGCATTTGACAAATCTGGGAGATGATGATGATGATGATGATGATGAT 1080
QY 1398 TGGTTTGAAGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1457
Db 1081 TGGTTTGAAGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1458 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1517
Db 1141 GTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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QY 1518 CTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1577
Db 1201 CTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1578 AGTGGTAGTAAAGAGGCTCGCAGGATAAGGAGGCTTCAAGGATGAGAGGCTTCAAGGCT 1637
Db 1261 AGTGGTAGTAAAGAGGCTCGCAGGATAAGGAGGCTTCAAGGATGAGAGGCTTCAAGGCT 1320
QY 1638 ATGTACACAGCTGCCAAGGACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681
Db 1321 ATGACATCAGCTCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1364

RESULT 9
BU517714 902 bp mRNA linear EST 12-SEP-2002
LOCUS AGENCOURT 10165932 NCI CGAP Mam2 Mus musculus cDNA clone
IMAGE:6515330 5', mRNA_sequence.
BU517714
BU517714.1 GI:22825240
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 902)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14092 row: b column: 03
High quality sequence stop: 700.
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/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:6515330"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 38.1%; Score 681.2; DB 5; Length 902;
Best Local Similarity 87.3%; Pred. No. 8.5e-170;
Matches 757; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

QY 525 GACAGTCCACGGCTCTGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
Db 1 GACAGTCCGATGGCTCAGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 585 GGCGCAGTAAATGATGAGAGCAAGTCTGACAGGCTGAAAGCTGATGATGATGATGATGATGATGAT 644
Db 61 GGCTCATTTATGATGAGAGCAAGCTGTCAGGCTGAGCTGATGATGATGATGATGATGATGATGAT 120
QY 645 GCACCTTGGGCGAGCGTCTTTTATGAACCCAGTGTGGTGGATTCCTGTGGGGCTAT 704
Db 121 GTCAACATGGGCGAGCGTCTTTTATGAACCCAGTGTGGTGGATTCCTGTGGGGCTAT 180
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Db      661  TCTGCCAACTCGCAGCAGGAGAAATGCTTTT -- GTTTGGAGTGGTAGTAAAGGGCT 718
Qy      1597  GCAGGATAAGAGGCCATTTCAGGCTACTCTGAGTCTCTGATGTCACCAAGCTCCAGG 1656
Db      719  CCCAGGTAAGAGGCCATTTCAGGCTACTCTGAGTCTCTGATGTCACCAAGCTCCAGG 778
Qy      1657  GCAGGCTGCTCAAGAGGCCAGCTGAGGCTGAGGCTCCAAAGACACACAGGCCCCCAAA-- 1714
Db      779  GCAGGCTGCTCAAGAGGCCAGCTATAGGCTCTGAGGCTCTGAGGACACTATAAGCCCCCAAC 838
Qy      1715  CCTGATAGCTGTCAGACAGCCATCCAGCCCTCAGCCCTACACCC 1755
Db      839  CTGATTAGCTTGGTCAAGACAGCAACCCAGCTCTCTAAAGCC 879

RESULT 11
BM553238 1088 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6572721 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5467120
5', mRNA sequence.
ACCESSION BM553238
VERSION BM553238.1 GI:18791793
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo
1 (bases 1 to 1088)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1968 row: j column: 17
High quality sequence stop: 698.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5467120"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 37.9%; Score 677.6; DB 3; Length 1088;
Best Local Similarity 78.5%; Pred. No. 8.2e-169;
Matches 849; Conservative 0; Mismatches 229; Indels 4; Gaps 3;

Qy      330  ATCCCTGTACCTTCTACTGTGCGTCTACTTCTTCGAGGTGGTCAATCCAGCAGGATC 389
Db      1 ATCCCTATCCCTCTATCTCTCGTCTACTTCTTTCGAGTCAATGACCCAGGATC 60
Qy      390  CTAAGGGTGAGAGCCAGTAGTGGGAGCGGTGGACCCCTATGCTACAGGGAATTGAGA 449

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RESULT 12
B0917716

Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 35.7%; Score 639; DB 2; Length 907;
Best Local Similarity 84.4%; Pred. No. 1.5e-158;
Matches 754; Conservative 0; Mismatches 135; Indels 4; Gaps 3;
QY 804 GGGCTCTTCACTGTGTTACGGGGTCCAGAACTTCAGCAAGATCCACCTGGTGACAGA 863
Db 1 GGGGTCTTCACTGTCTTACGGGGTCCAGAACTTCAGCAAGATCCACCTGGTGACAAA 60
QY 864 TGGATGGCTCAGCAAGTCACTACTGCGATTCAGAGAGTGCACATGATCAATGGC 923
Db 61 TGGACGGACTCAGCAAGATCGATTATTTGGCAATTCAGAGCAGTGTAAATGATCAATGGG 120
QY 924 ACTTCCGGGAGATGTGGGCAACCATTCATGACACCCAGTCTCGCTGGAAATTTCTAGT 983
Db 121 ACTTCCGGGAGATGTGGGCAACCATTCATGACACCCAGTCTCGCTGGAAATTTCTAGC 180
QY 984 CCGAAGCTTCAGGTCTATGAAGTCACTACCATGATTCAGGGGTGTTTGAAGGCATC 1043
Db 181 CCGGAGGCATCGAGTCCATGAAGCTGACCTTACACGAATCAAGGGTGTGTTGAAGGCATT 240
QY 1044 CCGACCTATCGCTTCAGAGCCCTTAAACTTTGTTTGGCAATGGTCTGTTTACCCACC 1103
Db 241 CCGACGATCGCTTCAGGGCCCTGATCTCTGTTTGGCAACGGGTCCGTCTACCCACC 300
QY 1104 AATGAAGTCTTCTCGGCTGCTTGAATCCGGCATTCAGAAATGTCAGCACTTGCAGGTTT 1163
Db 301 AACGAAGCTTCTCGCCATGCGGAGTCTGGCATTCAGAAATGTCAGCACTTGCAGGTTT 360
QY 1164 GGTGACCCCTGTTTCTGTCAACCCCTCACTTCTACATGAGACCCCTGTGCTATCAGAA 1223
Db 361 GGTGCGCTCTGTTTCTCTCCACCCCTTACAGCGCGACCTGTGTTGTCAGAA 420
QY 1224 GCGTCTGGTCTGAACCTTGACCAAGGAGCATTTCTTGTCTTGAATCCATCCG 1283
Db 421 GCTGTTCTGTGCTGAACCTTAAACCAAGGAGCATTTCTTGTCTTGAATCCATCCG 480
QY 1284 GTCACTGGATCCCATGAACTGTTCTGTAAGTTGCGATTAAGCTTACATCAAGCT 1343
Db 481 GTCACTGGATCCCATGAACTGTTCTGTAAGTGAAGTGAAGTGAAGCTTACATCAATCT 540
QY 1344 GTCAAGGGCATTTGGGCAACAGGGAAGATCGAGCGCTGCTCTCCATGCTGTGTTT 1403
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QY 1404 GAGCAGCGGTGCGATGGGCGGAGCCCTGAACTGATCTTCAAGCAGCTGGTGTG 1463
Db 601 GAAACAGCGGAGCAATGGGTGGCAAGCCCTGAGCAGCTTCTACAGCAGCTGGTGTG 660
QY 1464 ATG-CCCCAGTACTTCAATGATGCGATGATGCTGCTGGGCTGGGCGCTCTGCT 1522
Db 661 ATGCCCCAGTACTTCAATGATGCGATGATGCTGCTGGGCTGGGCGCTCTGCT 720
QY 1523 GCTGGTGGCTCTATCTACCAAGTTCGCGAGCGAGGAAATGCTTTTATTTGAGTGG 1582
Db 721 TGCTGGTGGCTCTATCT- GCACTGGCGAGCGAGGAAATGCTTTTGTAGGAGTGG 779
QY 1583 TA--GTAAAAAGGCTCGCAGATAAGAGGCCATTCAGGCTTACTCTGAGTCTCTGAT 1640
Db 780 TACGTGAAGAGGCTCCAGGATAGCGAGGCCATTCAGGCTTACTCTGAGTCTCTGTTG 839
QY 1641 TCACAGCTGCGAGGCGAGCTGCTGCAAGAGCCAGCTGTAGGTCCCAA 1693
Db 840 TCCAGTGTGCAAGGGGCGGCTGGTGGCAGAAAGCCAGGTATAGGGGCTGAA 892

RESULT 14

BQ877329 968 bp mRNA linear EST 16-AUG-2002
LOCUS BQ877329
DEFINITION AGENCOURT 8074145 NIH_MGC_102 Homo sapiens cdna clone IMAGE:6087067
5', mRNA sequence.

ACCESSION
VERSION BQ877329.1 GI:22269337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: ATCC

cdna Library Preparation: Rubin Laboratory

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LNCM2323 row: a column: 20

High quality sequence stop: 728.

Location/Qualifiers

1. 968

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6087067"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 102"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cdna made by oligo-dt priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCAGAG(G). Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA

synthesis kit (Stratagene) and Superscript II RT (Life

Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.9%; Score 624.8; DB 5; Length 968;

Best Local Similarity 79.0%; Pred. No. 9.2e-155;

Matches 743; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 496 TGGAGCAGCCGAGCTTCATTTCCAGCGGACAGGTCCACGGCTCTGAGATGACTACA 555

Db 4 TCGAGTACCCGACCTTCCAGTTCAGCCCTCCCAAGTCCACGGCTCGAGGAGGACTACA 63

QY 556 TTATACCTGCTAACTTCTGCTTTGGGGGGCGCAGTAATGATGGAGCAAGTCTGCAG 615

Db 64 TCGTATGCCCAACATCTCTGCTTTGGGTGCGGGGTGATGATGGAGAAATAGCCCATGA 123

QY 616 GCCTGAAGCTGATGATGACCTTGGGGGTGCGCCACCTTTGGGCCAGCGTSCCTTTATGAACC 675

Db 124 CCCTGAAGCTCATGATGACCTTGGCATTCACACCTCCGCGAAGCGTCTTCATGAACC 183

QY 676 GAACAGTTGTGTGATCTCTGTGGGGCTATGAGATTCCTTCGTGAAATTTATCAACAAAT 735

Db 184 GCATGTGGGTGATCATGTGGGGCTTACAAGGACCCCTTTGTGAATCTCATCAACAAAT 243

QY 736 ACTTACCAGACATGTTCCCATCAAGGGCAAGTTCCGCGCTGTTTGTGAGATGAACAACT 795

Db 244 ACTTTCAGGCGATGTTCCCTTCAAGGACAAAGTTTCGATTTATTTGAGCTCAACAACT 303

QY 796 CAGACTCTGGGCTCTTCACTGTGTTCACGGCGCTCCAGAACTTCAGCAAGATCCACCTCG 855

Db 304 CCGACTCTGGGCTCTTCACTGTGTTCACGGCGCTCCAGAACTTCAGCAAGATCCACCTCG 363

QY 856 TGGACAGATGGATGGGCTCAGCAAGTCAACTATCTGGCATTTCAAGAGAGTGCACAAATGA 915

Db 364 TGGACAGTGGAAACGGGCTGAGCAAGGTTGACTTCTGGCATTCGATTCAGTGCACAAATGA 423

Qy	1582	GTAGTAAAGGGCTCGCAGATAGGAGGCCATTTCAGGCCTA---CTCTGAGTCTCTGA	1638
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Qy	1639	TGTCACCAAGTCCCAAGGCGCGTGTGCAAGGCCAAGCTGTAGGGTCCCAAGACA	1698
Db	840	GTCCACCAAGTCCCAAGGCGCGTGTGCAAGGCCAAGCTGTAGGGTCCCAAGACA	899
Qy	1699	CCACGAGCCCCCAACCTGATAGCTTGGTCAGACCCAGCCATCCAGCCCCCTACACCCCGC	1758
Db	900	ACCTATAGGCCCAAACTGATAGCTTGGTCAGACCCAGCCATCCAGCCCCCTACACCCCGC	959
Qy	1759	TTCTTGA	1765
Db	960	TTGAGGA	966

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Job time : 7298.62 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 18:01:48 ; Search time 308.759 Seconds
(without alignments)
10293.724 Million cell updates/sec

Title: US-08-765-108-3
Perfect score: 1788
Sequence: 1 GCCACTGACGGCTACTGC.....CTCTCAGCGGACAGTCGC 1788

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1788	100.0	1788	2	US-08-559-505-1
2	1788	100.0	1788	2	US-08-749-907-1
3	1788	100.0	1788	3	US-09-241-581B-3
4	1788	100.0	1788	3	US-08-265-428-3
5	1788	100.0	1788	3	US-09-385-799-1
6	1788	100.0	1788	6	PCT-US95-07721-3
7	1786	99.9	1825	3	US-08-890-980-3
8	1786	99.9	1825	3	US-08-890-979-3
9	1786	99.9	1825	3	US-09-032-894-3
10	1786	99.9	1825	3	US-09-031-626-3
11	1369.8	76.6	1785	2	US-08-559-505-3
12	1369.8	76.6	1785	2	US-08-749-907-3
13	1369.8	76.6	1785	3	US-09-241-581B-7
14	1369.8	76.6	1785	3	US-09-385-799-3
15	1369.8	76.6	1785	6	PCT-US95-07721-7
16	1139.4	63.7	2630	2	US-08-890-980-1
17	1139.4	63.7	2630	3	US-08-890-979-1
18	1139.4	63.7	2630	3	US-09-032-894-1
19	1139.4	63.7	2630	3	US-09-031-626-1
20	1136.2	63.5	2566	3	US-09-270-542-124
21	1136.2	63.5	2566	3	US-09-054-272-58
22	1136.2	63.5	2566	3	US-10-024-396-3
23	971	54.3	2595	3	US-09-949-016-2296
24	285	15.9	719	3	US-10-024-396-11

25	193.2	10.8	465	3	US-09-949-016-2027	Sequence 2027, Ap
26	189	10.6	485	3	US-10-024-396-12	Sequence 12, Appl
27	132.6	7.4	397	3	US-09-513-999C-2451	Sequence 2451, Ap
28	131.8	7.4	41322	3	US-10-024-396-13	Sequence 13, Appl
29	131.8	7.4	90472	3	US-09-949-016-14038	Sequence 14038, A
30	128.6	7.2	481	2	US-08-890-980-11	Sequence 11, Appl
31	128.6	7.2	481	3	US-08-890-979-11	Sequence 11, Appl
32	128.6	7.2	481	3	US-09-032-894-11	Sequence 11, Appl
33	128.6	7.2	481	3	US-09-031-626-11	Sequence 11, Appl
34	123	6.9	526	2	US-08-890-980-8	Sequence 8, Appl
35	123	6.9	526	3	US-08-890-979-8	Sequence 8, Appl
36	123	6.9	526	3	US-09-032-894-8	Sequence 8, Appl
37	123	6.9	526	3	US-09-031-626-8	Sequence 8, Appl
38	117.6	6.6	1002	2	US-08-890-980-5	Sequence 5, Appl
39	117.6	6.6	1002	3	US-08-890-979-5	Sequence 5, Appl
40	117.6	6.6	1002	3	US-09-032-894-5	Sequence 5, Appl
41	117.6	6.6	1002	3	US-09-031-626-5	Sequence 5, Appl
42	117	6.5	479	2	US-08-890-980-6	Sequence 6, Appl
43	117	6.5	479	3	US-08-890-979-6	Sequence 6, Appl
44	117	6.5	479	3	US-09-032-894-6	Sequence 6, Appl
45	117	6.5	479	3	US-09-031-626-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-559-505-1
; Sequence 1, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MITT150
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683
; encode the amino acid sequence for the Hamster Scavenger Recept

US-08-559-505-1

Query Match 100.0%; Score 1788; DB 2; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGGCTACTGCTGCTCGGGCCACCTGCCTGAGACTCACCTTGCTGGAACTGG 60
DB 1 GCCACCTGCAGGGCTACTGCTGCTCGGGCCACCTGCCTGAGACTCACCTTGCTGGAACTGG 60

QY 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTCGCTTCTGTGCTGTGCTGCTGCTGCTGCT 120
DB 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTCGCTTCTGTGCTGTGCTGCTGCTGCTGCT 120

QY 121 CCTGAGCCCCGAGCCCCGGGCGCGCACACCGGACATGGCGCGCAGGGCGCGCT 180
DB 121 CCTGAGCCCCGAGCCCCGGGCGCGCACACCGGACATGGCGCGCAGGGCGCGCT 180

QY 181 GGGTGGGGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 240
DB 181 GGGTGGGGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 240

QY 241 TCCTCGGTGATGCTCTCATCAACAGCAGGACTACTGAAGATGTCGCGATAGACCCCA 300
DB 241 TCCTCGGTGATGCTCTCATCAACAGCAGGACTACTGAAGATGTCGCGATAGACCCCA 300

QY 301 GCAGCTGTCTTGCATGTGGAAGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACT 360
DB 301 GCAGCTGTCTTGCATGTGGAAGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACT 360

QY 361 TCCTCGAGGTGGTCAATCCAGCGAGATCCCTAAGGGTGAGAACCCAGTGTGCGGGAGC 420
DB 361 TCCTCGAGGTGGTCAATCCAGCGAGATCCCTAAGGGTGAGAACCCAGTGTGCGGGAGC 420

QY 421 GTGACCCCTATGTCTACAGGGAAATTCAGACATAGGCCCAACATCACCTTCAATGACAAATG 480
DB 421 GTGACCCCTATGTCTACAGGGAAATTCAGACATAGGCCCAACATCACCTTCAATGACAAATG 480

QY 481 ATACTGTGCTTGTGGAGCAGCGAGCTCCATTTCCAGCGCGACAGTCCCAAGCT 540
DB 481 ATACTGTGCTTGTGGAGCAGCGAGCTCCATTTCCAGCGCGACAGTCCCAAGCT 540

QY 541 CTGAGAGTACTACATTAATCTGCTAACTTCTGCTTGTGGGGGGCGAGTAATATGG 600
DB 541 CTGAGAGTACTACATTAATCTGCTAACTTCTGCTTGTGGGGGGCGAGTAATATGG 600

QY 601 AGACAAAGTCTGACGGCTGAGGCTGATGATACCTTGGGGCTGGCCACCTTGGGGCAGC 660
DB 601 AGACAAAGTCTGACGGCTGAGGCTGATGATACCTTGGGGCTGGCCACCTTGGGGCAGC 660

QY 661 GTGCTTTATGAACCGAAGCTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTGTGTA 720
DB 661 GTGCTTTATGAACCGAAGCTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTGTGTA 720

QY 721 ATTTTATCAAAATATCTTACGACATGTTCCCATCAAGGGCAAGTTCGGCTGTTTG 780
DB 721 ATTTTATCAAAATATCTTACGACATGTTCCCATCAAGGGCAAGTTCGGCTGTTTG 780

QY 781 TTGAGATGAACAACTCAGACTCTGGGCTTCTCACTGTGTTTTCAGGGCGTCCAGAACTTCA 840
DB 781 TTGAGATGAACAACTCAGACTCTGGGCTTCTCACTGTGTTTTCAGGGCGTCCAGAACTTCA 840

QY 841 GCAAGATCCACCTGGTGAGATGGAATGGGCTCAGCAGGTCMACTACTGGCATTCAG 900
DB 841 GCAAGATCCACCTGGTGAGATGGAATGGGCTCAGCAGGTCMACTACTGGCATTCAG 900

QY 901 AGCAGTCAACATGATCAATGGCACTTCCGGGCGAGATGGGCACTTATGACACCCC 960
DB 901 AGCAGTCAACATGATCAATGGCACTTCCGGGCGAGATGGGCACTTATGACACCCC 960

QY 961 AGTCTCGCTGGAAATCTTTCAGTCCGGAAGCTGTCAGGCTCTATGAAGCTCACCTTACCATG 1020
DB 961 AGTCTCGCTGGAAATCTTTCAGTCCGGAAGCTGTCAGGCTCTATGAAGCTCACCTTACCATG 1020

QY 1021 ATTCAGGGTGTGTTGAAGGCATCCACCTATCGCTTTCACAGCCCTAAAACTTTGTTTG 1080
DB 1021 ATTCAGGGTGTGTTGAAGGCATCCACCTATCGCTTTCACAGCCCTAAAACTTTGTTTG 1080

QY 1081 CCAATGGGTCTGTTTACCACCAATGAAGGTTTCTGCCCCGTGCTTGAATCCGGCATTC 1140
DB 1081 CCAATGGGTCTGTTTACCACCAATGAAGGTTTCTGCCCCGTGCTTGAATCCGGCATTC 1140

QY 1141 AAAATGTGAGCACTTTCAGGTTTGGTGACCCCTGTTTCTGTCTGTCACACCTCTCTACA 1200
DB 1141 AAAATGTGAGCACTTTCAGGTTTGGTGACCCCTGTTTCTGTCTGTCACACCTCTCTACA 1200

QY 1201 ATGCGAGCCCTGCTGATCAGAAAGCGTTCTGCGTCTGAACCTGACCCCAAGGAGCAT 1260
DB 1201 ATGCGAGCCCTGCTGATCAGAAAGCGTTCTGCGTCTGAACCTGACCCCAAGGAGCAT 1260

QY 1261 CTTTGTCTTCCATGACATCCATCCGGTCACTGGGATCCCAATGAATGTTCTGTGAAGTTGC 1320
DB 1261 CTTTGTCTTCCATGACATCCATCCGGTCACTGGGATCCCAATGAATGTTCTGTGAAGTTGC 1320

QY 1321 AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCG 1380
DB 1321 AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCG 1380

QY 1381 TGGTCTCTCCATTTGCTGTTTGAAGCAGAGCGGTGCCATGGCGCGAGCCCTGAAACA 1440
DB 1381 TGGTCTCTCCATTTGCTGTTTGAAGCAGAGCGGTGCCATGGCGCGAGCCCTGAAACA 1440

QY 1441 CGTTCTACACGAGCTGTGCTGATGCCCCAGGTACTTCAGTATGTGCAAGTATGCTGCTGC 1500
DB 1441 CGTTCTACACGAGCTGTGCTGATGCCCCAGGTACTTCAGTATGTGCAAGTATGCTGCTGC 1500

QY 1501 TGGGGCTGGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 TGGGGCTGGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

QY 1561 AATGCTTTTATTTTGGAGTGGTGTAAAGGGCTCGCAGGATAGAGGGCCATTCAGG 1620
DB 1561 AATGCTTTTATTTTGGAGTGGTGTAAAGGGCTCGCAGGATAGAGGGCCATTCAGG 1620

QY 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCACGGTGTGCAAGAGCCAAAGC 1680
DB 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCACGGTGTGCAAGAGCCAAAGC 1680

QY 1681 TGTAGGGTCCAAAGACACACAGAGCCCCCCCCAACCCTGATAGCTTGGTCAGACCCCAT 1740
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QY 1741 CCAGCCCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCGC 1788
DB 1741 CCAGCCCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCGC 1788

RESULT 2
US-08-749-907-1
; Sequence 1, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

QY 1681 TGTTAGGTTCCCAAGACACACACGAGCCCGCCCAACCTGATAGCTTGGTCAGACACGCCAT 1740
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QY 1741 CGAGCCCTTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTGGC 1788
DB 1741 CGAGCCCTTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTGGC 1788

RESULT 3

US-09-241-581B-3
; Sequence 3, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through
; 1683 encode the amino acid sequence for
; the Hamster Scavenger Receptor Class
; B-1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-241-581B-3
Query Match 100.0%; Score 1788; DB 3; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 421 GTGGACCCCTATGCTACAGGGAAATTCAGACATAAGGCCAAATCATCCTTCAATGACAAATG 480
QY 481 ATACTGTGTCCTTTGTGGAGCACCGCAGCCTCCATTTCCAGCGGACAGGTCCCAAGCT 540
DB 481 ATACTGTGTCCTTTGTGGAGCACCGCAGCCTCCATTTCCAGCGGACAGGTCCCAAGCT 540
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DB 541 CTGAGAGTGACTACATATATATGCTGCTTAACATTTCTGGTCTTGGGGGGCGGAGTAATG 600
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QY 721 ATTTTATCAACAATACTTACCAGACATGTTCCCATCAAGGGCAGTTGGGGCTTTTG 780
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QY 781 TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGGCGTCCAGAACTTCA 840
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QY 841 GCAAGATCCACCTGGTGGACAGATGGAAATGGGCTCAGCAAGGTCAACTACTTGGCAATTCAG 900
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QY 961 AGTCCTCGCTGGAATTTCTTCACTGCGGAAGCTTCAAGGTCTATGAAGCTCACCTACCATG 1020
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Qy 1261 CTTTGTCTCTTGACATCCATCCGCTCACTGGGATCCCCCATCAACTGTTCTGTGAAGTTGC 1320
Db 1261 CTTTGTCTCTTGACATCCATCCGCTCACTGGGATCCCCCATCAACTGTTCTGTGAAGTTGC 1320
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Db 1381 TGGTCTCCCATTTGCTGTGTTTGGAGCAGAGCGGTGCCATGGGCGGAGCCCTGGAACA 1440
Qy 1441 CGTTCTACACGAGTGTGTGCTGATGCCCCCAGGTACTTTCAGTATGTGAGTATGTGCTGC 1500
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Qy 1561 AATCGCTTTTATTTTGGAGTGTGTGTTTGGAGTGTGTGTTTGGAGTGTGTGTTTGGAG 1620
Db 1561 AATCGCTTTTATTTTGGAGTGTGTGTTTGGAGTGTGTGTTTGGAGTGTGTGTTTGGAG 1620
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Db 1621 CCTACTCTGAGTCTCTGATGTCAACAGCTGCAAGGGGCAAGGCTGTGCAAGGCAAGC 1680
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Db 1681 TGTAGGCTTCCAAAGACACACAGAGCCCCCAACCTGATAGTGTGTCAGACAGCCAT 1740
Qy 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTGTGTGTTTGGAGTGTGTGTTTGGAGTGTGT 1788
Db 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTGTGTGTTTGGAGTGTGTGTTTGGAGTGTGT 1788

RESULT 4

US-08-265-428-3
; Sequence 3, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683 encode the amino
; US-08-265-428-3

Query Match 100.0%; Score 1788; DB 3; Length 1788;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCACCTGCAGGGCTACTGCTCCGGCCACTGCTGAGACTCACCTTGTGTAAGCTG 60
Db 1 GCCACCTGCAGGGCTACTGCTCCGGCCACTGCTGAGACTCACCTTGTGTAAGCTG 60
Qy 61 AGCTCTGGCTTCTGTCACTCTGTGGCTCTGTGCTGCTGTGCTGCTGCTGCTGCTGCT 120
Db 61 AGCTCTGGCTTCTGTCACTCTGTGGCTCTGTGCTGCTGTGCTGCTGCTGCTGCTGCT 120
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Db 121 CTTAGAGCCCGCAGAGCCCGGGCCGCAACACGCGACATGGGCGGAGCCGAGGCGGCT 180
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Qy 721 ATTTTATCAAAATATCTTACAGAGATGTTCCCATCAAGGGCAAGTTCGGCTGTTT 780
Db 721 ATTTTATCAAAATATCTTACAGAGATGTTCCCATCAAGGGCAAGTTCGGCTGTTT 780
Qy 781 TTGAGATGACAACTCAGACTCTGGGCTCTTCACTGTGTTTCAAGGGGCTCCAGACTTCA 840
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Qy 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTTGGCATTCAG 900

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Db 841 GCAAGATCCACCTGGTGGACAGATGAATGGGCTCAGCAAGGTCAACTACTGCGCAATTCAG 900
Qy 901 AGCAGTGCACATGATCAATGGCACTTCGGGGCAGATGTGGGCACCATTCATGACACCCC 960
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Qy 1021 ATTACGGGGTGTGGAAGGCATCCCACTATCGCTTTCACAGCCCTTAAACCTTTGTTG 1080
Db 1021 ATTACGGGGTGTGGAAGGCATCCCACTATCGCTTTCACAGCCCTTAAACCTTTGTTG 1080
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Db 1081 CCAATGGGTCTGTATACCAACCAATGAAGTCTTTCGCGGCTGCTGAATCCGGCATTC 1140
Qy 1141 AAAATGTCAGCACTTGCAAGTGTGGTGACCCCTGTTTCTGTACACCCCTCACTTCTACA 1200
Db 1141 AAAATGTCAGCACTTGCAAGTGTGGTGACCCCTGTTTCTGTACACCCCTCACTTCTACA 1200
Qy 1201 ATGCAGACCTGTGCTATCAGAAGCGTTCCTGGTCTGAACCTGACCCCAAGGAGCAT 1260
Db 1201 ATGCAGACCTGTGCTATCAGAAGCGTTCCTGGTCTGAACCTGACCCCAAGGAGCAT 1260
Qy 1261 CTTTGTCTTGCATCCATCCGCTCACTGGGATCCCATGAAGTCTTCTGTGAAGTTC 1320
Db 1261 CTTTGTCTTGCATCCATCCGCTCACTGGGATCCCATGAAGTCTTCTGTGAAGTTC 1320
Qy 1321 AGATAAGCTCTACATCAAAAGCTGTCAAGGCAATGGGCAAAAGGAGATCGAGCCCG 1380
Db 1321 AGATAAGCTCTACATCAAAAGCTGTCAAGGCAATGGGCAAAAGGAGATCGAGCCCG 1380
Qy 1381 TGGTCTCTCCATCTGTGTGTTGAGCAGAGCGGTGCAATGGGCGGCGAGCCCTGAACA 1440
Db 1381 TGGTCTCTCCATCTGTGTGTTGAGCAGAGCGGTGCAATGGGCGGCGAGCCCTGAACA 1440
Qy 1441 CGTCTACAGCAGCTGTGCTGATGACCCCGAGTACTTCAATGATGTGCAATGATGCTGC 1500
Db 1441 CGTCTACAGCAGCTGTGCTGATGACCCCGAGTACTTCAATGATGTGCAATGATGCTGC 1500
Qy 1501 TGGGGCTGGGCGGCTCCTGCTGCTGGTCCCGCTCATCTACCAAGTTCGCGCAGCAGGAGA 1560
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Qy 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAAGGAGCCATTCAAG 1620
Db 1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAAGGAGCCATTCAAG 1620
Qy 1621 CCTACTCTGAGTCTCTGATGTACACGCTGCAAGGCGAGGCTGCTGCAAGAGCCAGC 1680
Db 1621 CCTACTCTGAGTCTCTGATGTACACGCTGCAAGGCGAGGCTGCTGCAAGAGCCAGC 1680
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Db 1681 TGTAGGGTCCCAAGACACCAAGGCGGCGGCTGATGATGCTGCTGCAAGAGCCAGCAT 1740
Qy 1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCG 1788
Db 1741 CCAGCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCG 1788
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RESULT 5

US-09-385-799-1

; Sequence 1, Application US/09385799

; Patent No. 6962688

; GENERAL INFORMATION:

; APPLICANT: Money Krieger, Attilio Rigotti, and Karen Kozarsky

; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

```
ADDRESS: Patrea L. Pabat, Arnall Golden & Gregory
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,799
FILING DATE: 30-Aug-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,907
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabat, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 156..1683
OTHER INFORMATION: /function= "Nucleotides 156 through 1683
encode the amino acid sequence for the Hamster Scavenger Receptor Class
B-I."
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-385-799-1
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Query Match 100.0%; Score 1788; DB 3; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCACCTGCAGGGCTACTGCTGCTCGGCCACTGCTGAGACTCACCTTGTGGAACGTG 60
Db 1 GCCACCTGCAGGGCTACTGCTGCTCGGCCACTGCTGAGACTCACCTTGTGGAACGTG 60
Qy 61 AGCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 AGCTCGGCTTCTGTCATCTCTGTGGCCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 CCTGAGCCCGGAGCCCGGCGGCACACCGGACATGGCGGCGGCGGCGGCGGCT 180
Db 121 CCTGAGCCCGGAGCCCGGCGGCACACCGGACATGGCGGCGGCGGCGGCGGCT 180
Qy 181 GGTGCGGCTGGGGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 GGTGCGGCTGGGGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 241 TCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 TCCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 301 GCAGCCTGCTCTTTCGCAATGTGAAGAGATCCCTGTACCTTCTACTTCTGCTGCTGCTGCT 360
Db 301 GCAGCCTGCTCTTTCGCAATGTGAAGAGATCCCTGTACCTTCTACTTCTGCTGCTGCTGCT 360
Qy 361 TCTTCGAGGTGGTCAATCCAGCAGATCCTAAAGGTTGAGAGCCAGTAGTTCGGGAGC 420
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Query Match	99.9%;	Score 1786;	DB 2;	Length 1825;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1786;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GCCACCTGCAGGGCTACTGTGCTCCGGCCACTGCCTGAGACTCACCTTGTCTGAAACGTG	60	
Db	1	GCCACCTGCAGGGCTACTGTGCTCCGGCCACTGCCTGAGACTCACCTTGTCTGAAACGTG	60	
QY	61	AGCCTCGGCTTCTGTCACTCTGTGTGGCCTCTGTGCGCTTCTGTGCTGTCCCCCTTCAGTC	120	
Db	61	AGCCTCGGCTTCTGTCACTCTGTGTGGCCTCTGTGCGCTTCTGTGCTGTCCCCCTTCAGTC	120	
QY	121	CTTGAGCCCCCGAGACCCCGGCCGCAACACGCGGACATGGGCGGAGCGCCAGAGCGCGCT	180	
Db	121	CTTGAGCCCCCGAGACCCCGGCCGCAACACGCGGACATGGGCGGAGCGCGCGCGCT	180	
QY	181	GGGTGGCGGTGGGGCTGGGGCTGGTGGGGCTGTGTGGCTGTGTGCTCGGTGTGGTTATGA	240	
Db	181	GGGTGGCGGTGGGGCTGGGGCTGGTGGGGCTGTGTGGCTGTGTGCTCGGTGTGGTTATGA	240	
QY	241	TCCTCGTGATGSCCCTCGCTCATCAAAACAGCAGAGTACTGAAGAATGTCCGATAGACCCCA	300	
Db	241	TCCTCGTGATGSCCCTCGCTCATCAAAACAGCAGAGTACTGAAGAATGTCCGATAGACCCCA	300	
QY	301	GCAGCTGTCTTTGCATGTGGAGAGATCCCTGTATCCCTTCTACTTGTTCGCTTACT	360	
Db	301	GCAGCTGTCTTTTGCAATGTGGAGAGATCCCTGTATCCCTTCTACTTGTTCGCTTACT	360	
QY	361	TCCTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGTGAAGACCACTAGTCGGGAGC	420	
Db	361	TCCTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGTGAAGACCACTAGTCGGGAGC	420	
QY	421	GTGGACCTATGTCTACAGGGAATTCAGACATAAGGCCAAATCACCTTCAATGACAATG	480	
Db	421	GTGGACCTATGTCTACAGGGAATTCAGACATAAGGCCAAATCACCTTCAATGACAATG	480	
QY	481	ATACTGTGCTTTGTGGAGACACCGAGCCTCCATTTTCAGCGCGGACAGGTCCACCGGT	540	
Db	481	ATACTGTGCTTTGTGGAGACACCGAGCCTCCATTTTCAGCGCGGACAGGTCCACCGGT	540	
QY	541	CTGAGAGTGACTACATTATATGCTTAACATTCTGTGCTTTGGGGGGCGCAGTAATGATGG	600	
Db	541	CTGAGAGTGACTACATTATATGCTTAACATTCTGTGCTTTGGGGGGCGCAGTAATGATGG	600	
QY	601	AGAGCAAGTCTGCAGGCCTGAAGCTGATGATGACCTTTGGGGCTTGGCCACCTTGGGCCAGC	660	
Db	601	AGAGCAAGTCTGCAGGCCTGAAGCTGATGATGACCTTTGGGGCTTGGCCACCTTGGGCCAGC	660	
QY	661	GTGCGCTTATGAACCGAAAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA	720	
Db	661	GTGCGCTTATGAACCGAAAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA	720	

RESULT 8

US-08-890-979-3
; Sequence 3, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 156..1682
US-08-890-979-3

Query Match 99.9%; Score 1786; DB 3; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	361	TCCTCGAGGTGTCATCCACGCGAGATCCTAAAGGGTGAGAAGCCAGTAGTCGGGAGC	420
DB	361	TCCTCGAGGTGTCATCCACGCGAGATCCTAAAGGGTGAGAAGCCAGTAGTCGGGAGC	420
QY	421	GTGGACCCCTATGCTACAGGGAATTCAGACATAAGGCCAAACATCACCTTCAATGACAATG	480
DB	421	GTGGACCCCTATGCTACAGGGAATTCAGACATAAGGCCAAACATCACCTTCAATGACAATG	480
QY	481	ATATCTGTCTCTTTGTGGAGCACCCGAGCCTCCATTTCCAGCCGGACAGGTCCACGGCT	540
DB	481	ATATCTGTCTCTTTGTGGAGCACCCGAGCCTCCATTTCCAGCCGGACAGGTCCACGGCT	540
QY	541	CTGAGAGTCACTACATATTACTATGCTTAAACATTTCTGGTCTTGGGGGCGCAGTAATGATGG	600
DB	541	CTGAGAGTCACTACATATTACTATGCTTAAACATTTCTGGTCTTGGGGGCGCAGTAATGATGG	600
QY	601	AGAGCAAGTCTGAGGCCCTGAAGCTGATGATGACCTTTGGGGCTTGGCCA CTTGGGGCAGC	660
DB	601	AGAGCAAGTCTGAGGCCCTGAAGCTGATGATGACCTTTGGGGCTTGGCCA CTTGGGGCAGC	660
QY	661	GTGCCCTTTATGAACCGACAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA	720
DB	661	GTGCCCTTTATGAACCGACAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA	720
QY	721	ATTATTATCAACAATACTATTACAGACATGTTCCCATCAAGGGCAAGTTTCGGGCTGTTTG	780
DB	721	ATTATTATCAACAATACTATTACAGACATGTTCCCATCAAGGGCAAGTTTCGGGCTGTTTG	780
QY	781	TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTTCAGAACTTCA	840
DB	781	TTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGGCTTCAGAACTTCA	840
QY	841	GCAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGTCAACTACTGGCATTCAG	900
DB	841	GCAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGTCAACTACTGGCATTCAG	900
QY	901	AGCAGTGCAACATGATCAATGGCACTTCCGGGCGAGATGTGGGCACCATTCATGACACCCC	960
DB	901	AGCAGTGCAACATGATCAATGGCACTTCCGGGCGAGATGTGGGCACCATTCATGACACCCC	960
QY	961	AGTCTCTCGCTGGAAATTTCTTCACTGTCGGAAAGCCTGCAAGTCTATGAAGCTCACTCAATG	1020
DB	961	AGTCTCTCGCTGGAAATTTCTTCACTGTCGGAAAGCCTGCAAGTCTATGAAGCTCACTCAATG	1020
QY	1021	ATTTCAGGGGTGTTGAAGGCATCCCACTATCGCTTTCAGCCCTTCAAGCCCTTAACTTTGTTG	1080
DB	1021	ATTTCAGGGGTGTTGAAGGCATCCCACTATCGCTTTCAGCCCTTCAAGCCCTTAACTTTGTTG	1080
QY	1081	CCAATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGCGCTTGAATCCGGCATTC	1140
DB	1081	CCAATGGGTCTGTTTACCCCAATGAAGGTTTCTGCGCGCTTGAATCCGGCATTC	1140
QY	1141	AAATCTCAGCACTTCAGGTTTGGTGCAACCTGTTTCTGTCAACCTTCATTTCTTACA	1200
DB	1141	AAATCTCAGCACTTCAGGTTTGGTGCAACCTGTTTCTGTCAACCTTCATTTCTTACA	1200
QY	1201	ATGCAACCTGTGCTATCAGAACCGTTCTGGGCTCTGAACCTTGAACCCAGGAGCATTC	1260
DB	1201	ATGCAACCTGTGCTATCAGAACCGTTCTGGGCTCTGAACCTTGAACCCAGGAGCATTC	1260
QY	1261	CTTTGTTCTTGCATCTCAGGTCATCCGGTCACTGGGATCCCATGAATCTTCTGTGAAGTTGC	1320
DB	1261	CTTTGTTCTTGCATCTCAGGTCATCCGGTCACTGGGATCCCATGAATCTTCTGTGAAGTTGC	1320
QY	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCAATGGGCAAAACAGGGAAGATCGAGCCCG	1380
DB	1321	AGATAAGCCTCTACATCAAAAGCTGTCAAGGGCAATGGGCAAAACAGGGAAGATCGAGCCCG	1380
QY	1381	TGCTCTCCATTCGTGTGTTGACAGAGCGGTGCCATGGGCGGAGCCCTCTGAACA	1440
DB	1381	TGCTCTCCATTCGTGTGTTGACAGAGCGGTGCCATGGGCGGAGCCCTCTGAACA	1440
QY	1441	CGTTCTACAGCAGCTGGTGTGATGCCCGAGGTACTTTCAGTATGTGCAATGTGTCTGC	1500

1441 CGTTCTACAGCAGCTGGTCTGATGCCCCCAGGTACTTTCAGTATGTGTCGTC 1500
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1501 TGGGGCTGGGCGGCTCTCTGCTGCTGGTCCCGTCTATCAACAGTTGCGCAGCAGGAGA 1560
1501 TGGGGCTGGGCGGCTCTCTGCTGCTGGTCCCGTCTATCAACAGTTGCGCAGCAGGAGA 1560
1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAGGAGGCCATTCAGG 1620
1561 AATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAGGAGGCCATTCAGG 1620
1621 CCTACTCTGAGTCTCTGATGCTCAACAGTCCCAAGGCGCGTCTGCAAGAGGCCAAGC 1680
1621 CCTACTCTGAGTCTCTGATGCTCAACAGTCCCAAGGCGCGTCTGCAAGAGGCCAAGC 1680
1681 TGTAGGGTCCCAAGACACACAGGAGCCCCCCCCCTGATAGTTGGTCAAGACGCCAT 1740
1681 TGTAGGGTCCCAAGACACACAGGAGCCCCCCCCCTGATAGTTGGTCAAGACGCCAT 1740
1741 CCAGCCCTACACCCCGCTTTTGGAGTCTCTCAGCGGACAGTC 1786
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RESULT 10
US-09-031-626-3
; Sequence 3, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031.626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)

US-09-031-626-3
Query Match 99.9%; Score 1786; DB 3; Length 1825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGGCTACTGCTGCTCCGSCCACTGCCTGAGACTCACCTTCGTCGAACTG 60
DB 1 GCCACCTGCAGGGCTACTGCTGCTCCGSCCACTGCCTGAGACTCACCTTCGTCGAACTG 60
QY 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTTCTGTGCTGCTCCCTTCAGTC 120
DB 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTTCTGTGCTGCTCCCTTCAGTC 120
QY 121 CCTGAGCCCGGAGCCCGGCGCCACACGCGGACATGGGCGGAGCGCGCGCT 180
DB 121 CCTGAGCCCGGAGCCCGGCGCCACACGCGGACATGGGCGGAGCGCGCGCT 180
QY 181 GGGTGGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 240
DB 181 GGGTGGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 240
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QY 301 GCAGCTGTCCCTTTCGCAATGTGGAAGGAGATCCCTGTACCCCTTCTACTTGTCCGTCTACT 360
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DB 421 GTGGAGCCCTATGTCTACAGGGAATTCAGACATAAGGCCAAATCATCCTTCAATGACAATG 480
QY 481 ATACTGTGTCTTGTGGAGCACCGCAGCTCCATTTCCAGCGGACAGCTCCACCGCT 540
DB 481 ATACTGTGTCTTGTGGAGCACCGCAGCTCCATTTCCAGCGGACAGCTCCACCGCT 540
QY 541 CTGAGAGTGACTACATTAATTAATCTGCCTAAATCTTGTCTTGGGGGGCGCAGTAATGATG 600
DB 541 CTGAGAGTGACTACATTAATTAATCTGCCTAAATCTTGTCTTGGGGGGCGCAGTAATGATG 600
QY 601 AGAGCAAGTCTGAGGCTTGAAGCTGATGATGACCTTGGGGGTGGCCACCTTGGGGCGAGC 660
DB 601 AGAGCAAGTCTGAGGCTTGAAGCTGATGATGACCTTGGGGGTGGCCACCTTGGGGCGAGC 660
QY 661 GTGCCCTTATGAACCGAAGTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA 720
DB 661 GTGCCCTTATGAACCGAAGTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTGA 720
QY 721 ATTATTAACAACAATACTTACCAGACATGTTCCTCCATCAAGGGCAAGTTTCGGCTCTTTG 780
DB 721 ATTATTAACAACAATACTTACCAGACATGTTCCTCCATCAAGGGCAAGTTTCGGCTCTTTG 780
QY 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTCACGGGGTCCAGAACTTCA 840
DB 781 TTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTGTTCACGGGGTCCAGAACTTCA 840
QY 841 GCNAGATCCACCTGGTGGGACAGATGGAATGGGCTCAGCAAGTCACTACTGCGATTCAG 900
DB 841 GCNAGATCCACCTGGTGGGACAGATGGAATGGGCTCAGCAAGTCACTACTGCGATTCAG 900
QY 901 AGCAGTGCACACATGATCAATGGCATTCCGGGCGAGATGTGGGCAACCATTCATGACACCCC 960
DB 901 AGCAGTGCACACATGATCAATGGCATTCCGGGCGAGATGTGGGCAACCATTCATGACACCCC 960
QY 961 AGTCCTCGCTGGAAATTTCTTCAGTCCGGAAGCTGCAAGTCTATGAAGCTCACCTACATG 1020
DB 961 AGTCCTCGCTGGAAATTTCTTCAGTCCGGAAGCTGCAAGTCTATGAAGCTCACCTACATG 1020
QY 1021 ATTCAGGGGTGTTTGAAGGCATCCCACTATCGCTTTCAGCGCCCTTAAACCTTTGTTTG 1080
DB 1021 ATTCAGGGGTGTTTGAAGGCATCCCACTATCGCTTTCAGCGCCCTTAAACCTTTGTTTG 1080
QY 1081 CCAATGGGCTGTGTTTACCAACCAATGAAAGGTTTCTGCGCGCTTGAATCCGGCATTC 1140
DB 1081 CCAATGGGCTGTGTTTACCAACCAATGAAAGGTTTCTGCGCGCTTGAATCCGGCATTC 1140
QY 1141 AAAATGTACAGCTTTCAGGTTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
DB 1141 AAAATGTACAGCTTTCAGGTTTGGTGCACCCCTGTTTCTGTCAACCCCTCACTTCTACA 1200
QY 1201 ATGCAGACCTGTGCTATCAGAGCCGTTCTGGGCTGTAACCTTGACCCCAAGGAGCAT 1260
DB 1201 ATGCAGACCTGTGCTATCAGAGCCGTTCTGGGCTGTAACCTTGACCCCAAGGAGCAT 1260
QY 1261 CTTTGTCTTGTACATCATCCGCTCACTGGGATCCCAATGAACTGTTCGTGAAAGTTC 1320
DB 1261 CTTTGTCTTGTACATCATCCGCTCACTGGGATCCCAATGAACTGTTCGTGAAAGTTC 1320
QY 1321 AGATAAGCTCTTACATCAAGAGCTGTCAAGGGCAATGGGCAAAACAGGAAAGATCGAGCCCG 1380
DB 1321 AGATAAGCTCTTACATCAAGAGCTGTCAAGGGCAATGGGCAAAACAGGAAAGATCGAGCCCG 1380

1070 AACTTTGTTTGGCAATGGGTCTGTTTACCCACCAATGAAGTTTCTGCGCGTCTTGA 1129
1129 TATCTGTTTGGCAATGGGTCTGTTTACCCACCAATGAAGTTTCTGCGCGTCTTGA 1024
1130 ATCCGCAATCAAAATGTGACACTTGCAGTTTGGTGACCCCTGTTTCTGTCACACC 1189
1189 GTCTGGCAATCAGATGTGACACTTGCAGTTTGGTGACCCCTGTTTCTGTCACACC 1084
1190 TCACTTCTACAAATGACACCTGTGTATCAGAACGGTCTGCGGTCTGAACCTGACCC 1249
1249 CCACCTTTTACACCGCCGACCTGTGTGTGTCAGAACGTTTCTGTCAGAACCTAACCC 1144
1250 AAGGGAGCACTTTGTTCTTGCATCCATCCGTCCTGCTGCTGCTGCTGCTGCTGCT 1309
1309 AAGGGAGCACTTTGTTCTTGCATCCATCCGTCCTGCTGCTGCTGCTGCTGCTGCT 1204
1310 TGTGAAGTTGTCAGATAGCTTACATCAAGCTGTCAAGGGCATTTGGGCAACAGGGAA 1369
1369 TGTGAAGTTGTCAGATAGCTTACATCAAGCTGTCAAGGGCATTTGGGCAACAGGGAA 1264
1370 GATCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1429
1429 GATCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
1430 GCCCTTGAACACAGCTTACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
1489 GCCCTTGAACACAGCTTACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1384
1490 GTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
1549 GTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
1550 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCGAGGATGAAGA 1609
1609 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCGAGGATGAAGA 1504
1610 GGCATTTCAGGCTTACTCTGAGTCTCTGATGTCCAGCTGCTGCTGCTGCTGCTGCTG 1669
1669 GGCATTTCAGGCTTACTCTGAGTCTCTGATGTCCAGCTGCTGCTGCTGCTGCTGCTG 1564
1670 AGAAGCCAACTGTAGGCTTCTGAGTCTCTGATGTCCAGCTGCTGCTGCTGCTGCTG 1729
1729 AGAAGCCAACTGTAGGCTTCTGAGTCTCTGATGTCCAGCTGCTGCTGCTGCTGCTG 1624
1730 AGACCGCATCCAGCCCTTACACCCGCTTCTTGGAGTCTCTCTAGCGGACAGTC 1786
1786 AGACCGCATCCAGCTTCTTACACCCGCTTCTTGGAGTCTCTCTAGCGGACAGTC 1681
1681 AGACCGCATCCAGCTTCTTACACCCGCTTCTTGGAGTCTCTCTAGCGGACAGTC 1681

RESULT 12

US-08-749-907-3
; Sequence 3, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907

FILING DATE: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1577
OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
OTHER INFORMATION: encode the amino acid sequence for the murine Scavenger Recept
US-08-749-907-3
Query Match 76.6%; Score 1369.8; DB 2; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 110 CCCCTTCAGTCCCTGAGCCCGCGAGCCCGCGGCGCACACGCGGACATGGCGGCGAGCCG 169
DB 5 CTCCTTCAGTCCCTGAGCCCGCGAGCCCGCGGCGCACACGCGGACATGGCGGCGAGCTC 64
QY 170 CAGGGCGCGCTGGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGG 229
DB 65 CAGGGCGCGCTGGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGG 124
QY 230 TGTGGTGTATGATCCTCGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289
DB 125 GGTGTGATGATCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
QY 290 CATAGACCCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 349
DB 185 CATAGACCCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 350 GTCCGCTACTTCTTTCAGGTGGTCAATCCCGAGGATCCTTAAAGGGTGAGAGCCAGT 409
DB 245 GTCTGTCTACTTCTTCGAAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCGAGAGCCAGT 304
QY 410 AGTGGCGGAGCGTGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
DB 305 AGTGGCGGAGCGTGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
QY 470 CAATGCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
DB 365 CAATGCAACGACACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
QY 530 GTCCCAAGGCTGAGAGTGATCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
DB 425 GTCCCAAGGCTGAGAGTGATCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
QY 590 AGTAATGATGAGAGCAAGTGTGCGGCTGAGGCTGATGATGATGATGATGATGATGATGAT 649
DB 485 GATATTGATGAGAGCAAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 544
QY 650 CTTGGGCGAGCGTGGCTTTTATGAACCGAAGCAGTTGGTGAGATCCTGTGGGGCTATGAGGA 709
DB 545 CATGGGCGAGCGTGGCTTTTATGAACCGAAGCAGTTGGTGAGATCCTGTGGGGCTATGAGGA 604
QY 710 TCCCTTCGTGAATTTTATCAACAAATACTTACAGACATGTTTCCCATCAAGGGCGAGTT 769
DB 605 TCCCTTCGTGAATTTTATCAACAAATACTTACAGACATGTTTCCCATCAAGGGCGAATTT 664

305 AGTCCGGAGCGTGGACCCCTATGCTACAGGGAGTTTACAGAAAGGTCAACATCACCTT 364
Db
470 CAATGACATGATACATGTGTCTTTTGGAGCACCGCAGCCTCATTTCAGCCGACAG 529
Qy
365 CAATGACACGACACCGTGTCTTTCGTGGAGAACCGCAGCCTCATTTTCAGCCTGACAA 424
Db
530 GTCCCGCTCTGAGAGTGAATACATTAATCTGCTTAACTTCTGCTTTGGGGGGCGC 589
Qy
425 GTGCATGGCTCAGAGTGAATCAATTTGCTTACCTTACATCTTGGTCTTGGGGGGCTC 484
Db
590 AGTAATGATGAGAGCAAGTCTGAGCCTGAAGCTGAAGTGAATGATGATGATGATGATG 649
Qy
485 GATATTGATGAGAGCAAGCTGTGAGCCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 544
Db
650 CTGGGCGCAGCGTCTTATGATGAACGACAGTTGGTGAATCTCTGGGGCTATCAGGA 709
Qy
545 CATGGGCGCAGCGTCTTATGATGAACGACAGTTGGTGAATCTCTGGGGCTATCAGGA 604
Db
710 TCCTCTCGTGAATTTTATCAACAAATACCTTACAGACATGTTCCCATCAAGGGCAAGTT 769
Qy
605 TCCTCTCGTGAATTTTCAACAGTACCTCCAGACATGCTTCCCATCAAGGGCAATTT 664
Db
770 CGGCTGTTTGGATGAAGAACTCAGACTCTGGGCTTTCACGTGTGTTCACGGGCGT 829
Qy
665 TGGCTGTTTGGATGAAGAACTCAGAACTCTGGGCTTTCACGTGTTCACGGGCGT 724
Db
830 CCAGAACTTCAGAAAGTCCACTGGTGGACAGATGGAATGGGCTCAGCAAGTCAACTA 889
Qy
725 CCAGAACTTCAGAGGATTCATCTGGTGGACAAATGGAAGGACTCAGCAAGTCAATTA 784
Db
890 CTGGCTTCAGAGCAGTCAACATGATCAATGGCACTTCCGGGCGAGATGGGCGACCAAT 949
Qy
785 TTGGCTTCAGAGCAGTGAACATGATCAATGGCACTTCCGGGCGAGATGGGCGACCTT 844
Db
950 CATGACACCCGATCTCTCGTGAATTTTCAAGGCTTCCAGCCGAGGATGCAAGTCCATGA 1009
Qy
845 CATGACACCCGATCTCTCGTGAATTTTCAAGGCTTCCAGCCGAGGATGCAAGTCCATGA 904
Db
1010 CACTTACCATGATTCAGGGGTGTTTGAAGCATCCCGACCTATCGCTTCACAGCCCTTAA 1069
Qy
905 GACCTACACGAATCAAGGGGTGTTTGAAGCATTCGCCAGTATCGCTTCACGGCCCGCA 964
Db
1070 AACTTTGTTTGGCAATGGGTCTGTTTACCACCAATGAAGGTTTTCGCCGTCGCTTGA 1129
Qy
965 TACTCTGTTTGGCAATGGGTCTGTTTACCACCAATGAAGGTTTTCGCCGTCGCTTGA 1024
Db
1130 ATCCGGCAATTCAGAAATGTCAGACTTGCAGGTTTGGTGCACCCCTGTTTCTGTCACACC 1189
Qy
1025 GTCTGGCAATTCAGAAATGTCAGACTTGCAGGTTTGGTGCACCCCTGTTTCTCTCCACCC 1084
Db
1190 TCACCTTCTAAGTGCAGACCTGCTGCTATCAGAGCGGTTCTGGGTCTGAACCTGACCC 1249
Qy
1085 CCACCTTTTCAACGCGCAGCCTGTTGTTGTCAGAGGTTTCTGGGTCTGAACCTTAAACC 1144
Db
1250 AAGGGAGCATCTTTGTTCTTGCATCCATCCGCTCAGTGGGATCCCATGAACCTGTTTC 1309
Qy
1145 AAGGGAGCATCTTTGTTCTTGCATCCATCCGCTCAGTGGGATCCCATGAACCTGTTTC 1204
Db
1310 TGTGAAGTTCAGATGAAGCTCTTACATCAAGAGTGTCAAGGGATTTGGGCAACAGGAA 1369
Qy
1205 TGTGAAGATCAGCTGAGCCTTACATCAAACTGTCAAGGGATTCGGGCAACAGGAA 1264
Db
1370 GATCGAGCCCGTGTCTCTCCATGCTGTGTTGTTGAGCAGCGGTGCCATGGGCGCGA 1429
Qy
1265 GATCGAGCCCGTGTCTCTCCATGCTGTGTTGTTGAGCAGCGGTGCCATGGGCGCGA 1324
Db
1430 GCCCTTGAACACAGTCTTACACGAGCTGTTGATGCCCTCAGGATCTTCAAGTATGTGA 1489
Qy
1325 GCCCTTGAACACAGTCTTACACGAGCTGTTGATGCCCTCAGGATCTTCAAGTATGTGA 1384
Db
1490 GTATGTGCTGTGGGGTGGGGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
Qy
1385 GTATGTGCTGTGGGGTGGGGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
Db

1550 CAGCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAAAGGCTCGCAGGATAAGGA 1609
Qy
1445 CAGCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAAAGGCTCGCAGGATAAGGA 1504
Db
1610 GGCCATTCAAGGCTTACTCTGAGTCTCTGATGTCCACAGCTGCCAAGGGCACGCTGTGCA 1669
Qy
1505 GGCCATTCAAGGCTTACTCTGAGTCTCTGATGTCCACAGCTGCCAAGGGCACGCTGTGCA 1564
Db
1670 AGAAGCAAGCTGTAGGTCCCAAGACACACAGAGGCCCCCCCAACCTGATAGCTTGGTC 1729
Qy
1565 AGAAGCAAGCTGTAGGTCCCAAGACACACATTAAGCCCCCCCCAACCTGATAGCTTGGTC 1624
Db
1730 AGAAGCAAGCTGTAGGTCCCAAGACACACCTTCTTGGAGTCTCTCAGCGGACAGTC 1786
Qy
1625 AGAAGCAAGCTGTAGGTCCCAAGACACACCTTCTTGGAGTCTCTCAGCGGACAGTC 1681
Db

RESULT 14

US-09-385-799-3
; Sequence 3, Application US/09385799
; Patent No. 6982688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385,799
; FILING DATE: 30-Aug-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
; encode the amino acid sequence for the murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-385-799-3

Query Match 76.6%; Score 1369.8; DB 3; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

SEQUENCE CHARACTERISTICS:

LENGTH: 1785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1577 /Function = "Nucleotides 51 through 1577 encode the amino acid sequence for the murine Scavenger Receptor Class B1."
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:

PCT-US95-07721-7

Query Match 76.6%; Score 1369.8; DB 6; Length 1785;

Best Local Similarity 88.6%; Pred. No. 0;

Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY	110	CCCTTCAGTCCTGAGCCCGGAGCCCGGGCGGCACACGCGGACATGGCGGCGAGCGC	169
DB	5	CTCCTTCAGTCTCGAGCCCGGAGAGCCCTTCCGCGCACGCGGACATGGCGGCGAGCTC	64
QY	170	CAGGGCGCGTGGTGGCGGTGGGGCTGGGCGTCTGGGGCTGCTGTGCGCTGTGCTCGG	229
DB	65	CAGGGCGCGTGGTGGCGCTGGGGTGGGCGCTGGGGCTGCTGTGCTGCTCGGCTCGG	124
QY	230	TGTGGTATGATCCTCGTGTATGCTCGCTCATCAACACGACGAGTACTGAAGAATGTCCG	289
DB	125	CGTTGTATGATCCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAATGTCCG	184
QY	290	CATGACCCGAGCAGCTGTCTTGCATGTGGAAGGAGATCCCTGTACCTTCTACTTT	349
DB	185	CATGACCCGAGCAGCTGTCTTGCAGATGTGGAAGGAGATCCCGTCCCTTCTACTTT	244
QY	350	GTCCGTCTACTTCTCGAGGTGTCTAATCCAGCAGATCTTAAGGGTGAGAAGCCAGT	409
DB	245	GTCTGTCTACTTCTCGAAGTGTCAACCAACAGAGGTCTCTCAACGCGCAGAGCCAGT	304
QY	410	AGTCCGGAGCGTGGACCCCTATGCTACAGGGAAATCAGACATPAAGCCCAACATCACTT	469
DB	305	AGTCCGGAGCGTGGACCCCTATGCTACAGGGAGTTCAGACAAAGGTCAACATCACTT	364
QY	470	CAATGACAAATGATCTGTGTCTTGTGGAGCACCGCAGCTCCATTTCCAGCGGACAG	529
DB	365	CAATGACAAACGACACCGTGTCTTGTGGAGAACCGCAGCTCCATTTCCAGCTTGACAA	424
QY	530	GTCCACCGCTCTGAGAGTGACTTACATTAATGCTTACCTTAACATTTCTGGTCTGGGGGCGC	589
DB	425	GTGCGATGGCTCAGAGAGTACTATCTGCTTACTGCTTAACTCTTGGTCTGGGGGGCTC	484
QY	590	AGTAATGATGGAGAGCAAGCTCTGAGGCTCTGAAGCTGATGATGATGATGATGATGATGAT	649
DB	485	GATATTGATGGAGAGCAAGCTCTGAGGCTCTGAAGCTGATGATGATGATGATGATGATGAT	544
QY	650	CTTGGGCGAGGTGCTTTATGAACCGAACAGTTGGTGGATCTGTGGGGCTATGAGGA	709
DB	545	CATGGGCGAGGTGCTTTATGAACCGCACAGTTGGTGGATCTGTGGGGCTATGACGA	604
QY	710	TCCCTTCGTGAATTTTATCAACAAATCTTACCAGACATGTTCCCATCAAGGGCAAGTT	769
DB	605	TCCCTTCGTGAATTTTCTCAACAGTACTTCCAGACATGCTTCCCATCAAGGGCAAGTT	664
QY	770	CGGCTGTGTTGTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGCGT	829
DB	665	TGGCTGTGTTGTGGATGAACAACTCGAATCTTGGGGTCTTCACTGTCTTTCACGGGCGT	724
QY	830	CCGAACTTCAGCAGATCCACCTGGGTGGACAGATGGAAATGGGCTCAGCAAGGTCAACTA	889
DB	725	CCGAAATTCAGCAGGATTCATCTGTTGGGACAAATGGAAACGGACTCAGCAAGATCGATTA	784

QY	890	CTGGCAATTCAGAGCAGTGCACATGATCAATGGCACTTCCGGGCGAGATGTGGGCAACATT	949
DB	785	TTGGCAATTCAGAGCAGTGTAAATGATCAATGGCACTTCCGGGCGAGATGTGGGCAACATT	844
QY	950	CATGACACCCAGTCTCGTGGAAATCTTCACTCGGAGGCTGCAGGTCTATGAGCT	1009
DB	845	CATGACACCCGAATCTCGTGGAAATCTTCAAGCCGGAGGATGCAGGTCTCATGAAGCT	904
QY	1010	CACCTACCATGATTCAGGGGTGTTGAAGGCATCCCACTATCGCTTCACAGCCCTTAA	1069
DB	905	GACCTACAAGAAATCAAGGTGTTTGAAGCAATCCACGTATCGCTTCAGGCCCTCGA	964
QY	1070	AACTTTGTTGGCAATGGGTCTGTATACCCCAATGAAGTTCCTGCGGTGCTTGA	1129
DB	965	TACTCTGTTTGCACAGCGGTCTGTACCCACCAACGAAGGCTTCTGCCCATGCCGAGA	1024
QY	1130	ATCCGGCATTCAAATGTGAGCACTTCAGAGTTGGTGCACCCCTGTTTCTGTCAACCC	1189
DB	1025	GTCTGGCAATTCAGAAATGTGAGCACTTCAGAGTTGGTGCACCCCTGTTTCTCTCCACCC	1084
QY	1190	TCACCTTACAAATGCAGACCCCTGTGTATCAGAAGCGTTCCTGGGTCTGAACCCCTGACCC	1249
DB	1085	CCACTTTTACAAGCGGACCCCTGTGTGTGCAAGCTGTCTTGGTCTGAACCCCTTAAACC	1144
QY	1250	AAGGGAGCAATCTTTGTTCTTGAATCCATCCGCTCACTGGGATCCCATGAACCTGTTT	1309
DB	1145	AAGGAGCAATCTTTGTTCTTGAATCCATCCGCTCACTGGATCCCATGAACCTGTTT	1204
QY	1310	TGTGAAGTTGCAAGTAAGCTCTTACATCAAGCTGTCAAGGGCATTTGGGCAACAGGGAA	1369
DB	1205	TGTGAAGATGCAGCTGAGCTCTATCAATAATCTGTCAAGGGCATTCGGGCAACAGGGAA	1264
QY	1370	GATCAGACCCGTGCTCTCCATTCGTGTGTTTGAAGAGAGCGGTGCCATGGGCGCGA	1429
DB	1265	GATCAGACCCGTGCTCTCCATTCGTGTGTTTGAAGAGAGCGGTGCCATGGGCGCGA	1324
QY	1430	GCCTCTGAAACAGCTTCTACACGAGCTGTGTGATGCCCCCAGGTACTTTCAGTATGCA	1489
DB	1325	GCCTCTGAGCACGTTCTACACGAGCTGTGTGATGCCCCCAGGTACTTTCAGTATGCA	1384
QY	1490	GTATGTGCTGTGGGGCTGGGCGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1549
DB	1385	GTATGTGCTGTGGGGCTGGGCGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1444
QY	1550	CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCCGAGGATAAGGA	1609
DB	1445	CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTAGTAAAGGGCTCCGAGGATAAGGA	1504
QY	1610	GGCAATTCAGGCTTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAAGGTGTGCA	1669
DB	1505	GGCAATTCAGGCTTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAAGGTGTGCA	1564
QY	1670	AGAGCCAAAGTGTAGGTTCCTCAAGACACACAGAGCCCTCCCAACCTGATAGCTTGGTC	1729
DB	1565	AGAGCCAAAGTGTAGGTTCCTCAAGACACATTAAGCCCTCCCAACCTGATAGCTTGGTC	1624
QY	1730	AGACCAAGCATCCAGCCCTTACACCCGCTTCTTGAAGTCTCTCAGCGGACAGTC	1786
DB	1625	AGACCAAGCATCCAGTCCCTTACACCCGCTTCTTGAAGTCTCTCAGCGGACAGTC	1681

Search completed: February 23, 2006, 18:13:43

Job time : 310.759 secs

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 156..1683
OTHER INFORMATION: /function= "Nucleotides 156 through 1683
encode the amino acid sequence for the Hamster Scavenger Receptor Class
B-I."
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-178-611-1

Query Match 100.0%; Score 1788; DB 6; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTGCTGGAAGCTG 60
DB 1 GCCACCTGCAGGGCTACTGCTGCTCCGGCCACTGCTGAGACTCACCTGCTGGAAGCTG 60

QY 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 AGCCTCGGCTTCTGTCATCTCTGTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120

QY 121 CTTGAGCCCGCGAGCCCGGCGCCGACACGCGGACATGCGCGGCGAGCGCGCGCT 180
DB 121 CTTGAGCCCGCGAGCCCGGCGCCGACACGCGGACATGCGCGGCGAGCGCGCGCT 180

QY 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
DB 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240

QY 241 TCCTCGTGATGCTCCCTCGCTCATCAAAACAGCAGAGTACTGAAGATGTCGCGATAGACCCCA 300
DB 241 TCCTCGTGATGCTCCCTCGCTCATCAAAACAGCAGAGTACTGAAGATGTCGCGATAGACCCCA 300

QY 301 GCAGCCTGTCCTTTGCAATGGAAGAGATCCCTGTACCCCTTCTACTTGTCCGCTTACT 360
DB 301 GCAGCCTGTCCTTTGCAATGGAAGAGATCCCTGTACCCCTTCTACTTGTCCGCTTACT 360

QY 361 TCTTCGAGGTGCTCAATCCCGAGGAGATCTTAAGGCTGAGAGCCAGTGTGGGAGC 420
DB 361 TCTTCGAGGTGCTCAATCCCGAGGAGATCTTAAGGCTGAGAGCCAGTGTGGGAGC 420

QY 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCAACATCACCTTCAATGACAAATG 480
DB 421 GTGACCCCTATGCTACAGGGAATTCAGACATAGGCAACATCACCTTCAATGACAAATG 480

QY 481 ATACTGTGTCCTTTGTGGAGCACCGGAGCTTCCATTTCCAGCCGAGCAGGTCCACGGCT 540
DB 481 ATACTGTGTCCTTTGTGGAGCACCGGAGCTTCCATTTCCAGCCGAGCAGGTCCACGGCT 540

QY 541 CTGAGAGTACTACATTTACTGCTTAACATTTCTGGTCTTGGGGGGGCGAGTAATGATGG 600
DB 541 CTGAGAGTACTACATTTACTGCTTAACATTTCTGGTCTTGGGGGGGCGAGTAATGATGG 600

QY 601 AGAGCAAGTCTGACGGCTGAAGCTGATGATGACCTTTGGGGGGGCGAGTAATGATGG 660
DB 601 AGAGCAAGTCTGACGGCTGAAGCTGATGATGACCTTTGGGGGGGCGAGTAATGATGG 660

QY 661 GTGCTTTTATGAACCGAACAGTGTGGTGGAGATCTGTGGGGGCTATGAGGATCCCTTCGTGA 720
DB 661 GTGCTTTTATGAACCGAACAGTGTGGTGGAGATCTGTGGGGGCTATGAGGATCCCTTCGTGA 720

QY 721 ATTTTATCAACAAATATTACAGACATGTTCCCATCAAGGGGCAAGTTCGGCTGTTTG 780
DB 721 ATTTTATCAACAAATATTACAGACATGTTCCCATCAAGGGGCAAGTTCGGCTGTTTG 780

QY 781 TTGAGATGAACACTCAGACTCTGGCTTCTCACTGTGTTCAAGGGGCTCCAGACTTCA 840
DB 781 TTGAGATGAACACTCAGACTCTGGCTTCTCACTGTGTTCAAGGGGCTCCAGACTTCA 840

QY 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCGCATTCAG 900

DB 841 GCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTACTGCGCATTCAG 900
QY 901 AGCAGTGCAACATGATCAATGGCACTTCGGGGCAGATGTGGGCACCATTCATCAGACCCC 960
DB 901 AGCAGTGCAACATGATCAATGGCACTTCGGGGCAGATGTGGGCACCATTCATCAGACCCC 960
QY 961 AGTCCTCGCTGGAAATCTTTTCAGTCGGAAGCCCTGCGAGTCTATGAAGCTCAGCTACCATG 1020
DB 961 AGTCCTCGCTGGAAATCTTTTCAGTCGGAAGCCCTGCGAGTCTATGAAGCTCAGCTACCATG 1020

QY 1021 ATTTCAGGGTGTGGAAGGATCCCACTATCGCTTCACAGCCCTTAAACCTTTGTTG 1080
DB 1021 ATTTCAGGGTGTGGAAGGATCCCACTATCGCTTCACAGCCCTTAAACCTTTGTTG 1080

QY 1081 CCAATGGGCTGTGTTTACCAACCAATGAAGTTCCTGCGGCTGCTTGAATCGGCAATC 1140
DB 1081 CCAATGGGCTGTGTTTACCAACCAATGAAGTTCCTGCGGCTGCTTGAATCGGCAATC 1140

QY 1141 AAAATGTCAGCACTTCGAGGTTTGTGTCACCCCTGTTTCTGTCAACCCCTCACTTCTTACA 1200
DB 1141 AAAATGTCAGCACTTCGAGGTTTGTGTCACCCCTGTTTCTGTCAACCCCTCACTTCTTACA 1200

QY 1201 ATGCGAGCCCTGTGCTATCAGAAAGCCGTTCTGGGCTGTAACCCCTGACCCCAAGGAGCAT 1260
DB 1201 ATGCGAGCCCTGTGCTATCAGAAAGCCGTTCTGGGCTGTAACCCCTGACCCCAAGGAGCAT 1260

QY 1261 CTTTGTTCCTTGACATCCATCCGCTCACTGGGATCCCATGAACTGTTCTGTGAAGTTGC 1320
DB 1261 CTTTGTTCCTTGACATCCATCCGCTCACTGGGATCCCATGAACTGTTCTGTGAAGTTGC 1320

QY 1321 AGATAAGCCCTTACATCAAGAGCTGTCAAGGGCAATGGGCAAAACAGGGAAGATCGAGCCCG 1380
DB 1321 AGATAAGCCCTTACATCAAGAGCTGTCAAGGGCAATGGGCAAAACAGGGAAGATCGAGCCCG 1380

QY 1381 TGCTCTCCCATGCTGTGTTTGAAGAGCGGTGCGCATGGGCGGCGAGCCCTGAAACA 1440
DB 1381 TGCTCTCCCATGCTGTGTTTGAAGAGCGGTGCGCATGGGCGGCGAGCCCTGAAACA 1440

QY 1441 CGTTCTACAGCAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 CGTTCTACAGCAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

QY 1501 TGGGGCTGGGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 TGGGGCTGGGCGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

QY 1561 AATGCTTTTATTTTGGAGTGTGTAATAAAGGGCTCGCAGGATAGAGGGCCATTCAGG 1620
DB 1561 AATGCTTTTATTTTGGAGTGTGTAATAAAGGGCTCGCAGGATAGAGGGCCATTCAGG 1620

QY 1621 CCTACTCTGAGTCTGATGCTACAGCTGCGCAAGGGCAGGCTGCTGCAAGAGCCAAAGC 1680
DB 1621 CCTACTCTGAGTCTGATGCTACAGCTGCGCAAGGGCAGGCTGCTGCAAGAGCCAAAGC 1680

QY 1681 TGTAGGGTCCCAAGACACACAGGAGCCCGCCCAACCTGATGCTGCTGAGCAGCCAT 1740
DB 1681 TGTAGGGTCCCAAGACACACAGGAGCCCGCCCAACCTGATGCTGCTGAGCAGCCAT 1740

QY 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGTCCG 1788
DB 1741 CCAGCCCTTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGTCCG 1788

RESULT 3

US-10-164-863-1
; Sequence 1, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; APPLICANT: Miettinen, Helena
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094

; CURRENT APPLICATION NUMBER: US/10/164,863
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (156)..(1683)
; OTHER INFORMATION: Encodes amino acid sequence for the Hamster Scavenger Receptor Cl
; OTHER INFORMATION: ass B-1
US-10-164-863-1

Query Match 100.0%; Score 1788; DB 6; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCAGGCGTACTGCTGCTCCGGCCACTGCTGCTGAGACTCACCTTCTGCGAACTG 60
DB 1 GCCACCTGCAGGCGTACTGCTGCTCCGGCCACTGCTGCTGAGACTCACCTTCTGCGAACTG 60
QY 61 AGCTCGGCTTCTGTCATCTCTGTGCGCTCTGTGCGCTCTGTGCGCTCTGTGCGCTCTGTG 120
DB 61 AGCTCGGCTTCTGTCATCTCTGTGCGCTCTGTGCGCTCTGTGCGCTCTGTGCGCTCTGTG 120
QY 121 CCTGAGCCCCGCGAGCCCGGCGCACACGCGGACATGCGCGCAGCGCCAGCGCGCGCT 180
DB 121 CCTGAGCCCCGCGAGCCCGGCGCACACGCGGACATGCGCGCAGCGCCAGCGCGCGCT 180
QY 181 GGGTGGCGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 240
DB 181 GGGTGGCGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 240
QY 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGACTGTAAGAATGTCCGATAGACCCCA 300
DB 241 TCCTCGTGATGCCCTCGCTCATCAACAGCAGGACTGTAAGAATGTCCGATAGACCCCA 300
QY 301 GCAGCTGCTCTTTGCAATGTGAAGAGATCCTGTACCCTTCTACTTCTCGCTCTACT 360
DB 301 GCAGCTGCTCTTTGCAATGTGAAGAGATCCTGTACCCTTCTACTTCTCGCTCTACT 360
QY 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGTGAGAGCCAGTAGTCCGGAGC 420
DB 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGGTGAGAGCCAGTAGTCCGGAGC 420
QY 421 GTGACCTATGTCTACAGGGAATTCAGACATTAAGGCCAATCATCTTCAATGACATG 480
DB 421 GTGACCTATGTCTACAGGGAATTCAGACATTAAGGCCAATCATCTTCAATGACATG 480
QY 481 ATACTGTGCTCTTTGTGGACACCGCAGCTCCATTTCCAGCCGACAGTCCACCGCT 540
DB 481 ATACTGTGCTCTTTGTGGACACCGCAGCTCCATTTCCAGCCGACAGTCCACCGCT 540
QY 541 CTGAGAGTACTACATTAATCTGCTAACATTTCTGCTTTGGGGGGCGCAGTAATATGG 600
DB 541 CTGAGAGTACTACATTAATCTGCTAACATTTCTGCTTTGGGGGGCGCAGTAATATGG 600
QY 601 AGAGCAAGTCTGAGGCTGAGCTGATGATGACCTTTGGGGCTGGCCACCTTGGGGCAGC 660
DB 601 AGAGCAAGTCTGAGGCTGAGCTGATGATGACCTTTGGGGCTGGCCACCTTGGGGCAGC 660
QY 661 GTGCTTTATGAACCGAAAGTGTGTCAGATCCTGTGGGCTATGAGATCCCTTGTGTA 720
DB 661 GTGCTTTATGAACCGAAAGTGTGTCAGATCCTGTGGGCTATGAGATCCCTTGTGTA 720
QY 721 ATTTTATCAAAATACTTACCAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTGTTG 780

DB 721 ATTTTATCAAAATACTTACCAGACATGTTCCCATCAAGGGCAAGTTCGGCTGTGTTG 780
QY 781 TTGAGATGAACAATCTCAGACTCTGGGCTCTTCACTGTGTTCAAGGGCGTCCAGAACTTCA 840
DB 781 TTGAGATGAACAATCTCAGACTCTGGGCTCTTCACTGTGTTCAAGGGCGTCCAGAACTTCA 840
QY 841 GCAAGATCCACCTGGTGGACAGATGGAATGGCTCAGCAAGGTCAACTACTGGCATTCAG 900
DB 841 GCAAGATCCACCTGGTGGACAGATGGAATGGCTCAGCAAGGTCAACTACTGGCATTCAG 900
QY 901 AGCAGTGCACATGATCAATGGCACTTCGGGCGAGATGCGGACCAATTCATGACACCCC 960
DB 901 AGCAGTGCACATGATCAATGGCACTTCGGGCGAGATGCGGACCAATTCATGACACCCC 960
QY 961 AGTCTCTGCTGAAATCTTCACTCGGAGCCTGAGGTCTATGAGCTCACTACCATG 1020
DB 961 AGTCTCTGCTGAAATCTTCACTCGGAGCCTGAGGTCTATGAGCTCACTACCATG 1020
QY 1021 ATTACGGGGTGTGGAAGGCATCCCACTATCGCTTCAAGCCCTCAAACTTTGTTG 1080
DB 1021 ATTACGGGGTGTGGAAGGCATCCCACTATCGCTTCAAGCCCTCAAACTTTGTTG 1080
QY 1081 CCAATGGGCTCTGTTTACCAACCAATGAAGTTCCTGCCGCTGCTTGAATCGGCAATTC 1140
DB 1081 CCAATGGGCTCTGTTTACCAACCAATGAAGTTCCTGCCGCTGCTTGAATCGGCAATTC 1140
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DB 1141 AAAATGTACGACTTGCAGGTTTGGTGACCCCTGTTCTGTCAACCCCTCACTTCTACA 1200
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DB 1201 ATGCAGACCTCTGTCTATCAGAAAGCGTTCTGGGCTGTAACCTGACCCCAAGGAGCAT 1260
QY 1261 CTTTGTCTTCAATCCGCTCATCGGTCATCGGATCCCAATGAATCTGTTGTGAAGTTGC 1320
DB 1261 CTTTGTCTTCAATCCGCTCATCGGTCATCGGATCCCAATGAATCTGTTGTGAAGTTGC 1320
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DB 1321 AGATAGCCCTTACATCAAGCTGTCAGGGCATTTGGGCAACAGGGAAGATCGAGCCCG 1380
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DB 1381 TGGTCTCTCCATTTGCTGTGTTGAGCAGAGCGTGCCATGCGCGCGAGCCCTGAACA 1440
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DB 1441 CGTTCTACACGAGCTGTGCTGATGCGCCAGGTACTTCAGTATGTGCAATGTGCTGC 1500
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DB 1501 TGGGGCTGGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 AATGCTTTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAGAGAGCCATTCAG 1620
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QY 1681 TGTAGGGTCCCAAGACACACGAGCCCGCCCACTGATAGCTGCTGCTGCTGCTGCTGCTG 1740
DB 1681 TGTAGGGTCCCAAGACACACGAGCCCGCCCACTGATAGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 CCAGCCCTTACACCCCGCTTCTTGAAGTCTCTCTCAGCGGACAGTCCG 1788
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; Sequence 1, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MT8299
; CURRENT APPLICATION NUMBER: US/10706,073
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Hamster
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (156)..(1683)
; OTHER INFORMATION: Encodes amino acid sequence for the Hamster
; OTHER INFORMATION: Scavenger Receptor Class B-1
; US-10-706-073-1

Query Match 100.0%; Score 1788; DB 7; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACCTGCGAGGCTACTGCTGCTCCGGCCACTGCTGAGACTCCTTGTGGAAGCTG 60
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QY 61 AGCTCGGCTTCTGCTCATCTCTGCGCTCTGTCGCTTCTGTCGCTGCCCTTCAATC 120
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QY 121 CCTGAGCCCGCGAGCCCGCGCCGCAACAGCGGAGCATGGGCGGCGAGCGCGCGCT 180
DB 121 CCTGAGCCCGCGAGCCCGCGCCGCAACAGCGGAGCATGGGCGGCGAGCGCGCGCT 180

QY 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 240
DB 181 GGGTGGCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 240

QY 241 TCCTCGTGATGCTGCTCATCAACAGCAGGCTACTGAAGATGTCCGATAGACCCCA 300
DB 241 TCCTCGTGATGCTGCTCATCAACAGCAGGCTACTGAAGATGTCCGATAGACCCCA 300

QY 301 GCAGCTGTCTTTGCAATGTGAAGGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360
DB 301 GCAGCTGTCTTTGCAATGTGAAGGAGATCCCTGTACCTTCTACTTGTCCGTCTACT 360

QY 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAAGGCTGAAGCCAGTAGTTCGGGAGC 420
DB 361 TCTTCGAGGTGGTCAATCCAGCGAGATCCTAAAGGCTGAAGCCAGTAGTTCGGGAGC 420

QY 421 GTGACCTATGCTACAGGGAATTCAGACATAGGCAATCATTCAATGACATG 480
DB 421 GTGACCTATGCTACAGGGAATTCAGACATAGGCAATCATTCAATGACATG 480

QY 481 ATACTGTGCTCTTTGTGGAGCAGCGAGCTTCAATTTCCAGCCGAGAGTCCACGGCT 540
DB 481 ATACTGTGCTCTTTGTGGAGCAGCGAGCTTCAATTTCCAGCCGAGAGTCCACGGCT 540

QY 541 CTGAGAGTACTACATTAATCTGCTTAACATTTCTGGTCTTTGGGGGGCGCAGTAATG 600
DB 541 CTGAGAGTACTACATTAATCTGCTTAACATTTCTGGTCTTTGGGGGGCGCAGTAATG 600

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DB 601 AGACCAAGTCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660
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QY 721 ATTTTATCAACAATATCTTACAGACATGTTCCCATCAAGGCAAGTTCCGCTGTTG 780
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QY 781 TTGAGATGAACAACTCTGAGCTCTGGGCTCTTCACTGTGTTACGGGCTCCAGAACTTCA 840
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QY 901 AGCAGTGCAACATGATCAATGGCACTTCGGGCGAGATGTGGGCAACCATTCATGACACCCC 960
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DB 1021 ATTCAGGGGTGTTTGAAGGCATCCCACTATCGCTTTCACAGCCCTTAAACTTTGTTG 1080

QY 1081 CCAATGGGCTGTTTACCAACCAATGAAAGTTTTCGCGCTTGAATCCGGCATTC 1140
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QY 1321 AGATAAGCTCTTACATCAAGCTGTCAAGGCAATTCGGGCAACAGGAGATCGAGCCCG 1380
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QY 1621 CTTACTCTGAGTCTCTGATGTCACAGCTGCCAAGGCGACGCTGCTGCAAGAGCAAGCAAGC 1680
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QY 1681 TGTAGGGTCCCAAGACACACAGAGCCCCCCCCCACTGATAGCTTGGTTCAGACCCCAT 1740
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665	DB	TGCGCTGTTTGGTGGATGAACAACTCGAAATCTTGGGGTCTTCACTGCTTTCACGGCGGT	724
830	QY	CCAGAACTTCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTA	889
725	DB	CCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAACTCAGCAAGATCGATT	784
890	QY	CTGGCAATTCAGACGATGCAACATGATCAATGGCACTTCGGGCGAGATGTGGGCAACCAT	949
785	DB	TTGGCAATTCAGACGATGCAACATGATCAATGGCACTTCGGGCGAGATGTGGGCGACCCCT	844
950	QY	CATGACACCCCACTCTCGCTGGAAATCTTTCAGTCCGGAAGCCCTGCAGGTCTATGAAGCT	1009
845	DB	CATGACACCCCAATCTCTCGCTGGAAATCTTTCAGTCCGGAAGCCCTGCAGGTCTCATGAAGCT	904
1010	QY	CACCTACCATGATTCAGGGGTGTTGAAGGATCCCACTATCGCTTCACAGCCCTAA	1069
905	DB	GACCTACACGAATCAAGGGTGTGTAAGGCAATTCACCGTATCGCTTCACGGCCCCGGA	964
1070	QY	AACCTTTGTTTGCCAATGGGTCGTGTTACACCAACCAATGAAGGTTCTGCGCGGTGCTTGA	1129
965	DB	TACTCTGTTTGGCAACGGGTCCGTCTACCCACCAACGAAGGCTTCTGCCCATGCGGAGA	1024
1130	QY	ATCCGGCAATTCAAAATGTCAGCACTTTCAGGTTTGGTGACCCCTGTTTCTGTCAACACC	1189
1025	DB	GTCCTGGCAATTCAGAAATGTCAGCACTTCAGGTTTGGTGCGCTCTGTTTCTCTCCACCC	1084
1190	QY	TCACTTCTCAATTCAGACACCTGTGCTATCAGAAAGCGGTTCTGGGCTGAACCCCTGACCC	1249
1085	DB	CCACTTTTACAAACGCGCACCTGTGTGTTGTCAGAAAGCTGTTCTTTGGTCTGAACCTTAACCC	1144
1250	QY	AAGGGAGCATCTCTTGTTCCTTCACATCCATCCGCTCAGTGGATCCCATGAAGCTGTTTC	1309
1145	DB	AAAGGAGCATCTCTTGTTCCTTCAGACATCCATCCGCTCAGTGGATCCCATGAAGCTGTTTC	1204
1310	QY	TGTGAAGTTGCGAGTAAGCCCTCTACATCAAGCTGTCAAGGGCAATTTGGGCAAAACAGGAA	1369
1205	DB	TGTGAAGATGCAGCTGAGCCCTCTACATCAATCTGTCAAGGGCATCGGCAAAACAGGAA	1264
1370	QY	GATCGAGCCCGTGGTCTCCCATCTGTGTGGTTTGACAGAGCGGTGCCATATGGGCGGCGA	1429
1265	DB	GATCGAGCCAGTAGTTCTGTGCGTTGTGCTGTGTCGAAACAGAGCGGAGCAATGGGTGGCAA	1324
1430	QY	GCCCTCTGAACACAGTTTTCACACGACGTGTGCTGATGATGCCCCAGGTACTTCAGTATGTGCA	1489
1325	DB	GCCCTCTGAGCACGTTTTCACACGACGTGTGCTGATGATGCCCCAGGTCTTTCATCAGCGCA	1384
1490	QY	GTAATGCTGCTGGGGCTGGGCGGCTCTCTGCTGCTGGTGGCGCTCATCTACCAAGTTGCG	1549
1385	DB	GTAATGCTGCTGGGGCTGGGCGGCTCTCTGCTGCTGGTGGCGCTCATCTACCAAGTTGCG	1444
1550	QY	CAGCCAGGAGAAATGCTTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGATTAAGGA	1609
1445	DB	CAGCCAGGAGAAATGCTTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGATTAAGGA	1504
1610	QY	GGCCATTCAGGCGCTACTCTGAGTCTCTGATGTACACAGCTGCCAAGGGCACGGTGTGCA	1669
1505	DB	GGCCATTCAGGCGCTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGGCACGGTGTGCA	1564
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1565	DB	AGAAGCAAGCTCTAGGGTCCCTGAAGACACTATAAGCCCCCCCCAACTGATAGTTGGTCT	1624
1730	QY	AGACCAAGCCATCAGGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC	1786
1625	DB	AGACCAAGCCATCAGGTCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTC	1681

RESULT 12

US-10-178-611-3

US-10-178-611-3
; Sequence 3, Application US/10178611

Sequence 3, Application US/10175A1
Publication No. US20030167475A1

; PUBLICATION NO. CS2003
; GENERAL INFORMATION:

APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky

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1 TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
2
3 NUMBER OF SEQUENCES: 4
4
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
7 ADDRESS: 2800 One Atlantic Center
8 STREET: 1201 West Peachtree Street
9 CITY: Atlanta
10 STATE: Georgia
11 COUNTRY: USA
12 ZIP: 30309-3450
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/10/178,611
22 FILING DATE: 24-Jun-2002
23 CLASSIFICATION: <Unknown>
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US/08/749,907
27 FILING DATE: <Unknown>
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Pabst, Patrea L.
31 REGISTRATION NUMBER: 31,284
32 REFERENCE/DOCKET NUMBER: MI17538
33
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (404) 873-8794
36 TELEFAX: (404) 873-8795
37
38 INFORMATION FOR SEQ ID NO: 3:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 1785 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: double
43 TOPOLOGY: linear
44
45 MOLECULE TYPE: DNA (genomic)
46 HYPOTHETICAL: NO
47 ANTI-SENSE: NO
48 FEATURE:
49
50 NAME/KEY: CDS
51 LOCATION: 51..1577
52
53 OTHER INFORMATION: /Function = "Nucleotides 51 thro
54 encode the amino acid sequence for the murine Scaveng
55 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
56
57 US-10-178-611-3

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Query Match	76.6%	Score 1369.8	DB 6	Length 1785
Best Local Similarity	88.6%	Pred. No. 0		
Matches 1495	Conservative 0	Mismatches 192	Indels 0	Gaps 0
Qy	110	CCCTTCAGTCCCTGAGCCCGGAGCCCGGCGCCGACACGCGGACATGCGCGCAGCGC	169	
Db	5	CTCCTTCAGTCTGAGCCCGGAGAGCCCTTCGCGCAGCGGACATGCGCGCAGCTC	64	
Qy	170	CAGGGCGCGCTGGGTGGCGGTGGGGCTGGGCGCTGCTGGGGCTCTCTGTGCCTCTGTGCTCGG	229	
Db	65	CAGGGCGCGCTGGGTGGCGCTGGGGCTGGGGCGCCCTGGGGCTGCTGTTGCTGGCGCTCGG	124	
Qy	230	TGTGGTTATGATCCTCGTGAATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAATGTCCG	289	
Db	125	CGTTGTATGATCCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAATGTCCG	184	
Qy	290	CATGACCCCGACAGCGCTGCTCTTGCATGTGGAGGAGATCCCTGTACCCCTTCTACTT	349	
Db	185	CATGACCCCGACAGCGCTGCTCTTGGGATGTGGAAGGAGATCCCCGTCCCTTCTACTT	244	
Qy	350	GTCCGTCTACTTCTTCGAGTGTCTAATCCACCGAGATCCTAAAGGGTGAGAAGCCAGT	409	
Db	245	GTCTGTCTACTTCTTCGAGTGTCAACCCAAACAGGTCTCTCAA CGGCGAGAAGCCAGT	304	
Qy	410	AGTGGGGAGCGTGGACCTTATGCTACAGGGAATTCAGACATATAGGCCAAATACACCTT	469	
Db	305	AGTCCGGGAGCGTGGACCTTATGCTACAGGAGTTCAGACAAAGGTCAACATCACCTT	364	

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QY 470 CAATGACATGATATCTGTGCTCTTTGTGGAGCACCGCAGCCTCAATTTCCAGCCGACAG 529
Db 365 CAATGACACGACACCGGTGCTCTGTGGAGAACCGCAGGCTCAATTTCCAGCCTGACAA 424
QY 530 GTCCACGGCTCTGAGAGTGAATACATTAATGATGCTTAACTTCTGCTGTGGGGGGCGC 589
Db 425 GTCCGATGGCTCAGAGAGTGAATACATTAATGATGCTTAACTTCTGCTGTGGGGGGCTC 484
QY 590 AGTAATGATGAGACGAGTCTGAGGCTGAGGCTGAGTGAATGATGATGATGATGATGATG 649
Db 485 GATATGATGAGAGCAGGCTGTGAGCCTGAGGCTGAGTGAATGATGATGATGATGATGATG 544
QY 650 CTTGGGCGACGCTGCTTATGAAACGAAACAGTTGATGATGATGATGATGATGATGATGAT 709
Db 545 CATGGGCGACGCTGCTTATGAAACGAAACAGTTGATGATGATGATGATGATGATGATGATG 604
QY 710 TCCTCTGCTGAATTTATCAACAAATATCTTACAGACATGTTCCCTCATCAAGGGCAAGTT 769
Db 605 TCCTCTGCTGAATTTATCAACAGTACCTCCAGACATGCTTCCCTCATCAAGGGCAAAAT 664
QY 770 CGGCTGTTTGTGAGATGAACACTCAGACTCTGGGCTCTTCACTGTGTTACGGGCGT 829
Db 665 TGGCCTGTTTGTGGGATGAACACTCGAATTTCTGGGCTCTTCACTGTGTTACGGGCGT 724
QY 830 CCAAGACTTCCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTA 889
Db 725 CCAGATTTCCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCAATTA 784
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Db 785 TTGGCATTCAGAGCAGTGAACATGATCAATGGCACTTCCGGGAGATGTTGGGCAACAT 844
QY 950 CATGACACCCAGTCTCGCTGGAAATCTTTCAGTCCGGAAGCCTGCAAGTCTATGAAGCT 1009
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QY 1010 CACTCATCATGATTTCAGGGGTGTTTGAAGGCATCCACCATCTGCTTTCACACCCCTTAA 1069
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QY 1070 AACTTTGTTTCCCAATGGGCTGTGTTTACCCACCAATGAAGGTTTCTGCGCGTGCCTTGA 1129
Db 965 TACTCTGTTTCCCAATGGGCTGTGTTTACCCACCAATGAAGGTTTCTGCGCGTGCCTTGA 1024
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Db 1025 GTCTGGCATTCAGAAATGTCAGCCTGTCAGGTTTGTGCGCCTCTGTTTCTCTCCACCC 1084
QY 1190 TCACCTTCAAAATGTCAGACCTGTCATCAGAAAGCCTGTTCTGCTGCTGAACCCCTGACC 1249
Db 1085 CCACCTTTTCAACGCCGACCTGTTTGTGTCAGAAAGCTGTTCTGCTGCTGAACCCCTGACC 1144
QY 1250 AAGGGAGCATTTCTTTGTTCTTACATCCATCCGCTCAGTGGATCCCCATGAATGTTTC 1309
Db 1145 AAGGGAGCATTTCTTTGTTCTTACATCCATCCGCTCAGTGGATCCCCATGAATGTTTC 1204
QY 1310 TGTGAAGTTCAGATTAAGCCTCTACATCAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAA 1369
Db 1205 TGTGAAGATGAGTGAAGCCTCTACATCAAAATCTGTCAAGGGCATTTGGGCAAAACAGGGAA 1264
QY 1370 GATCGAGCCGCTGCTCTCCATTTGCTGCTTGTGAGCAGAGCGGTGCCATGGGCGGCGA 1429
Db 1265 GATCGAGCCGCTGCTCTCCATTTGCTGCTTGTGAGCAGAGCGGTGCCATGGGCGGCGA 1324
QY 1430 GCCCTTGAACACAGTCTTACACGAGCTGGTGTGATGCTCCCGAGTACTTTCAGTATGTGCA 1489
Db 1325 GCCCTTGAACACAGTCTTACACGAGCTGGTGTGATGCTCCCGAGTACTTTCAGTATGTGCA 1384
QY 1490 GTATGCTGCTGGGGCTGGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
Db 1385 GTATGCTGCTGGGGCTGGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
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QY 1550 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAAAGGGCTCCGAGGATAAGGA 1609
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QY 1610 GGCCATTCAGGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAACGGTGTGCA 1669
Db 1505 GGCCATTCAGGGCTACTCTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAACGGTGTGCA 1564
QY 1670 AGAAGCCAGCTGTAGGTGCCAAGACACACAGAGCCCCCCCCAACCTCATAGCTTGGTC 1729
Db 1565 AGAAGCCAGCTGTAGGTGCCAAGACACACAGAGCCCCCCCCAACCTCATAGCTTGGTC 1624
QY 1730 AGACAGCCCATCCAGCCCCCTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGTC 1786
Db 1625 AGACAGCCCATCCAGCCCCCTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGTC 1681
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RESULT 13

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US-10-164-863-3
; Sequence 3, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; APPLICANT: Miettinen, Helena
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)..(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine Scavenger Receptor
; OTHER INFORMATION: Class BI
US-10-164-863-3
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Query Match 76.6%; Score 1389.8; DB 6; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
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QY 110 CCCCCTTCAGTCCCTGAGCCCCCGGAGCCCGGCGCACACGCGGACATGGGGGCGAGCGC 169
Db 5 CTCCTTCAGTCCCTGAGCCCCCGGAGCCCGGCGCACACGCGGACATGGGGGCGAGCTC 64
QY 170 CAGGGCGCGCTGGTGGCGGTGGGGCTGCGTGGGGCTGCTGTGGCGCTGTGCTCGG 229
Db 65 CAGGGCGCGCTGGTGGCGGTGGGGCTGCGTGGGGCTGCTGTGGCGCTGTGCTCGG 124
QY 230 TGTGGTTATGATCCTCGTGATGCCCTCGCTCATCAAAACAGCAGGTAATGATGTCG 289
Db 125 CGTTGTGATGATCCTCATGGTGCCTCCCTCATCAAGCAGCAGGTCCTCAAGAATGTCG 184
QY 290 CATAGACCCAGCAGCCTGCTCTTTCGAATGTGGAGGAGATCCCTGTACCTTCTACTTT 349
Db 185 CATAGACCCAGCAGCCTGCTCTTTCGAATGTGGAGGAGATCCCTGTACCTTCTACTTT 244
QY 350 GTCGCTACTACTTCTTCGAGGTGGTCAATCCAGCGAGATCTCTAAAGGGTGAGAGCCAGT 409
Db 245 GTCTGTCTACTTCTTCGAAAGTGGTCAACCCAAACGAGGTCTCTCAACGCGCAGAGCCAGT 304
QY 410 AGTGGGGAGCGGTGGAGCCCTATGTCTPACAGGGAATTCAGACATTAAGGCCAACATACCTT 469
Db 305 AGTCCGGGAGCGTGGAGCCCTATGTCTPACAGGAGTTCAGACAAAGGTCAACATACCTT 364
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QY 470 CAATGACAAATGATGCTCTTTTGGAGACACCGAGCGCTCCATTTTCAGCCGAGCAG 529
DB 365 CAATGACAAACACACCGCTGCTCTTGGAGAACCGAGCGCTCCATTTTCAGCCGAGCAA 424
QY 530 GTCCACAGGCTCTGAGAGTACTACATTAATGCTGCTAAATCTGCTGCTTGGGGGGCGC 589
DB 425 GTCCATGCTCTGAGAGTACTACATTAATGCTGCTAAATCTGCTGCTTGGGGGGCGC 484
QY 590 AGTAATGATGAGAGCAAGCTCTGAGGCTCTGAAGCTGATGATGACCTTTGGGGCTGGCCAC 649
DB 485 GATATTGATGAGAGCAAGCTCTGAGGCTCTGAAGCTGATGATGACCTTTGGGGCTGGCCAC 544
QY 650 CTGGGCGAGCGCTGCTTTATGAAACCGAAAGTTGGTGAGATCTGCTGGGGCTATGAGGA 709
DB 545 CATGGGCGAGCGCTGCTTTATGAAACCGCACAGTTGGTGAGATCTGCTGGGGCTATGAGGA 604
QY 710 TCCCTTCGTGAATTTTATCAACAAATCTTACACAGACATGTTCCCATCAAGGGCAAGTT 769
DB 605 TCCCTTCGTGAATTTTCTCAACAGTCTCTCCAGACATGCTTCCCATTAAGGGCAATTT 664
QY 770 CGGCTGTTTGTGAGATGAACAACCTCAGACTCTGGGCTCTTCACTGTTTACGGGCGT 829
DB 665 TGGCTGTTTGTGGATGAACAACCTCGAATTTCTGGGCTCTTCACTGTTTACGGGCGT 724
QY 830 CCAGAACTTCAGCAAGATCCACCTGGTGAGAGTGAAGTGGGCTCAGCAAGGTCAACTA 889
DB 725 CCAGAACTTCAGCAAGATCCACCTGGTGAGAGTGAAGTGGGCTCAGCAAGATCGATTA 784
QY 890 CTGGCTTCAGAGCAGTCAACATGATCAATGACATTCGGGCTCAGGAGATGGGCAACATT 949
DB 785 TTGGCATTCAGAGCAGTCAACATGATCAATGACATTCGGGCTCAGGAGATGGGCAACATT 844
QY 950 CATGACACCCAGTCTCGTGGGAATTTCTTCAGTCCGGAAGCCCTGAGGCTCTATGAAGCT 1009
DB 845 CATGACACCCAGTCTCGTGGGAATTTCTTCAGTCCGGAAGCCCTGAGGCTCTATGAAGCT 904
QY 1010 CACTCAATGATTCAGGGGTGTTGAAGGATCCCACTATCGTTCACAGCCCTCA 1069
DB 905 GACCTCAACGAATCAAGGGGTGTTGAAGGATTCCTCCACGATTCGCTTCACGGCCCCGA 964
QY 1070 AACTTTGTTGCCAATGGGCTGTTTACCCACCAATGAAGGTTTTCGCCGCTGCTTGA 1129
DB 965 TACTCTGTTTGCCCAACGGGCTCGTCTACCCACCAACGAAGGCTTCTGCCCATCCGAGA 1024
QY 1130 ATCCGGCAATTCAAATGTCAGCACTTGCAAGTGGTGGTCCACCTGTTTCTGTCAACACC 1189
DB 1025 GTCTGGCAATTCAGAAATGTCAGCACTTGCAAGTGGTGGTCCACCTGTTTCTTCCCAACC 1084
QY 1190 TCACCTTCTACAAATGACACCTGCTGCTATCAGAAAGCCGTTCTGGGCTGAACCCCTGACC 1249
DB 1085 CCACCTTTTACAAACCGGACCTGTTGTTGTCAGAAAGCTGTTCTTGGTCTGAACCCCTAACCC 1144
QY 1250 AAGGAGCATTTCTTGTTCATCATCCATCCGCTCACTGGGATCCCATGAATCTGTTTC 1309
DB 1145 AAGGAGCATTTCTTGTTCATCATCCATCCGCTCACTGGGATCCCATGAATCTGTTTC 1204
QY 1310 TGTGAAGTTGAGATAAGCTCTTACATCAAGCTGTCAGGGCAATTCGGGCAACAGGAA 1369
DB 1205 TGTGAAGATGAGCTGAGCTCTTACATCAATCTGTCAAGGGCAATTCGGGCAACAGGAA 1264
QY 1370 GATCAGCCCGTGTGCTTCCATTTGCTGTTGTTGAGCAGAGCGGTGCCATTTGGGCGCGA 1429
DB 1265 GATCAGCCCGTGTGCTTCCATTTGCTGTTGTTGAGCAGAGCGGTGCCATTTGGGCGCGA 1324
QY 1430 GCCCTGAAACAGCTTTTACAGCAGCTGCTGATGATGATGATGATGATGATGATGATGAT 1489
DB 1325 GCCCTGAGCAAGCTTTTACAGCAGCTGCTGATGATGATGATGATGATGATGATGATGAT 1384
QY 1490 GTATGCTGCTGGGCTGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549
DB 1385 GTATGCTGCTGGGCTGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
QY 1550 CAGCCAGGAGAAATGCTTTTTTATTTTGGAGTGGTAGTAAAAAAGGGCTCGCAGGATAGGA 1609

DB 1445 CAGCCAGGAGAAATGCTTTTTTGTGGAGTGTAGTAAAAAGGGCTCCAGGATAGGA 1504
QY 1610 GGCATTTCAGGCTTACTCTGAGTCTCTGAGTGTCAACAGCTGCAAGGCGACGGTGTGCA 1669
DB 1505 GGCATTTCAGGCTTACTCTGAGTCTCTGAGTGTCAACAGCTGCAAGGCGACGGTGTGCA 1564
QY 1670 AGAAGCAAGCTGTAGGCTCCAAAGACACACAGAGCCCCCAACCTGATAGCTTGGTC 1729
DB 1565 AGAAGCAAGCTATAGGCTCTGAGAGACATATAAGCCCCCAACCTGATAGCTTGGTC 1624
QY 1730 AGACCAAGCTATAGGCTCTGAGAGACATATAAGCCCCCAACCTGAGCGACAGTC 1786
DB 1625 AGACCAAGCTATAGGCTCTGAGAGACATATAAGCCCCCAACCTGAGCGACAGCC 1681

RESULT 14
US-10-706-073-3
; Sequence 3, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: In The Treatment Of Steroidal Overproduction
; CURRENT APPLICATION NUMBER: US/10706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51)-(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine
; OTHER INFORMATION: Scavenger Receptor Class BI
US-10-706-073-3

Query Match 76.6%; Score 1369.8; DB 7; Length 1785;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 110 CCCCTTCAGTCCCTGAGCCCCCGAGCCCGGCGCACACGCGGACATGCGGCGAGCGC 169
DB 5 CTCCTTCAGGTCTGAGCCCCCGAGAGCCCCCTTCGCGCACGCGGACATGCGGCGAGCTC 64
QY 170 CAGGGCGGCTGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 229
DB 65 CAGGGCGGCTGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 124
QY 230 TGTGGTTATGATCCTCGTGTATGCCCTCGCTCATCAAAACAGCAGTACTGAAGATGTCG 289
DB 125 CGTTGTATGATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGTGTCTCAAGATGTCG 184
QY 290 CATAGACCCCGAGCAGCTGTCTTTGCAATGTGGAAGGAGATCCCTGTACCTTTTACTT 349
DB 185 CATAGACCCCGAGCAGCTGTCTTTGCAATGTGGAAGGAGATCCCTGTCTTCTTACTT 244
QY 350 GTCCGTCTACTTCTTGGAGTGTCTAATCCAGCAGATCTCTAAGGGTGAGAGCCAGT 409
DB 245 GTCTGTCTACTTCTTGGAGTGTCTAATCCAGCAGATCTCTAAGGGTGAGAGCCAGT 304
QY 410 AGTGGCGGAGCGGCGGCTTATCTGTACAGGGGATTTACAGACATAAGSCCAACATCACCT 469
DB 305 AGTGGCGGAGCGGCGGCTTATCTGTACAGGGGATTTACAGACATAAGSCCAACATCACCT 364
QY 470 CAATGACAAATGATGCTGTGTCTTTTGTGGAGCACCGCAGCTCCATTTTCCAGCGGACAG 529

Db 65 CAGGCGCGCTGGGTGGCTTTGGGGTGGGGCCCTGGGGCTGCTGTTGCTGGCGCTCGG 124
Qy TGTGGTATGATCTCGTGATGCCCTCGCTCATCAAAACAGCAGGTACTGAAGAATGTCGG 289
Db 125 CGTTGTATGATCTCATGTTGGCTCCCTCATCAGCAGCAGGTGTCAAGAATGTCGG 184
Qy 290 CATAGACCCAGCAGCTGTCTTTGCAATGTGAAGAGAGATCCCTGTACCTTTCTACTT 349
Db 185 CATAGACCCAGCAGCAGCTGTCTTTGGGATGTGAAGAGAGATCCCTGTCTTTCTACTT 244
Qy 350 GTCCGCTACTCTTCAGAGTGTCAATCCAGCAGATCTTAAGGGTGAAGCCAGT 409
Db 245 GTCTGTCTACTCTTCGAAGTGGTCAACCCAAACAGGTCTCAACGGCCAGAGCCAGT 304
Qy 410 AGTCGGGAGCGTGGACCTATGCTACAGGGAATTCAGACATTAAGGCCAAACATCACTT 469
Db 305 AGTCGGGAGCGTGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCACTT 364
Qy 470 CAATGACAAATGATACTGTCTTTGGAGACCCGAGCCTCCATTTCCAGCCGGACAG 529
Db 365 CAATGACAAACGACACCGTGTCTTGGTGGAGAACCGCAGCCTCCATTTCCAGCCTGACAA 424
Qy 530 GTCCACGGCTCTCAGAGTACTATTAATGATGCTGCTTAACTTGTGCTTTGGGGGGCGC 589
Db 425 GTCCATGGCTCAGAGAGTACTATTAATGATGCTGCTTAACTTGTGCTTTGGGGGGCGC 484
Qy 590 AGTAATGATGAGAGCAAGTCTGAGCGCTGAAGCTGATGATGACCTTTGGGGCTGGCCAC 649
Db 485 GATATTGATGAGAGCAAGCTGTGAGCCTGAAGCTGATGATGACCTTTGGGGCTGGTCAC 544
Qy 650 CTTGGGGCAGCGTCTTTATGAACCGAACAGATTTGGTGAATCTGTGGGGCTATGAGGA 709
Db 545 CATGGGCCAGCGTCTTTATGAACCGCACAGATTTGGTGAATCTGTGGGGCTATGAGGA 604
Qy 710 TCCCTTCGTGAATTTATCAAAATTAATTAACAGATTTCCCAATGATGATGATGATGATG 769
Db 605 TCCCTTCGTGAATTTATCAAAATTAATTAACAGATTTCCCAATGATGATGATGATGATG 664
Qy 770 CGGCTCTTTGTCAGATGAACACTCAGACTCTGGGCTCTTCACTGCTGTTCAGGGCGT 829
Db 665 TGGCTCTTTGTCAGATGAACACTCAGACTCTGGGCTCTTCACTGCTGTTCAGGGCGT 724
Qy 830 CCAGAACTTCAGCAAGATCCACCTGTGTGAAGATGGAATGGGCTCAGCAAGGTCAACTA 889
Db 725 CCAGAACTTCAGCAAGATCCACCTGTGTGAAGATGGAATGGGCTCAGCAAGGTCAACTA 784
Qy 890 CTGGCATTCAGAGCAGTGCATGATCAATGGCACTTCGGGGCAGATGTGGGCACCAAT 949
Db 785 TTGGCATTCAGAGCAGTGCATGATCAATGGCACTTCGGGGCAGATGTGGGCACCAAT 844
Qy 950 CATGACACCCAGTCCCTCGCTGGAATTTCTTCAGTCCGGAGCCCTGCAAGTCTATGAGCT 1009
Db 845 CATGACACCCAGTCCCTCGCTGGAATTTCTTCAGTCCGGAGCCCTGCAAGTCTATGAGCT 904
Qy 1010 CACCTACCATGATTCAGGGGTGTTGAAGGATCCCAACCTATCGCTTCAGAGCCCTAA 1069
Db 905 GACCTACAAAGATCAAGGGTGTGGAAGCATTTCCACGATGCTTCAGGGCCCGGA 964
Qy 1070 AACTTTGTTGCCAATGGGTGTTTACCAACCAATGAAGGTTTTCGCCGCTGCTTGA 1129
Db 965 TACTCTGTTGCCAACGGGTCCGTCTACCCCAACCAAGAGGCTTCGCGCATGCGCGAGA 1024
Qy 1130 ATCCGGCATTCAGATGTCAGACTTCAGAGTTCGAGTTCGACCCCTGTTCTGTACACCC 1189
Db 1025 GTCTGGCATTCAGATGTCAGACTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 1084
Qy 1190 TCACCTTCAGATGTCAGACTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 1249
Db 1085 CCACCTTTACAAACCGGACCCCTGTTGTGAGAGCTGTTCTGAGTTCGAGTTCGAGTTCGAG 1144
Qy 1250 AAGGGAGCATTTTGTTCCTTGAATTCATCCAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAG 1309

Db 1145 AAAGGAGCATTCCTTGTTCCTAGACATCCATCCGCTCAGTGGATCCCCATGAATGTTTC 1204
Qy 1310 TGTGAAGTTTCAGATAAGCTCTTACATCAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAA 1369
Db 1205 TGTGAAGATGCAGCTGAGCTCTTACATCAATCTGTCAAGGGCATCGGGCAAAACAGGGAA 1264
Qy 1370 GATCGAGCCCGTGGTCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCCATGCGGCGCA 1429
Db 1265 GATCGAGCCAGTAGTTCTGCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1324
Qy 1430 GCGCCCTGACACAGTTCTTACACGAGCTGGTGTGATGTCGCCCCCAGGTACTTCAGTATGCA 1489
Db 1325 GCGCCCTGAGCACAGTTCTTACACGAGCTGGTGTGATGTCGCCCCCAGGTACTTCACATCGCGCA 1384
Qy 1490 GTATGTGCTGCTGGGCTGGGCGGCTCTCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGG 1549
Db 1385 GTATGTGCTGCTGGGCTGGGCGGCTCTCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGG 1444
Qy 1550 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTATTAAGGGCTTCGAGGATAGGA 1609
Db 1445 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGTGTATTAAGGGCTTCGAGGATAGGA 1504
Qy 1610 GGCATTTCAGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAGCGTGTGCA 1669
Db 1505 GGCATTTCAGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAGCGTGTGCA 1564
Qy 1670 AGAAGCCAGCTCTAGGGTCCCAAGACACACAGAGCCCCCAGCTGATGATGATGATGATG 1729
Db 1565 AGAAGCCAGCTATAGGGTCTGAGACACTATAGCCCCCAGCTGATGATGATGATGATGATG 1624
Qy 1730 AGACCCAGCCATCCAGCCCCCTTACACCCCGCTTTCTTGAAGTCTCTCAGCGGACAGTC 1786
Db 1625 AGACCCAGCCATCCAGCCCCCTTACACCCCGCTTTCTTGAAGTCTCTCAGCGGACAGTC 1681

Search completed: February 23, 2006, 23:37:58
Job time : 1479.74 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	1788	100.0	1788	12	US-11-128-061-1074	Sequence 1074, Ap	
2	1788	100.0	1788	12	US-11-128-049-1074	Sequence 1074, Ap	
3	1424.6	79.7	2497	12	US-11-136-527-2943	Sequence 2943, Ap	
4	1255.8	70.2	1531	9	US-11-222-745-3	Sequence 3, Appl1	
C	5	1137.8	63.6	2569	8	US-10-821-234-66	Sequence 66, Appl
	6	1136.2	63.5	2566	9	US-11-072-175-90	Sequence 90, Appl
	7	1136.2	63.5	2566	12	US-11-055-309A-11	Sequence 11, Appl
	8	1061.2	59.4	1530	9	US-11-222-745-8	Sequence 8, Appl1
9	623.4	34.9	1400	12	US-11-136-527-7039	Sequence 7039, Ap	
10	600	33.6	600	12	US-11-128-061-4716	Sequence 4716, Ap	
11	600	33.6	600	12	US-11-128-049-4716	Sequence 4716, Ap	
12	172.6	9.7	2076	12	US-11-136-527-1803	Sequence 1803, Ap	
13	132.6	7.4	1400	12	US-11-136-527-5899	Sequence 5899, Ap	
14	70.6	3.9	2216	8	US-10-909-125-1747	Sequence 1747, Ap	
15	65	3.6	506	6	US-09-925-065A-515554	Sequence 515554,	
16	63	3.5	2675	12	US-11-136-527-2950	Sequence 2950, Ap	
17	59.4	3.3	645	6	US-09-925-065A-675492	Sequence 675492,	
18	52.2	2.9	1910	12	US-11-128-061-1101	Sequence 1101, Ap	
19	52.2	2.9	1910	12	US-11-128-049-1101	Sequence 1101, Ap	
20	46.2	2.6	2718	6	US-09-925-065A-701020	Sequence 701020.	

[illegible]

RESULT 3
US-11-136-527-2943

Query Match	79.7%	Score 1424.6;	DB 12;	Length 2497;
Best Local Similarity	87.3%;	Pred. No. 0;		
Matches 1557;	Conservative 23;	Mismatches 192;	Indels 11;	Gaps 2;
Qy	1	GCACCTGCAAGGCTACTGTGTCGGGCCATGCCTCGAGACTCACCTTCTCGAACGTG	60	
'				
Db	59	GCACCTGCAAGGCTACTGTGCKCTGGCCACTGTGAGGCACACACCTTGCTG	-----	111

Qy	1355	TGGGCAAA	CAGGGAAT	CGAGCC	TGCTCT	CCATGCT	GTGTT	TGAG	CAGAGCGG	1414
Db	1201	CGGGCAAA	CAGGGAAT	CGAGCA	GATCGAG	CTGTCT	CGCCAT	TGCTGT	CGAA	1260
Qy	1415	TGCAT	TGGGCGG	CGAGCC	CTGAA	CAACG	TTCTAC	AGCAG	CTGGT	1474
Db	1261	GATGAT	TGGGTGG	CAAGAC	CTTGA	ACACG	TTCTAC	AGCAG	CTGGT	1320
Qy	1475	ACTTCAG	TATGTGC	AGTATG	CTGCTG	GGGCTG	GGGCG	CTCTC	TCTGCT	1534
Db	1321	TCCTTCA	CTACG	CGCAG	TATG	TGCTGT	GGGCTT	TGAGG	CGCTCT	1380
Qy	1535	CATCTAC	CAGTTG	CGCAG	CCAGC	AGAAAT	GTCTTT	TATTTT	TGGAGT	1594
Db	1381	CATTTAC	CAACTCG	CGCAG	CCAGC	AGAAAT	GTCTTT	TATTTT	TGGAGT	1440
Qy	1595	CTCGCAG	GATAGG	GGCCAT	TTCAG	CGCTACT	CTGAGT	CTCTG	ATGTC	1654
Db	1441	CTCGCAG	GATAGG	GGCCAT	TTCAG	CGCTACT	CTGAGT	CTCTG	ATGTC	1500
Qy	1655	GGSCAC	GGTGTCT	GCAAG	AGCCAA	CGCTGT	AG			1685
Db	1501	GGSCAC	GGTGTAGT	GCAAG	AGCCAA	CGCTGT	AG			1531

RESULT 5
US-10-821-234-66/c
; Sequence 66, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

Query Match	63.6%	Score 1137.8	DB 8	Length 2569	
Best Local Similarity	80.1%	Pred. No. 1.1e-307			
Matches 1337	Conservative	0	Mismatches 332	Indels 0	Gaps 0
QY	120	CCCTGAGCCCGCGAGCCCGGGCCGCACACGCGGACATGGCGGGCAGCGCCAGGGCGCGC	179		
DB	2536	CCCTGGAGCCCGGGTGGCCCCAGCGCGCAGACATGGGCTGTCTCCGCCAAGCGCGC	2477		
QY	180	TGGGTGGCGTGGGGCTGGGCGTGTGGGCTGCTGTGGCTGTGTCTGGTGTGGTTATG	239		
DB	2476	TGGGCTGCCGGGCGCTGGGCGTTCGGGGGCTACTGTGCGTGTGTCTGGGCGCTGTCTATG	2417		
QY	240	ATCCTCGTGATGCCCTCGCTCATCAACACAGCAGGTACTGAAGAATGTCCGCATAGACCCC	299		
DB	2416	ATCGTGATGGTGGCTCGCTCATCAGCAGCAGGTCTCTTAAGAACGTGGCGCATCGACCCC	2357		
QY	300	AGCAGCCTGTCTTTGCAATGTGGAAGGAGATCCCTGTACCCCTTCTACTTGTTCGGTCTAC	359		
DB	2356	AGTAGCTGTCTTCAACATGTGAAGGAGATCCCTATCCCTTCTATCTCTCCGTCTAC	2297		
QY	360	TTCTTCGAGGTGGTCAATCCGACGAGATCTTAAGGGTGAAGAAGCCAGTAGTTCGGGAG	419		
DB	2296	TTCTTTGAGCGTCATGAACCCACGCGAGATCTGAAGGGGAGAAGCGCAGGTGCGGGAG	2237		

Qy	420	CGTGGACCCCTATGCTCTACAGGGAAATTCAGACATTAAGGCCAAATCACTCTCAATGACAAT	479
Db	2236	CGCGGGCCCTACGCTGTATACGGGAGTCAGGCACAAAAGAACAAATCACTTTCAACAACAAC	2177
Qy	480	GATACTGTGTCTTTGTGGAGACCGGCAGAGCTCCATTTCCAGCGCGACAGGTCCCACGGC	539
Db	2176	GACACGGTGTCTTCCTCGAGTACCGGACCTTTCAAGTTCAGCGCTTCAAGTCCCACGGC	2117
Qy	540	TCTGAGAGTGACTACATTATATCTGCCCTAAATTTCTGGTCTTTGGGGGGCGCAGTAATGATG	599
Db	2116	TCGGAGAGCGACTACATCGTCATGCCCAAATCCTGGTCTTTGGTGGCGGTGATGATG	2057
Qy	600	GAGAGCAAGTCTGCGAGCCCTGAAGCTGATGATGACCTTTGGGGCTGGCCACCTTTGGGGCAG	659
Db	2056	GAGAAATAGCCCATGAGCCCTGAAGCTCATCATGACCTTGGCATTTCAACACCTCGCGGAA	1997
Qy	660	CGTGCCTTTATGAACCCGAACAGTTGGTGAGATCCTGTGGGGCTATGAGGATCCCTTCGTG	719
Db	1996	CGTGCCCTTCATGAACCCGACCTGTGGGTGAGATCATGTGGGGCTACAAGGACCCCTTGTG	1937
Qy	720	AATTTTATCAACAAATATCTTACCAGACATGTTCCCATCAAGGCCAAGTTTCGGCTGTGTTT	779
Db	1936	AATCTCATCAACAAGTACTTTCCAGGCATGTTCCCTTTCAGGACAAGTTCSGATATTTT	1877
Qy	780	GTTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTGTTCAAGGGCTCCAGAACTTC	839
Db	1876	GCTCAGCTCAACAACTCCGACTCTGGGCTCTTCAACGGTGTTCACGGGGTCCAGAAATC	1817
Qy	840	AGCAAGATCCACCTGGTGGACAGATGAATGGGCTCAGCAGGTCAACTACTCGCATTCAC	899
Db	1816	AGCAGGATCCACCTCGTGGCAAGTGGAAAGGGCTGAGCAAGGTGACTTTCTGGCATTC	1757
Qy	900	GAGCAGTGCACCATGATCAATGGCACCTTCGGGGCAGATGTGGGCACCATTCATGACACCC	959
Db	1756	GATCAGTGCACCATGATCAATGNACTTCTGGGGCAATGTGGCGGCTTCAAGCTCCT	1697
Qy	960	CAGTCTCGCTGGAAATCTTCAGTCCGGAAAGCCTGCAAGTCTATGAAGCTCACTTACCAT	1019
Db	1696	GAGTCTCTCGCTGGAGTTCTACAGCCCGAGGCGCTGCCGATCCATGAAGCTAATGTACAAG	1637
Qy	1020	GATTCAGGGTGTTTGAAGGCATCCCACTATCGCTTTCAGGCCCTTAAACCTTTGTTT	1079
Db	1636	GAGTCAAGGGTGTTTGAAGGCATCCCACTATCGCTTTCGTTGGCTCCCAAAACCTTGT	1577
Qy	1080	GCCAAATGGGTCTGTTTTACCAACCAATGAAGTTTCTGCCGCTGCTTGAATCCGGCAT	1139
Db	1576	GCCAAAGGGTCCATCTACCAACCAAGAGCTTCTGCCGCTGCTTGGAGTCTGNAAT	1517
Qy	1140	CAAAATGTACGACTTCGAGTTTGTGTCACCCCTGTTTCTGTACACCCCTCACTTCTAC	1199
Db	1516	CAGAACTGCAGCACTCGAGTTTCAGTGCCTTGTCTCTCCATCTCTCACTTCTCTC	1457
Qy	1200	AATCGACACCTGTGCTATCAGAAAGCGTTCTGGGTCTGAAACCTTGACCCCAAGGAGCAT	1259
Db	1456	AACGCCAGCCGGTCTCTGGCAGAGCGGTGACTGCGCTGCACCCCTAACCAGGAGGCACAC	1397
Qy	1260	TCTTTGTTCTTGACATCCATCCGTCACATGGGATCCCATGAACTCTTCTGTGAAGTTG	1319
Db	1396	TCCTTGTTCTTGACATCCACCCGGTCAACGGAAATCCCATGAATCTCTGTGAACCTG	1337
Qy	1320	CAGATAAGCCCTCTACATCAAGCTGTCAAGGGCATTTGGGCAAAACAGGGAAGATCGAGCCC	1379
Db	1336	CAGCTGAGCCCTTACATGAAATCTGTCGAGGCATTCGACAACTGGAAGATTGAGCCT	1277
Qy	1380	GTGCTCTCCATTTGCTGTGTTGAGCAGAGCGGTGCATGGGGCGGAGACCCCTGAAC	1439
Db	1276	GTGCTCTGCGCTGTCTGTGTTTTCAGAGAGCGGGGCCATGGAGGGGGAGACTCTTTCAC	1217
Qy	1440	ACGTTCTACAGCAGCTGTGCTCATGCCCAAGTACTTCAGATATGTCAGTATGTCCTG	1499
Db	1216	ACATCTACACTCAGCTGGTGTGATGCCCAAGGTGATGACATATGCCCATGCTCTCT	1157
Qy	1500	CTGGGGCTGGGGCGGCTCTCTGCTGTGTGTCGGCTCATCTACCAAGTTGGCGCAGCAGGAG	1559

RESULT, 6

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US-11-072-175-90
; Sequence 90, Application US/11072175
; Publication No. US2006029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCES: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 2566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-90
Query Match 63.5%; Score 1136.2; DB 9; Length 2566;

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Db 394 GACACGCTGCTCTCTCGAGTACCGCACCTTCCAGTTCCAGCCCTCCAAAGTCCCGGC 453
Qy 540 TCTGAGAGTACATACATTAATCTGCTTAAATCTCTGCTTCTGGGGGCGCAGTAATGATG 599
Db 454 TCGAGAGCGACTACATCGTCATGCCCAACATCTCTGCTCTTGGGTGGCGGTGATGATG 513
Qy 600 GAGAGCAAGTCTCGAGGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATG 659
Db 514 GAGAAAGAGCCCATGACCTTGAAGCTCATCATGACCTTGGCATTCACACCTCGGCGAA 573
Qy 660 CGTGCTTTATGAACCGAAGTGGTGAGATCTCTGGGGGCTATGAGGATCCCTTCGTG 719
Db 574 CGTGCTTTATGAACCGAAGTGGTGAGATCTCTGGGGGCTATGAGGATCCCTTCGTG 633
Qy 720 AATTTTATCAACAAATATCTTACAGACATGTTCCCATCAAGGGCAAGTTTCGGCTGTTT 779
Db 634 AATCTCATCAACAGTACTTTCCAGGCATGTTCCCTTCAAGGCAAGTTTCGATATTT 693
Qy 780 GTTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTGTCAAGGGGCTCCAGAACTTC 839
Db 694 GCTGAGCTCAACAACTCCGACTCTGGGCTCTTCACTGTGTGTCAAGGGGCTCCAGAACTTC 753
Qy 840 AGCAAGATCCACTGTGGGAGATGGAATGGGCTCAGCAAGGTCACTACTTGGCATTC 899
Db 754 AGCAGGATCCACTGTGGGAGATGGAATGGGCTCAGCAAGGTCACTACTTGGCATTC 813
Qy 900 GAGCAGTGAACATGATCAATGACATCTCGGGCAGATGGGCACCATTCATGACACCC 959
Db 814 GATCAGTGAACATGATCAATGACATCTCGGGCAGATGGGCACCATTCATGACACCC 873
Qy 960 CAGTCTCGCTGGAATCTTTCAGTCCGGAAGCTCGAGGTCTATGAGCTCACTACCAT 1019
Db 874 GAGTCTCGCTGGAATCTTTCAGTCCGGAAGCTCGAGGTCTATGAGCTCACTACCAT 933
Qy 1020 GATTGAGGGTGTGAGGATCCCACTATGCTTTCAGCCTTCAAGCCCTTAACTTGTGTT 1079
Db 934 GAGTCAAGGGGTGTGAGGATCCCACTATGCTTTCAGCCTTCAAGCCCTTAACTTGTGTT 993
Qy 1080 GCCAATGGGTCTGTTTACCCACCAATGAAGTCTTCTGCCGCTGCTTGAATCCGCAAT 1139
Db 994 GCCAAGGGTCTGTTTACCCACCAATGAAGTCTTCTGCCGCTGCTTGAATCCGCAAT 1053
Qy 1140 CAAATGTGACACTTTCAGGTTTGGTGACCCCTGTTTCTGTGACACCTCACTTCTAC 1199
Db 1054 CAGAGCTGACGACCTTTCAGGTTTGGTGACCCCTGTTTCTGTGACACCTCACTTCTAC 1113
Qy 1200 AATGACAGCTGTGCTATCAGAGCGGTCTCGGCTGTGAGCCCTGACCCCAAGGAGCAT 1259
Db 1114 AACGCGACCCGCTTCTGGCAGAGCGGTGACTGGCTTGACCTTAACAGGAGGACAC 1173
Qy 1260 TCTTGTCTTTCGACATCCATCCGCTCAGTGGGATCCCATGAATCTGTGAGGTG 1319
Db 1174 TCTTGTCTTTCGACATCCATCCGCTCAGTGGGATCCCATGAATCTGTGAGGTG 1233
Qy 1320 CAGATAAGCTCTTACATCAAGCTGTCAAGGGCAATTTGGGCAACAGGAGATCGAGCCC 1379
Db 1234 CAGCTGAGCTCTACATGAATCTGTGCGAGGATTTGGAACAACTGGAGATTTGAGCT 1293
Qy 1380 GTGGTCTCTCCATGCTGTGTTTGAAGAGAGCGGTGCCATGGCGCGGACCCCTTGAAC 1439
Db 1294 GTGGTCTCTCCGCTGCTGTTTGAAGAGAGCGGTGCCATGGAGGGGAGACTCTTTCAC 1353
Qy 1440 AGTCTTACAGCAGCTGGTGTGATGCCCGGACTTTCAGTATGTGAGTATGCTG 1499
Db 1354 ACATTTTACACTCAGTGTGTTTGAAGAGAGCGGTGCCATGGAGGGGAGACTCTTTCAC 1413
Qy 1500 CTGGGCTCTGGGCGCTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
Db 1414 CTGGGCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473
Qy 1560 AATGCTTTTATTTTGGAGTGTAGTAAAGGGCTTCGAGGATGAAGGGCCATTTCAG 1619

Db 1474 AATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCAAGGATGAAGGGCCATTTCAG 1533
Qy 1620 GCCTACTCTGAGTCTCTGATGTCCAGGCTGCGCAAGGCGACGCTGTGCAAGAGCAAG 1679
Db 1534 GCCTATTCTGAATCCCTGATGATCATGCTCCCAAGGGCTCTGTGCTGCAGGAGCAAA 1593
Qy 1680 CTGTAGGGTCCCAAGACACACGAGAGCCCGCCCACTGATAGCTTGGTTCAGACCGCA 1739
Db 1594 CTGTAGGGTCTGTAGGACACCGGTGAGCCAGCGGCTGTGGCGCTGACCGGCC 1653
Qy 1740 TCCAGGCTTACACCCCGCTTCTTGAAGGCTCTCTCAGCGGACAGTCCG 1788
Db 1654 CCAGGCTTACACCCCGCTTCTTCCGGACTCTTCCAGAGACAGCCCC 1702

RESULT 7

US-11-055-309A-11
; Sequence 11, Application US/11055309A
; Publication No. US20050282750A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: Treatment for Dark Adaptation
; FILE REFERENCE: HO-P02351U55
; CURRENT APPLICATION NUMBER: US/11/055,309A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 2566
; TYPE: DNA
; ORGANISM: HUMAN
US-11-055-309A-11

Query Match 63.5%; Score 1136.2; DB 12; Length 2566;
Best Local Similarity 80.0%; Pred. No. 3.2e-307;
Matches 1336; Conservative 0; Mismatches 333; Indels 0; Gaps 0;

Qy 120 CCTGAGCCCCCGAGCCCGCGCCGACACGCGGACATGGCGGCGAGCGCGCGCGCGC 179
Db 34 CCTGCGAGCCCGGGTGGGCCCGCGGCGGACATGGGCTGCTCCCGCAAGCGCGC 93
Qy 180 TGGGTGGCGGTGGGGCTGGCGCTGCTGGGGCTGCTGTGCGCTGTGCTCGGTGGTTATG 239
Db 94 TGGGCTGCGCGGCGCTGGCGCTGCTGGCGGCTACTGTGCGCTGTGCTGGGCGTGTGATG 153
Qy 240 ATCTCTGTGATGCCCTCGCTCATCAAAAGAGAGGTACTGAAGAAATGTCGCGATAGACCCC 299
Db 154 ATCTGTGATGGTCCGCTCGCTCATCAAGCAGCAGGCTCTTAAAGAACGTCGCGCATCGACCCC 213
Qy 300 AGCAGCTGCTCTTTTGCATGTGGAGGAGATCCCTGTACCTTCTTCTTCTTCTTCTTCTTCT 359
Db 214 AGTAGCTGTCTTCAACATGTGGAGGAGATCCCTTATCCCTTCTTCTTCTTCTTCTTCTTCT 273
Qy 360 TTCTTTGAGGTGGTCAATCCAGCAGAGATCTTAAAGGGTGAGAAGCCAGTAGTGGCGGAG 419
Db 274 TTCTTTGAGCTCATGAACCCCGAGGAGATCTTGAAGGGCGAGAGCGCGAGGTGGCGGAG 333
Qy 420 CGTGAGCCCTATGTCTACAGGGAATTCAGACATGAAGGCCAAATCACTCTTCAATGACAT 479
Db 334 CGCGGGCCCTACGTGTACAGGGAGTCCAGGCAAAAGCAACATCACCTTCAACACAAC 393

481 TTGGCATTACACCCCTCGGGAAGTGCCTTTCATGAACCGCACTGTGGGTGAGATCATG 540
696 TGGGGCTATGAGGATCCCTTCGTGAATTTTATCAACAAATATCTTACAGACATGTTTCCCC 755
541 TGGGGCTTACAAGGACCCCTTGTGAATCTCATCAACAAATATCTTACAGGATGTTTCCCC 600
756 ATCAAGGGCAAGTTCGGCTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 815
601 TTCAAGGACAAGTTCGGATTAATTTGTGAGCTCAACAACTCCGACTTCGGGCTCTTCACG 660
816 GTGTTCACGGGCTTCAGAACTTCAGCAAGATCCACCTGTGTGACAGATGATGATGATGATGAT 875
661 GTGTTCACGGGCTTCAGAACTTCAGCAAGATCCACCTGTGTGACAGATGATGATGATGATGAT 720
876 AGCAAGTCAACTTACCTGACATTCAGCAAGATCCACCTGTGTGACAGATGATGATGATGATGAT 935
721 AGCAAGTTCAGTTCGGATTCAGCAAGATCCACCTGTGTGACAGATGATGATGATGATGATGAT 780
936 ATGTGGGCACCATTCAGACACCCAGTCTCGCTGGAATTTCTCAGTCCGGAGGCTGC 995
781 ATGTGGGCACCATTCAGACACCCAGTCTCGCTGGAATTTCTCAGTCCGGAGGCTGC 840
996 AGGTCTATGAAGTCACTTACCTGATTCAGGGGTGTTTCAAGGCAATCCCACTATCGC 1055
841 CGATCCATGAAGTATGATCAAGAGTCAAGGGTGTGAGGATCCCACTATCGC 900
1056 TTCACAGCCCTTAAACTTTTGTGCAATTTGCGGTGTTTACCCCAATGAAGGTTTC 1115
901 TTGCTGGCTCCCAAAACCTGTTTGGCAACGGGTTCATCTACCCCAACGAAGGCTTC 960
1116 TGCCCGTGCCTTGAATCCGGCATTCAAATGTGAGCATTTGAGGTTTGTGACACCCCTG 1175
961 TGCCCGTGCCTTGAATTCGAATTCGAACGTGAGCATTCAGCATTCAGGTTTCAGTGCCTCTG 1020
1176 TTCTCTGTCACACCTCACTTCTCAATGACAGCCCTGTGTGATCAAGAGCGTTCCTGGT 1235
1021 TTCTCTCCCATCTCACTTCTCAAGCCGACCCGGTTCGCGAAGCGGTGACTGGC 1080
1236 CTGAACCTTGACCAAGGGAGCATTTCTTGTCTTGAATCCATCCGCTCACTGGGATC 1295
1081 CTGACCCCTAACAGGAGGACACTCTTGTCTTGGACATCCACCGGTCAAGGATC 1140
1296 CCATGAATGTTCTGTGAAGTTCAGATGAAGCTCTATCAATCAAGCTGCAAGGCAAT 1355
1141 CCATGAATGTTCTGTGAAGTTCAGATGAAGCTCTATCAATCAAGCTGCAAGGCAAT 1200
1356 GGGCAACAGGGAAGTTCAGAGCCGTGCTCTCCATTTGCTGTGTGAGCAGAGGCT 1415
1201 GGAACAACCTGGGAAGTTCAGAGCCGTGCTCTCCATTTGCTGTGTGAGCAGAGGCT 1260
1416 GCCATGGGGCGGAGCCCTGGAACAGCTTCTACAGCAGCTGTGTGATGATGATGATGATGATGAT 1475
1261 GCCATGGGGCGGAGCTTCTACACATTTCTACACTCAGTGTGTGATGATGATGATGATGATGAT 1320
1476 CTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1535
1321 ATGCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1536 ATCTACAGTTCGCGAGCCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1595
1381 ATCTGCAATTCGCGAGCCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1596 TCCAGAGTAAAGAGGCAATTCAGGCTTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGAT 1655
1441 TCAAGGATTAAGAGGCAATTCAGGCTTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGAT 1500
1656 GGCACGGTTCGCAAGAGCCAGGCTGATG 1685
1501 GGCTCTGTGCTGAGGAAGCAAACTGTAG 1530

RESULT 9

US-11-136-527-7039

; Sequence 7039, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7039
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-7039

Query Match 34.9%; Score 623.4; DB 12; Length 1400;
Best Local Similarity 89.6%; Pred. No. 5.7e-164;
Matches 657; Conservative 10; Mismatches 66; Indels 0; Gaps 0;

QY 1051 ATGCTTTCAGAGCCCTTAAACTTTGTTTCCCAATGGGTCTGTTTACCCACCCCAATGAAG 1110
Db 1 ATGCTTTCAGAGCCCTTAAACTTTGTTTCCCAATGGGTCTGTTTACCCACCCCAATGAAG 60
QY 1111 GTTTCGCGCTGCTTGAATCCGGCATTCGCAATTCAGCACTTCGAGCTTCGAGGTTTGGTGAC 1170
Db 61 GCTTTCGCGCTGCTTGAATCCGGCATTCGCAATTCAGCACTTCGAGCTTCGAGGTTTGGTGAC 120
QY 1171 CCCTGTTTCTGTACACCTCTCACTTCTACAATGCAGACCTGTGTATCAGAACCGGTTTC 1230
Db 121 CCCTGTTTCTCTCCAGCCCACTTCTACAATGCAGACCTGTGTATCAGAACCGGTTTC 180
QY 1231 TGCGTCTGAACCTGACCCAGGAGCATTTTGTTCCTTGACATCCATCCCGTCACTG 1290
Db 181 TTGGTCTGAACCTGACCCAGGAGCATTTTGTTCCTTGACATCCATCCCGTCACTG 240
QY 1291 GGATCCCAATGAAGTCTTCTGTGAAGTTCAGATAGCTCTACATCAAGCTGTCAAGG 1350
Db 241 GGATCCCAATGAAGTCTTCTGTGAAGTTCAGATAGCTCTACATCAAGCTGTCAAGG 300
QY 1351 GCATTTGGGCAACAGAGGAGATCGAGCCGCTGCTCTCCATTTGCTGTGTGAGCAGA 1410
Db 301 GCGTGGGCAACAGAGGAGATCGAGCAGTAGTCTGCTGCAATTTGCTGTGTTTGAACAGA 360
QY 1411 GCGTGGCCTATGGGCGGAGCCCTTGAAACAGTTCACAGCAGCTGTGTGATGATGATGATGATGAT 1470
Db 361 GCGGAT 420
QY 1471 AGGTCTTTCAGTATGTCAGTATGTCGTCTGGGCTGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
Db 421 ARGTTCTTCACTACGCGCAGTATGTCGTCTGGGCTGGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 1531 CCCTCATCTACAGTATGTCGAGCAGGAGGAGTGTCTTTTATTTTGGAGTGTGTGAGTGTGAGTGTGAGT 1590
Db 481 CCATCATTTACCACTGCGCGCAGGAGGAGTGTCTTTTATTTTGGAGTGTGTGAGTGTGAGTGTGAGT 540
QY 1591 AGGGCTTCGAGGATTAAGAGGCAATTCAGGCTTCTCTGAGTCTCTGATGATGATGATGATGATGATGAT 1650
Db 541 AGGGCTTCGAGGATTAAGAGGCAATTCAGGCTTCTCTGAGTCTCTGATGATGATGATGATGATGATGATGAT 600
QY 1651 CCAAGGCAAGGCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1710
Db 601 CCAAGGCAAGGCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 1711 CCAAGCTGAT 1770
Db 661 CCAAGCTGAT 720
QY 1771 CTCTCAGCGGACA 1783
|||||

Db 721 CTCTCAGCGGACA 733

RESULT 10

US-11-128-061-4716
; Sequence 4716, Application US/11128061
; Publication No. US2006003958A1
; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE OF INVENTION: TO MONITOR GENE EXPRESSION

; FILE REFERENCE: 01997.027701

; CURRENT APPLICATION NUMBER: US/11/128,061

; PRIOR FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; PRIOR FILING DATE: 2004-05-11

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4716

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Cricetulus griseus

US-11-128-061-4716

Query Match 33.6%; Score 600; DB 12; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.5e-157;

Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 CTCACCTTCTACAATGAGACCCCTGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACC 1248

Db 1 CTCACCTTCTACAATGAGACCCCTGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACC 60

QY 1249 CAAGGGAGCAATCTTTGTTCTTGACATCCATCCGGTCACTGGGATCCCATGAACCTGTT 1308

Db 61 CAAGGGAGCAATCTTTGTTCTTGACATCCATCCGGTCACTGGGATCCCATGAACCTGTT 120

QY 1309 CTGTGAAGTTGCAGATAAGCCTCTACATCAAGCTGTCAAGGCGCATTTGGGCAACAGGGA 1368

Db 121 CTGTGAAGTTGCAGATAAGCCTCTACATCAAGCTGTCAAGGCGCATTTGGGCAACAGGGA 180

QY 1369 AGATCGAGCCCGTGGTCTCTCCCATTTGCTGTGGTTTGAGCAGAGCGGTGCCATGGGCGCG 1428

Db 181 AGATCGAGCCCGTGGTCTCTCCCATTTGCTGTGGTTTGAGCAGAGCGGTGCCATGGGCGCG 240

QY 1429 AGCCCTGGAACAGCTTCTACACGAGCTGTGCTGATGCCCGCCAGGTACTTCAGTATGTGC 1488

Db 241 AGCCCTGGAACAGCTTCTACACGAGCTGTGCTGATGCCCGCCAGGTACTTCAGTATGTGC 300

QY 1489 AGTATGCTGCTGGGGCTGGGGCTCTCTGCTGTGGTGGCCGTCATCTACCAAGTTGC 1548

Db 301 AGTATGCTGCTGGGGCTGGGGCTCTCTGCTGTGGTGGCCGTCATCTACCAAGTTGC 360

QY 1549 GCAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGAGGGCTCCGAGGATAAGG 1608

Db 361 GCAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGAGGGCTCCGAGGATAAGG 420

QY 1609 AGGCCATTACGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAGGGCACGGTGTGC 1668

Db 421 AGGCCATTACGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAGGGCACGGTGTGC 480

QY 1669 AAGAAGCCAGCTGTAGGGTCCCAAGACACACAGAGCCCCCACTCATAGCTTGGT 1728

Db 481 AAGAAGCCAGCTGTAGGGTCCCAAGACACACAGAGCCCCCACTCATAGCTTGGT 540

QY 1729 CAGACCAAGCCATCCAGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCGC 1788

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Db 541 CAGACCAGCCATCCAGCCCTACACCCGCTTCTTTGAGGACTCTCTCAGCGGACAGTCGC 600

RESULT 11

US-11-128-049-4716

; Sequence 4716, Application US/11128049

; Publication No. US20060010513A1

; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.

; APPLICANT: Charlebois, Timothy S.

; APPLICANT: Mounts, William M.

; APPLICANT: Hann, Louane E.

; APPLICANT: Sinacore, Martin S.

; APPLICANT: Leonard, Mark W.

; APPLICANT: Brown, Eugene L.

; APPLICANT: Miller, Christopher P.

; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

; FILE OF INVENTION: MAKING AND USING SAME

; FILE REFERENCE: 01997.027700

; CURRENT APPLICATION NUMBER: US/11/128,049

; PRIOR FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; PRIOR FILING DATE: 2004-05-11

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4716

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Cricetulus griseus

US-11-128-049-4716

Query Match 33.6%; Score 600; DB 12; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.5e-157;

Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 CTCACCTTCTACAATGAGACCCCTGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACC 1248

Db 1 CTCACCTTCTACAATGAGACCCCTGTGCTATCAGAAGCCGTTCTGGGTCTGAACCCCTGACC 60

QY 1249 CAAGGGAGCAATCTTTGTTCTTGACATCCATCCGGTCACTGGGATCCCATGAACCTGTT 1308

Db 61 CAAGGGAGCAATCTTTGTTCTTGACATCCATCCGGTCACTGGGATCCCATGAACCTGTT 120

QY 1309 CTGTGAAGTTGCAGATAAGCCTCTACATCAAGCTGTCAAGGCGCATTTGGGCAACAGGGA 1368

Db 121 CTGTGAAGTTGCAGATAAGCCTCTACATCAAGCTGTCAAGGCGCATTTGGGCAACAGGGA 180

QY 1369 AGATCGAGCCCGTGGTCTCTCCCATTTGCTGTGGTTTGAGCAGAGCGGTGCCATGGGCGCG 1428

Db 181 AGATCGAGCCCGTGGTCTCTCCCATTTGCTGTGGTTTGAGCAGAGCGGTGCCATGGGCGCG 240

QY 1429 AGCCCTGGAACAGCTTCTACACGAGCTGTGCTGATGCCCGCCAGGTACTTCAGTATGTGC 1488

Db 241 AGCCCTGGAACAGCTTCTACACGAGCTGTGCTGATGCCCGCCAGGTACTTCAGTATGTGC 300

QY 1489 AGTATGCTGCTGGGGCTGGGGCTCTCTGCTGTGGTGGCCGTCATCTACCAAGTTGC 1548

Db 301 AGTATGCTGCTGGGGCTGGGGCTCTCTGCTGTGGTGGCCGTCATCTACCAAGTTGC 360

QY 1549 GCAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGAGGGCTCCGAGGATAAGG 1608

Db 361 GCAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGAGGGCTCCGAGGATAAGG 420

QY 1609 AGGCCATTACGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAGGGCACGGTGTGC 1668

Db 421 AGGCCATTACGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAGGGCACGGTGTGC 480

QY 1669 AAGAAGCCAGCTGTAGGGTCCCAAGACACACAGAGCCCCCACTCATAGCTTGGT 1728

Db 481 AAGAAGCCAGCTGTAGGGTCCCAAGACACACAGAGCCCCCACTCATAGCTTGGT 540

QY 1729 CAGACCAAGCCATCCAGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCGC 1788

|||||

Db 1544 CAGAGTCA 1552

RESULT 15

US-09-925-065A-515554
; Sequence 515554, Application US/0925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 515554
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-515554

Query Match 3.6%; Score 65; DB 6; Length 506;
Best Local Similarity 76.2%; Pred. No. 4.9e-08;
Matches 80; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1684 AGGGTCCCAAGACACACAGAGCCCCCCCCAAGCTGATAGCTGGTCAGACAGCCATCCA 1743
DB 384 AGGGTCTGAGGACACCGTGAGCCAGCCAGGCGCTGGCGCTGAGCGGCCCA 443
QY 1744 GCCCTACACCCCGCTTCTGAGGACTCTCTCAGCGGACAGTCGC 1788
DB 444 GCCCTACACCCCGCTTCTCCCGACTCTCCAGCGGACAGCCCC 488

Search completed: February 23, 2006, 18:46:01
Job time : 552.461 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:34:44 ; Search time 152 Seconds
(without alignments)
1471.341 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2881
Sequence: 1 MGSGARWVAVGLGVVGLL.....YSESLMSPAAGTGVLRAXL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	2	AAR88465 Hamster s
2	2681	100.0	509	2	AAR93574 Hamster s
3	2681	100.0	509	2	AAY44019 Hamster s
4	2681	100.0	509	5	ABG33056 Hamster s
5	2681	100.0	509	5	AAE21523 Hamster s
6	2681	100.0	509	6	ABO27241 Human sca
7	2681	100.0	509	8	ADJ46121 Human sca
8	2681	100.0	509	8	ADJ53335 Hamster s
9	2681	100.0	509	8	ADU51467 Hamster s
10	2525	94.2	509	9	ABO33938 Hamster s
11	2453	91.5	509	8	ADU51468 Mouse sca
12	2447	91.3	509	2	AAR93575 Mouse sca
13	2447	91.3	509	2	AAY44020 Mouse sca
14	2447	91.3	509	5	ABB57092 Mouse isc
15	2447	91.3	509	5	AAE21525 Murine sc
16	2447	91.3	509	8	ADJ53337 Murine SR
17	2447	91.3	509	9	ADZ13455 Murine ca
18	2447	91.3	509	9	ABO33940 Murine ca
19	2447	91.3	519	8	ABO84950 Murine ca
20	2447	91.3	519	8	ADR67033 Mouse can
21	2444	91.2	509	8	ADU51466 Rat Prote
22	2444	91.2	510	7	ADE56446 Rat Prote
23	2444	91.2	510	7	ADE56442 Rat Prote
24	2430	90.6	509	7	ADE55241 Rat Prote

25	2244	83.7	509	6	ABO27240 Human sca
26	2244	83.7	509	8	ADJ46119 Human sca
27	2244	83.7	509	9	ADZ13464 Human can
28	2244	83.7	509	9	ADZ13458 Human can
29	2244	83.7	514	9	ADZ13466 Human can
30	2237	83.4	509	2	AAW97900 Human SR-
31	2237	83.4	532	4	ABD12012 Human SR-
32	2237	83.4	532	7	ADE09273 Novel pro
33	2236	83.4	509	2	AAAY49573 Human CLA
34	2236	83.4	509	6	AAO31106 Human CD3
35	2236	83.4	509	8	ADL61295 Human sca
36	2236	83.4	510	7	ADE56448 Human Pro
37	2236	83.4	510	7	ADE56444 Human Pro
38	2234	83.3	506	9	ADZ13453 Murine ca
39	2227	83.1	509	2	AAW97899 Human SR-
40	2203	82.2	509	7	ADE40210 Human NOV
41	2117	79.0	481	7	ADE08291 Novel pro
42	2112.5	78.8	537	4	ABG22317 Novel hum
43	2086.5	77.1	552	6	ABR62035 Human SR-
44	2066.5	77.1	552	7	ADE55243 Human Pro
45	2066.5	77.1	552	8	ADP23287 PRO polyp

ALIGNMENTS

RESULT 1

AAR88465

ID AAR88465 standard; protein; 509 AA.

XX AC AAR88465;

XX DT 29-MAR-1996 (first entry)

XX DE Hamster scavenger receptor class B-I.

XX KW Scavenger receptor class BI; HASR-BI; low density lipoprotein;

XX KW atherosclerosis; CHO; Chinese hamster ovary; lipoprotein receptor;

XX KW cholesterol.

XX OS Cricetulus sp.

XX FH Key

FT Domain

FT Disulfide-bond

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

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FT Modified-site

FT Modified-site

XX 19-JUN-1995; 95WO-US007721.
 XX 23-JUN-1994; 94US-00265428.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Krieger M, Acton SL, Pearson AM, Rigotti A;
 XX WPI; 1996-068872/07.
 XX N-PSDB; AAT10116.
 XX Class BI and CI scavenger receptor proteins - used to develop products
 PT for treating or preventing atherosclerosis, fat uptake by adipocyte(s)
 PT and immune disorders.
 XX Claim 5; Page 57-58; 84pp; English.
 XX A new hamster class B-I scavenger receptor, hasR-BI (AAR88465),
 CC selectively binds to low density lipoprotein (LDL) and to acetylated LDL.
 CC It was obtd. by expression of a cDNA clone (AAT10116) isolated from an
 CC expression library prepd. from CHO line Var-261 mRNA. hasR-BI is used to
 CC screen for cpds. that alter binding of scavenger receptor proteins to LDL
 CC or modified lipoprotein, to remove LDL from patient blood, to inhibit
 CC uptake of lipoprotein or lipids by adipocytes, to develop anti-
 CC atherosclerosis drugs, to treat some immune disorders and to raise
 CC diagnostic or therapeutic antibodies
 XX SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
 DB 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
 QY 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 DB 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 QY 121 FQDRSHGSES DYIILPNILVLGAVNMESKSAKGLKMLMTLGLATLGLQAFMNRVTGVEIL 180
 DB 121 FQDRSHGSES DYIILPNILVLGAVNMESKSAKGLKMLMTLGLATLGLQAFMNRVTGVEIL 180
 QY 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 DB 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 QY 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 DB 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 QY 301 FTAPKTLFANGSVYPPNEGFCPCLESQI QNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 DB 301 FTAPKTLFANGSVYPPNEGFCPCLESQI QNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 QY 361 LNPDPREHSLFLDIHPVTGI PMNC SVKQLI SLYKAVKGIGOTGKIPPVVLPLLWFEQSG 420
 DB 361 LNPDPREHSLFLDIHPVTGI PMNC SVKQLI SLYKAVKGIGOTGKIPPVVLPLLWFEQSG 420
 QY 421 AMGGEPLNTFYTLVMPVLYQVYVLLGLGILLVVPYIQLRSQEKCFLFWSGSKG 480
 DB 421 AMGGEPLNTFYTLVMPVLYQVYVLLGLGILLVVPYIQLRSQEKCFLFWSGSKG 480
 QY 481 SQDKAATQAYSESLSMPAAKTGTVLQEAKL 509
 DB 481 SQDKAATQAYSESLSMPAAKTGTVLQEAKL 509

ID AAW93574 standard; protein; 509 AA.
 XX AAW93574;
 XX 17-JUN-1999 (first entry)
 XX Hamster scavenger receptor class B-I protein.
 XX Scavenger receptor class B type I; hamster; steroid production; HDL;
 KW cholesterol; cholesteryl ester transport; high-density lipoprotein;
 KW lipoprotein; liver; steroidogenic tissue; SR-BI; contraception;
 KW treatment; disorder; overproduction; underproduction; menopause;
 KW breast cancer; prostate cancer; endometriosis; fibroid tumour.
 XX Cricetulus griseus.
 XX WO9911288-A1.
 XX 11-MAR-1999.
 XX 04-SEP-1998; 98WO-US018463.
 XX 05-SEP-1997; 97US-0057943P.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Krieger M;
 XX WPI; 1999-204984/17.
 XX N-PSDB; AAX23403.
 XX Modification of steroid production in mammals - by administering
 PT modulator of SR-BI expression or activity.
 XX Disclosure; Page 79-80; 86pp; English.
 XX This invention describes a method for modifying steroid production in a
 CC mammal which comprises administering a compound that alters cholesterol
 CC or cholesteryl ester transport from high-density lipoprotein (HDL) or
 CC other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger
 CC receptor class B type I). This method is useful for female contraception,
 CC for treating disorders characterised by overproduction of steroids, for
 CC treating disorders characterised by underproduction of steroids,
 CC especially menopause, for treating disorders that can be treated by
 CC decreasing steroid production, especially breast cancer, prostate cancer,
 CC endometriosis or fibroid tumours
 XX SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
 DB 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
 QY 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 DB 61 VPYLSVYFVFNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
 QY 121 FQDRSHGSES DYIILPNILVLGAVNMESKSAKGLKMLMTLGLATLGLQAFMNRVTGVEIL 180
 DB 121 FQDRSHGSES DYIILPNILVLGAVNMESKSAKGLKMLMTLGLATLGLQAFMNRVTGVEIL 180
 QY 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 DB 181 WGYEDPFPVNFINKYLPDMFPIKGKFGLVFEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 QY 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
 DB 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300

QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKLQISLYIKAVKIGQTKIBPVVLPILWFQSG 420
 Db 361 LNPDPRHSLFLDIHPVTGIPMNCVKLQISLYIKAVKIGQTKIBPVVLPILWFQSG 420
 QY 421 AMGGEPLNTFYTLVLPQVLYVYVLLGLGGLLLVPVIYQLRSQEKCFLFWGSKKG 480
 Db 421 AMGGEPLNTFYTLVLPQVLYVYVLLGLGGLLLVPVIYQLRSQEKCFLFWGSKKG 480
 QY 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509
 Db 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509

RESULT 3
 AAY44019
 ID AAY44019 standard; protein; 509 AA.
 AC AAY44019;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 XX Hamster Scavenger receptor class BI protein.
 XX
 KW Hamster; scavenger receptor; modulation; cholesterol transport; lipid;
 KW lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;
 KW high density lipoprotein; ester; blood.
 XX
 OS Cricetulus sp.
 XX
 XX US5962322-A.
 XX
 PD 05-OCT-1999.
 XX
 PF 15-NOV-1996; 96US-00749907.
 XX
 PR 15-NOV-1996; 96US-00749907.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA (NASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Krieger M, Rigotti A, Kozarsky K;
 XX
 DR WPI; 1999-589717/50.
 DR N-PSDB; AAZ30615.
 XX
 XX Modulating cholesterol transport for the control of cholesterol levels in
 PT blood.
 PT
 XX
 PS Disclosure; Col 21-24; 23pp; English.
 XX
 CC This sequence represents the hamster scavenger receptor class BI (SR-BI)
 CC which is used in a method of modulating cholesterol transport. The method
 CC comprises selectively altering the transport of lipid, cholesterol and/or
 CC lipoproteins (or their components) into and out of mammalian cells to
 CC alter plasma cholesterol levels, by administering a compound which alters
 CC the expression or activity of the SR-BI scavenger protein receptor. This
 CC alters the rate of clearance of the protein component of high density
 CC lipoprotein (HDL) as compared to the ester component of HDL. The method
 CC may be used to control cholesterol levels in the blood plasma of mammals
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSARARWAVGLGVVGLLCVAVLGVVMIWMLPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVGLGVVGLLCVAVLGVVMIWMLPSLIKQVVKVNRIDPSSLSFAMWKEIP 60

QY 61 VPFLSYVFFEVVNPSEILKGEKPVVRGPPYVYRFRHKANITFNDNDTVSFVHRSLH 120
 Db 61 VPFLSYVFFEVVNPSEILKGEKPVVRGPPYVYRFRHKANITFNDNDTVSFVHRSLH 120
 QY 121 FQDRSHGSSDYIILPNILVLGAVNMESKAGLKMMTLGLATLGLQRAFMRNRTVGEIL 180
 Db 121 FQDRSHGSSDYIILPNILVLGAVNMESKAGLKMMTLGLATLGLQRAFMRNRTVGEIL 180
 QY 181 WGYEDFPVNFINKYLPDMFPFKGKFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNL 240
 Db 181 WGYEDFPVNFINKYLPDMFPFKGKFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNL 240
 QY 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLFFSPEACRSMKLYTHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLFFSPEACRSMKLYTHDSGVFEGIPTYR 300
 QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKLQISLYIKAVKIGQTKIBPVVLPILWFQSG 420
 Db 361 LNPDPRHSLFLDIHPVTGIPMNCVKLQISLYIKAVKIGQTKIBPVVLPILWFQSG 420
 QY 421 AMGGEPLNTFYTLVLPQVLYVYVLLGLGGLLLVPVIYQLRSQEKCFLFWGSKKG 480
 Db 421 AMGGEPLNTFYTLVLPQVLYVYVLLGLGGLLLVPVIYQLRSQEKCFLFWGSKKG 480
 QY 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509
 Db 481 SODKEATQAYSESLMSPAAGTIVLOEAKL 509

RESULT 4
 ABG33056
 ID ABG33056 standard; protein; 509 AA.
 AC ABG33056;
 XX
 DT 20-NOV-2002 (first entry)
 XX
 XX Hamster scavenger receptor type B1 (haSR-B1).
 KW Hamster; scavenger receptor protein type B1; low density lipoprotein;
 KW LDL; cholesterol; endothelial; adipose; macrophage; lipoprotein receptor;
 KW receptor.
 XX
 OS Cricetulus griseus.
 XX
 XX US6429289-B1.
 XX
 PD 06-AUG-2002.
 XX
 PF 23-JUN-1994; 94US-00265428.
 XX
 PR 23-JUN-1994; 94US-00265428.
 XX
 PA (NASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Krieger M, Acton SL, Pearson AM;
 XX
 DR WPI; 2002-689668/74.
 DR N-PSDB; ABS53744.
 XX
 XX New scavenger receptor protein type B1 useful for screening for drugs
 PT that inhibit the uptake of cholesterol in endothelial or adipose cells or
 PT macrophages.
 XX
 PS Claim 1; Col 29-32; 31pp; English.
 XX
 CC The present invention relates to a new scavenger receptor protein type B1
 CC which selectively binds to low density lipoprotein (LDL) and modified

CC lipoprotein with the characteristics of acetylated LDL. The invention is
 CC useful for screening for drugs that inhibit the uptake of cholesterol in
 CC endothelial or adipose cells or macrophages, and for screening for other
 CC lipoprotein receptors. The present amino acid sequence represents the
 CC hamster scavenger receptor protein type B1 (hasR-B1) of the invention
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 5; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVAGLVGVLGCAVLGVVMIIVMPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVAGLVGVLGCAVLGVVMIIVMPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFVFNVPNSILKGEKPVVRERGPVYVFRFRKANITFNDNDTVSFVHRSLH 120
 Db 61 VPFYLSVYFVFNVPNSILKGEKPVVRERGPVYVFRFRKANITFNDNDTVSFVHRSLH 120
 Qy 121 FQDRSHGSESDYIIILPNILVLGGAVMMESKSLAGLKMMTLGLATLGLQRAFMNRTVGEIL 180
 Db 121 FQDRSHGSESDYIIILPNILVLGGAVMMESKSLAGLKMMTLGLATLGLQRAFMNRTVGEIL 180
 Qy 181 WGYEDPPFVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPPFVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Qy 361 LNPDPRHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGQTKIPVVLPLLWPEQSG 420
 Db 361 LNPDPRHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGQTKIPVVLPLLWPEQSG 420
 Qy 421 AMGGEPLNTFYTLVLMQVQLVYVYLLGLGLLLLPVYIQLRSQEKCFLFWSGSKG 480
 Db 421 AMGGEPLNTFYTLVLMQVQLVYVYLLGLGLLLLPVYIQLRSQEKCFLFWSGSKG 480
 Qy 481 SQDKEATQAYSESLMSPAAGTVLQEA 509
 Db 481 SQDKEATQAYSESLMSPAAGTVLQEA 509
 RESULT 5
 AAE21523 standard; protein; 509 AA.
 AC AAE21523;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Hamster scavenger receptor type B-I (hasR-BI).
 XX
 KW Scavenger receptor protein type B1; low density lipoprotein; LDL;
 KW hamster; SR-BI.
 XX
 OS Cricetulus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 9..32
 FT /note= "Putative transmembrane domain"
 FT Modified-site 102..104
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 108..110
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 173..175
 FT /note= "Potential N-linked glycosylation site"

FT Modified-site 212..214
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 227..229
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 255..257
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 310..312
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 330..332
 FT /note= "Potential N-linked glycosylation site"
 FT Modified-site 383..385
 FT /note= "Potential N-linked glycosylation site"
 FT Domain 440..464
 FT /note= "Putative transmembrane domain"
 XX
 PN US6350859-B1.
 XX
 PD 26-FEB-2002.
 XX
 PF 02-FEB-1999; 99US-00241581.
 XX
 PR 23-JUN-1994; 94US-00265428.
 PR 27-MAR-1997; 97US-00765108.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Krieger M, Acton SL, Rigotti A;
 XX
 DR WPI; 2002-314680/35.
 DR N-PSDB; AAD33915.
 XX
 PT Antibody specific for scavenger receptor protein type B1 useful for
 PT detection, characterization or isolation of receptor proteins, as well
 PT inhibiting scavenger protein binding to low density lipoprotein.
 XX
 PS Claim 1; Col 33-36; 41pp; English.
 XX
 CC The invention relates to an antibody specific for scavenger receptor
 CC protein type B-I (SR-BI) derived from murine and hamster. Antibodies of
 CC the invention are useful for detection, characterization and isolation of
 CC receptor proteins and for inhibiting scavenger protein binding to low
 CC density lipoprotein (LDL). The present sequence is hamster (ha) SR-BI
 CC protein
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 5; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVAGLVGVLGCAVLGVVMIIVMPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVAGLVGVLGCAVLGVVMIIVMPSLIKQVLKQVLRIDPSSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFVFNVPNSILKGEKPVVRERGPVYVFRFRKANITFNDNDTVSFVHRSLH 120
 Db 61 VPFYLSVYFVFNVPNSILKGEKPVVRERGPVYVFRFRKANITFNDNDTVSFVHRSLH 120
 Qy 121 FQDRSHGSESDYIIILPNILVLGGAVMMESKSLAGLKMMTLGLATLGLQRAFMNRTVGEIL 180
 Db 121 FQDRSHGSESDYIIILPNILVLGGAVMMESKSLAGLKMMTLGLATLGLQRAFMNRTVGEIL 180
 Qy 181 WGYEDPPFVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPPFVNFINKYLPDMFPIKGFGLFVEMNNSDSGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Db 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFFSPSEACRSKMLTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFDHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420
 Db 361 LNPDPREHSLFDHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420
 Qy 421 AMGGEPLNTFTQVLMPQVLYVYVLLGGLLLVPVIYQLRSQKCFWFGSGKKG 480
 Db 421 AMGGEPLNTFTQVLMPQVLYVYVLLGGLLLVPVIYQLRSQKCFWFGSGKKG 480
 Qy 481 SODKEALQAYSESLMSPAAGTGLQEA 509
 Db 481 SODKEALQAYSESLMSPAAGTGLQEA 509

RESULT 6

ABO27241
 ID ABO27241 standard; protein; 509 AA.

XX AC ABO27241;

XX DT 10-SEP-2003 (first entry)

XX DE Human scavenger receptor BI , splice variant.

XX KW Human; receptor; scavenger receptor BI; SR-BI; cardiant; antilipemic;
 KW high density lipoprotein; HDL; hormone replacement therapy;
 KW postmenopausal female; cardiovascular disorder; coronary heart disease;
 KW atherosclerosis; stroke; ischaemia; restenosis; congestive heart failure;
 KW gangrene.

XX OS Homo sapiens.

XX PN US2003044782-A1.

XX PD 06-MAR-2003.

XX PF 08-FEB-2001; 2001US-00779152.

XX PR 10-JUL-1997; 97US-00890979.

XX PR 27-FEB-1998; 98US-00031626.

XX PA (ACTO/) ACTON S L.

XX PA (MCCA/) MCCARTHY J J.

XX PI Acton SL, McCarthy JJ;

XX PR WPI; 2003-503489/47.

XX DR N-PSDB; ACD44926.

PT Determining if a subject has or is at risk of developing abnormally low
 PT high density lipoprotein level, involves determining identity of allelic
 PT variant of polymorphic region of SR-BI gene of the subject.

PS Example 1; Fig 3; 84pp; English.

XX The invention relates to determining whether a subject has, or is at risk
 XX of developing, an abnormally low high density lipoprotein (HDL) level,
 XX involves determining the identity of the allelic variant of a polymorphic
 XX region of the SR-BI (scavenger receptor BI) gene of the subject, and
 XX comparing the allelic variant of the subject with allelic variants
 XX associated with abnormally low HDL levels. Also included are a kit for
 XX determining whether a subject has, or is at risk of developing, a low HDL
 XX level (comprises a probe or primer which is capable of hybridising to an
 XX SR-BI gene, and thus identifying whether the SR-BI gene contains an
 XX allelic variant of a polymorphic region which is associated with a low
 XX HDL level) and predicting the effect of hormone replacement therapy on
 XX the HDL level in a female subject (by identifying one or more allelic
 XX variants of the SR-BI gene which are associated with abnormally low HDL
 XX levels in females (especially postmenopausal females), thus predicting
 XX the effect of hormone replacement therapy on the HDL level in the
 XX subject). Also disclosed are methods of treating low HDL levels and
 XX resulting cardiovascular disorders (e.g. coronary heart disease,
 XX atherosclerosis, stroke, ischaemia, restenosis, congestive heart failure

CC and gangrene) by administering a compound that increases HDL levels, when
 CC the subject has been identified as having the common allele at residue 41
 CC of exon 8. The present sequence is a SR-BI protein
 XX Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 6; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCAVLGVVMIIVMSLTKQOVLKNVIRIDPSLSFAMWKEIP 60
 Db 1 MGSARARWAVGLGVVGLLCAVLGVVMIIVMSLTKQOVLKNVIRIDPSLSFAMWKEIP 60
 Qy 61 VPFYLSVYFPEVNPSEILKGEKPVVRERGPYVYVREPRHKANITFNNDVTVSFVHRSLSH 120
 Db 61 VPFYLSVYFPEVNPSEILKGEKPVVRERGPYVYVREPRHKANITFNNDVTVSFVHRSLSH 120
 Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGGEIL 180
 Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGGEIL 180
 Qy 181 WGYEDEPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKHLVDRWNL 240
 Db 181 WGYEDEPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKHLVDRWNL 240
 Qy 241 SKVNYWHSEOCNMINGTSGQWAPFMTQSSLSFFSPEACRSKMLTYHDSGVPEGIPTYR 300
 Db 241 SKVNYWHSEOCNMINGTSGQWAPFMTQSSLSFFSPEACRSKMLTYHDSGVPEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPDPREHSLFDHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420
 Db 361 LNPDPREHSLFDHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVLPLWFQSG 420
 Qy 421 AMGGEPLNTFTQVLMPQVLYVYVLLGGLLLVPVIYQLRSQKCFWFGSGKKG 480
 Db 421 AMGGEPLNTFTQVLMPQVLYVYVLLGGLLLVPVIYQLRSQKCFWFGSGKKG 480
 Qy 481 SODKEALQAYSESLMSPAAGTGLQEA 509
 Db 481 SODKEALQAYSESLMSPAAGTGLQEA 509

RESULT 7

ADJ46121

ID ADJ46121 standard; protein; 509 AA.

XX AC ADJ46121;

XX DT 06-MAY-2004 (first entry)

XX DE Human scavenger receptor CD36L1 variant.

XX KW Human; receptor; scavenger receptor class B type 1; CD36L1; SNP;
 KW single nucleotide polymorphism; coronary artery disease; atherosclerosis;
 KW cardiovascular disease; myocardial infarction; stroke; gangrene;
 KW high density lipoprotein; HDL; TG; triglyceride; diabetes; obesity;
 KW metabolic disorder.

OS Homo sapiens.

XX PN US2004023225-A1.

XX PD 05-FEB-2004.

XX PF 05-AUG-2002; 2002US-00212848.

XX PR 05-AUG-2002; 2002US-00212848.

PA (VITI-) VITIVITY INC.
 XX McCarthy J;
 XX WPI; 2004-224681/21.
 DR N-PSDB; ADJ46120.
 XX
 PT Determining the presence of abnormally high triglyceride (TG) level or
 PT TG:high density lipoprotein cholesterol ratio comprises determining if
 PT the subject has an allelic variant of a polymorphic region of the CD36L1
 PT gene.
 XX
 XX Disclosure; SEQ ID NO 4; 80pp; English.
 XX
 CC The invention relates to determining whether a subject has, or is at risk
 CC of developing, abnormally high triglyceride (TG) level or an abnormally
 CC high TG:high density lipoprotein cholesterol (HDL-C) ratio, comprises
 CC determining whether the subject has an allelic variant of a polymorphic
 CC region of the CD36L1 gene (scavenger receptor class B type 1) that is
 CC associated with abnormally high TG levels or TG:HDL-C ratios. Also
 CC included are a method of diagnosing or aiding in the diagnosis of
 CC abnormally high TG level or TG:HDL-C ratio in a subject, a method for
 CC treating a subject having a disease or disorder associated with specific
 CC allelic variants of a CD36L1 gene, a kit for determining whether a
 CC subject has, or is at risk of developing, abnormally high TG level or an
 CC abnormally high TG:HDL-C ratio (comprising a probe or primer capable of
 CC hybridizing to a polymorphic region of a CD36L1 gene and identifying
 CC whether the CD36L1 gene contains an allelic variant of a polymorphic
 CC region associated with abnormally high TG level or TG:HDL-C ratio, and
 CC instructions for use), a method for predicting the effect of hormone
 CC replacement therapy on the TG level or TG:HDL-C ratio in a female
 CC subject, a medical information system for assessing a subject's risk for
 CC developing an abnormally high TG level or TG:HDL-C ratio (comprising
 CC means for obtaining biological information from the individual to obtain
 CC a CD36L1 genetic profile, means for representing the CD36L1 genetic
 CC profile as digital molecular data, means for electronically processing
 CC the CD36L1 digital genetic profile to generate a risk assessment report
 CC for developing an abnormally high TG level or TG:HDL-C ratio and means
 CC for displaying the risk assessment report on an output device, where the
 CC presence of a polymorphic region of CD36L1 indicates an increased risk
 CC for developing an abnormally high TG level or TG:HDL-C ratio), a
 CC computerized method of providing medical advice to a subject, a method
 CC for a health care provider to generate a personal health assessment
 CC report for an individual and a method of assessing the health of an
 CC individual. The composition and methods are useful for identifying risk
 CC factors for abnormal lipid levels and their associated diseases and
 CC disorders. These may be used for diagnosing, prognosing or treating
 CC subjects having a disease or disorder associated with abnormal lipid
 CC levels, such as vascular (e.g. coronary artery disease, atherosclerosis,
 CC cardiovascular disease, myocardial infarction, stroke and gangrene) or
 CC metabolic (e.g. diabetes or obesity) diseases or disorders. The present
 CC sequence represents a human CD36L1 protein.
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 8; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-262;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSARARWAVGLGVGVLCAVLGVVILVPSLIIKQVLLKVRIDPSSLSFAMWKEIP 60
 Db 1 MGSARARWAVGLGVGVLCAVLGVVILVPSLIIKQVLLKVRIDPSSLSFAMWKEIP 60
 Qy 61 VPFLSYVFFVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLLH 120
 Db 61 VPFLSYVFFVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSLLH 120
 Qy 121 FQPRSHGSESDDIILPNILVLGAVVMESKAGLKMNTLGLATLQORAFMNTVGEIL 180
 Db 121 FQPRSHGSESDDIILPNILVLGAVVMESKAGLKMNTLGLATLQORAFMNTVGEIL 180
 Qy 181 WGYEDPPFVNFKYLPDMFPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPPFVNFKYLPDMFPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYWHSQCQNMINGTSCQMWPMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
 Db 241 SKVNYWHSQCQNMINGTSCQMWPMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFSLHSHPHFYNADPVLSEAVLG 360
 Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFSLHSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPDPRHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
 Db 361 LNPDPRHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
 Qy 421 AMGGEPLNTFYTLVLMPOVLQYVQVYVLLGGLLLLLLVPIYQLRSQEKCFLWMSGKKG 480
 Db 421 AMGGEPLNTFYTLVLMPOVLQYVQVYVLLGGLLLLLLVPIYQLRSQEKCFLWMSGKKG 480
 Qy 481 SODKBAIQAYSESLSMSPAAGTGLQEAKL 509
 Db 481 SODKBAIQAYSESLSMSPAAGTGLQEAKL 509
 RESULT 8
 ADJ53335
 ID ADJ53335 standard; protein; 509 AA.
 XX AC ADJ53335;
 XX AC
 DT 06-MAY-2004 (first entry)
 XX
 DE Hamster SR-BI scavenger receptor polypeptide.
 XX
 KW Hamster; SR-BI; scavenger receptor; HDL receptor; lipid; cholesterol;
 KW lipoprotein; bile acid; steroid hormone; vitamin A; atherosclerosis;
 KW adipocyte fat uptake; endocrine disorder; antiarteriosclerotic; receptor;
 KW scavenger receptor class BI.
 XX
 OS Cricetinae gen. sp.
 XX
 FN US2003167475-A1.
 PD 04-SEP-2003.
 XX
 PF 24-JUN-2002; 2002US-00178611.
 XX
 PR 15-NOV-1996; 96US-00749907.
 PR 30-AUG-1999; 99US-00385799.
 XX
 XX (KOZA/) KOZARSKY K.
 PA (RIGO/) RIGOTTI A.
 PA (KRIE/) KRIEGER M.
 XX
 PI Kozarsky K, Rigotti A, Krieger M;
 XX
 DR WPI; 2004-246237/23.
 DR N-PSDB; ADJ53334.
 XX
 PT Screening for agents that influence lipid transport, useful e.g. for
 PT treating or preventing atherosclerosis, based on modulation of the SR-BI
 PT scavenger receptor.
 XX
 PS Disclosure; SEQ ID NO 2; 22pp; English.
 XX
 CC The invention relates to a method for screening compounds that alter
 CC transport of lipids, cholesterol, lipoproteins or their components,
 CC mediated by the SR-BI scavenger receptor (SR-BI HDL receptor) or a
 CC homologue. The test compound is administered to an animal and cholesterol
 CC or bile acid levels, production levels of steroid hormones or alterations
 CC in chemical composition of lipids, lipoproteins, cholesterol, steroid
 CC hormones, bile acids and Vitamin A is measured. Agents that alter
 CC transport of lipids, cholesterol or lipoproteins are potentially useful
 CC for the treatment or prevention of atherosclerosis, fat uptake by

CC adipocytes and some endocrine disorders. This sequence represents the
 CC hamster SR-BI scavenger receptor of the invention.
 XX
 SQ Sequence 509 AA;

```

Query Match      100.0%; Score 2681; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-262;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
    |||
Db 1 MGSARARWAVAGLVGVLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
    |||

Qy 61 VPFYLSVYFFEVVNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSILH 120
    |||
Db 61 VPFYLSVYFFEVVNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSILH 120
    |||

Qy 121 FQDRSHGSESDYIIILPNILVLGGAVWMSKSAKGLMMTLGLATLGLQRAFMNRTVGEIL 180
    |||
Db 121 FQDRSHGSESDYIIILPNILVLGGAVWMSKSAKGLMMTLGLATLGLQRAFMNRTVGEIL 180
    |||

Qy 181 WGYEDPFFVNFINKYLPDMFPIKGKFGLVFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
    |||
Db 181 WGYEDPFFVNFINKYLPDMFPIKGKFGLVFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
    |||

Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
    |||
Db 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
    |||

Qy 301 FTAPKTLFANGSVYPNNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
    |||
Db 301 FTAPKTLFANGSVYPNNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
    |||

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPILLWFEQSG 420
    |||
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPILLWFEQSG 420
    |||

Qy 421 AMGGEPLNTFTYTLVLMPOVLYVQVYVLLGLGGLLLVPVIYQLRSQEKCFLFWSGSKKG 480
    |||
Db 421 AMGGEPLNTFTYTLVLMPOVLYVQVYVLLGLGGLLLVPVIYQLRSQEKCFLFWSGSKKG 480
    |||

Qy 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509
    |||
Db 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509
    |||
  
```

RESULT 9
 ADU51467
 ID ADU51467 standard; protein; 509 AA.
 XX
 AC ADU51467;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Hamster scavenger receptor class B type I-related protein - SEQ ID 2.
 XX
 KW monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
 KW SR-BI; spermatogenesis.
 XX
 OS Mesocricetus auratus.
 XX
 PN JP2004331633-A.
 XX
 PD 25-NOV-2004.
 XX
 PF 29-MAY-2003; 2003JP-00152800.
 XX
 PR 10-MAR-2003; 2003JP-00063407.
 XX
 PA (UYKA-) UNIV KANAZAWA TLO YG.
 XX
 DR WPI; 2004-810031/80.
 XX

PT Novel monoclonal antibody which belongs to mouse IgG1/kappa subclass and
 PT which specifically binds to scavenger receptor class B type I (SR-BI) of
 PT rat origin, useful for functional analysis of SR-BI.
 XX
 PS Disclosure; SEQ ID NO 2; 21pp; Japanese.

CC The invention comprises a monoclonal antibody that belongs to the mouse
 CC IgG1/kappa subclass which specifically binds to scavenger receptor class
 CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
 CC is useful for the detection and analysis of SR-BI. The monoclonal
 CC antibody of the invention is useful for analysing the influence of SR-BI
 CC on spermatogenesis in testis. The present amino acid sequence represents
 CC a golden hamster SR-BI-related protein.
 XX
 SQ Sequence 509 AA;

```

Query Match      100.0%; Score 2681; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-262;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
    |||
Db 1 MGSARARWAVAGLVGVLCAVLGVVMIWPSLIIKQVVKVRIIDPSSLSFAMWKEIP 60
    |||

Qy 61 VPFYLSVYFFEVVNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSILH 120
    |||
Db 61 VPFYLSVYFFEVVNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSILH 120
    |||

Qy 121 FQDRSHGSESDYIIILPNILVLGGAVWMSKSAKGLMMTLGLATLGLQRAFMNRTVGEIL 180
    |||
Db 121 FQDRSHGSESDYIIILPNILVLGGAVWMSKSAKGLMMTLGLATLGLQRAFMNRTVGEIL 180
    |||

Qy 181 WGYEDPFFVNFINKYLPDMFPIKGKFGLVFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
    |||
Db 181 WGYEDPFFVNFINKYLPDMFPIKGKFGLVFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
    |||

Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
    |||
Db 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMLKTYHDSGVFEGIPTYR 300
    |||

Qy 301 FTAPKTLFANGSVYPNNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
    |||
Db 301 FTAPKTLFANGSVYPNNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
    |||

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPILLWFEQSG 420
    |||
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVPVLPILLWFEQSG 420
    |||

Qy 421 AMGGEPLNTFTYTLVLMPOVLYVQVYVLLGLGGLLLVPVIYQLRSQEKCFLFWSGSKKG 480
    |||
Db 421 AMGGEPLNTFTYTLVLMPOVLYVQVYVLLGLGGLLLVPVIYQLRSQEKCFLFWSGSKKG 480
    |||

Qy 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509
    |||
Db 481 SQDKEATOAYSESLSMSPAAGTGLQEAKL 509
    |||
  
```

RESULT 10
 AEB03938
 ID AEB03938 standard; protein; 509 AA.
 XX
 AC AEB03938;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Hamster Scavenger Receptor Class B-1, SEQ ID 2.
 XX
 KW Antilipemic; transgenic animal; Scavenger Receptor Class B-1;
 KW high density lipoprotein receptor; cholesterol; lipid.
 XX
 OS Cricetulus griseus.
 XX
 PN US2005136005-A1.

Db 61 VPFLSVYFFVNVNPNVNLGQKPVVRERGYPVVRFRQKNITFNDNDTVSFVENSRLH 120
Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180
Qy 181 WGYEDDPFVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVNRWGL 240
Db 181 WGYDDPPVHFLNTYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVNRWGL 240
Qy 241 SKVNYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKIDYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKGIGQTKIBPVPVPLPLWFQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKGIGQTKIBPVPVPLPLWFQSG 420
Qy 421 AMGEPLNTFTQVLVMPQVLYQVYVLLGLGGLLLVPVYQVLRSEKCFLFWGSKKG 480
Db 421 AMGKPLSTFTQVLVMPQVLYQVYVLLGLGGLLLVPVYQVLRSEKCFLFWGSKKG 480
Qy 481 SQDKAIAQYSESLMSPAAGTGLQEA 509
Db 481 SQDKAIAQYSESLMSPAAGTGLQEA 509

RESULT 12

AAW93575
ID AAW93575 standard; protein; 509 AA.

XX AC AAW93575;

XX DT 17-JUN-1999 (first entry)

XX DE Mouse scavenger receptor class B-1 protein.

XX KW Scavenger receptor class B type I; mouse; steroid production; HDL;

XX KW cholesterol; cholesteryl ester transport; high-density lipoprotein;

XX KW lipoprotein; liver; steroidogenic tissue; SR-BI; contraception;

XX KW treatment; disorder; overproduction; underproduction; menopause;

XX KW breast cancer; prostate cancer; endometriosis; fibroid tumour.

XX OS Mus sp.

XX PN WO9911288-A1.

XX PD 11-MAR-1999.

XX PF 04-SEP-1998; 98WO-US018463.

XX PR 05-SEP-1997; 97US-0057943P.

XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX PI Krieger M;

XX XX WPI; 1999-204984/17.

XX DR N-PSDB; AAX23404.

XX XX Modification of steroid production in mammals - by administering

XX PT modulator of SR-BI expression or activity.

XX PS Disclosure; Page 81-82; 86pp; English.

XX XX This invention describes a method for modifying steroid production in a

XX CC mammal which comprises administering a compound that alters cholesterol

XX CC or cholesteryl ester transport from high-density lipoprotein (HDL) or

XX CC other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger

CC receptor class B type I). This method is useful for female contraception,
CC for treating disorders characterised by overproduction of steroids, for
CC treating disorders characterised by underproduction of steroids,
CC especially menopause, for treating disorders that can be treated by
CC decreasing steroid production, especially breast cancer, prostate cancer,
CC endometriosis or fibroid tumours

XX SQ Sequence 509 AA;

Query Match 91.3%; Score 2447; DB 2; Length 509;

Best Local Similarity 89.0%; Pred. No. 2e-238;

Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIILMPSLIKQVILKNVIRIDPSSLSFAMWKEIP 60

Db 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIILMPSLIKQVILKNVIRIDPSSLSFAMWKEIP 60

Qy 61 VPFLSVYFFVNVNPNVNLGQKPVVRERGYPVVRFRQKNITFNDNDTVSFVENSRLH 120

Db 61 VPFLSVYFFVNVNPNVNLGQKPVVRERGYPVVRFRQKNITFNDNDTVSFVENSRLH 120

Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180

Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180

Qy 181 WGYEDDPFVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVNRWGL 240

Db 181 WGYDDPPVHFLNTYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVNRWGL 240

Qy 241 SKVNYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300

Db 241 SKIDYHSEOCNMTNGTSGOMWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300

Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360

Db 301 FTAPDTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKGIGQTKIBPVPVPLPLWFQSG 420

Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISLYIKAVKGIGQTKIBPVPVPLPLWFQSG 420

Qy 421 AMGEPLNTFTQVLVMPQVLYQVYVLLGLGGLLLVPVYQVLRSEKCFLFWGSKKG 480

Db 421 AMGKPLSTFTQVLVMPQVLYQVYVLLGLGGLLLVPVYQVLRSEKCFLFWGSKKG 480

Qy 481 SQDKAIAQYSESLMSPAAGTGLQEA 509

Db 481 SQDKAIAQYSESLMSPAAGTGLQEA 509

RESULT 13

AAAY44020

ID AAAY44020 standard; protein; 509 AA.

XX AC AAAY44020;

XX DT 18-JAN-2000 (first entry)

XX DE Mouse Scavenger receptor class BI protein.

XX KW Hamster; scavenger receptor; modulation; cholesterol transport; lipid;

XX KW lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;

XX KW high density lipoprotein; ester; blood.

XX OS Mus sp.

XX PN US9562322-A.

XX PD 05-OCT-1999.

XX PF 15-NOV-1996; 96US-00749907.

XX PR 15-NOV-1996; 96US-00749907.

XX (UYPE-) UNIV PENNSYLVANIA.
PA (WASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Krieger M, Rigotti A, Kozarsky K;
XX WPI; 1999-589717/50.
DR N-PSDB; AA230616.
XX
PT Modulating cholesterol transport for the control of cholesterol levels in
PT blood.
XX
PS Disclosure; Col 29-32; 23pp; English.
XX
CC This sequence represents the mouse scavenger receptor class BI (SR-BI)
CC which is used in a method of modulating cholesterol transport. The method
CC comprises selectively altering the transport of lipid, cholesterol and/or
CC lipoproteins (or their components) into and out of mammalian cells to
CC alter plasma cholesterol levels, by administering a compound which alters
CC the expression or activity of the SR-BI scavenger protein receptor. This
CC alters the rate of clearance of the protein component of high density
CC lipoprotein (HDL) as compared to the ester component of HDL. the method
CC may be used to control cholesterol levels in the blood plasma of mammals
XX
SQ Sequence 509 AA;
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 2e-238;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSARARWAVGLGVVGLLCAVLGVVMIILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGSRRARWALGLGALGLLFAALGVVMIILVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVYFEVNVNPSBILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPFLSYVYFEVNVNPSBILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGGEIL 180
DB 121 FQPKSHGSESDYIIVLPNLIIVLGSILMESKPVSLKLMTLALVTMGQAFMNRVTGGEIL 180
QY 181 WGYEDDPFVFNKYLPMFPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYDDPFVFNLTLPDMLPIKGFGLFVGNMNSGCVFTVFTGVQNFSLHLVDKWNGL 240
QY 241 SKVNYHSEOCNMGTSQOMWAPFMTQSSLEFFSPEACRSKMLTYVHDSGVFEGIPTYR 300
DB 241 SKIDYHSEOCNMGTSQOMWAPFMTQSSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFCGAPLFLSHPHFYFNADPVLSEAVLG 360
DB 301 FTAPDTLFANGSVYPPNEGFCPCRESGQNVSTCRFCGAPLFLSHPHFYFNADPVLSEAVLG 360
QY 361 LNPDPREHSLFLDHPVTGIPMNGSVKLOISLYIKAVKGIGOTKIBPVVLPILWPFQSG 420
DB 361 LNPDPKESLFLDHPVTGIPMNGSVKQSLYIKSVKGIGOTKIBPVVLPILWPFQSG 420
QY 421 AMGGEPLNTFTQLVLPQVLYQVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480
DB 421 AMGKPLSTFTQLVLPQVLYQVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480
QY 481 SODKEATQAYSESLSMAKGTVLOEAKL 509
DB 481 SODKEATQAYSESLSMAKGTVLOEAKL 509
RESULT 14
ABB57092
ID ABB57092 standard; protein; 509 AA.
XX
AC ABB57092;
XX

DT 07-MAR-2002 (first entry)
XX Mouse ischaemic condition related protein sequence SEQ ID NO:202.
DE
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
OS Mus musculus.
XX
PN WO20018188-A2.
XX
PD 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-JP004192.
PF
XX 18-MAY-2000; 2000JP-00145977.
PR
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
PA
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
PI
XX WPI; 2002-034733/04.
DR N-PSDB; AB199330.
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
PS Claim 2; Page 576-579; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (AB199202 to AB199912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 509 AA;
Query Match 91.3%; Score 2447; DB 5; Length 509;
Best Local Similarity 89.0%; Pred. No. 2e-238;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSARARWAVGLGVVGLLCAVLGVVMIILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGSRRARWALGLGALGLLFAALGVVMIILVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVYFEVNVNPSBILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPFLSYVYFEVNVNPSBILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMMTLGLATLQORAFMNRVTGGEIL 180
DB 121 FQPKSHGSESDYIIVLPNLIIVLGSILMESKPVSLKLMTLALVTMGQAFMNRVTGGEIL 180
QY 181 WGYEDDPFVFNKYLPMFPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYDDPFVFNLTLPDMLPIKGFGLFVGNMNSGCVFTVFTGVQNFSLHLVDKWNGL 240
QY 241 SKVNYHSEOCNMGTSQOMWAPFMTQSSLEFFSPEACRSKMLTYVHDSGVFEGIPTYR 300
DB 241 SKIDYHSEOCNMGTSQOMWAPFMTQSSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFCGAPLFLSHPHFYFNADPVLSEAVLG 360

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:40:25 ; Search time 26 Seconds
(without alignments)
1883.628 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2681
Sequence: 1 MGSSARWVAVGLGVVGLL.....YSSLSMPAAKGVTLQEA 509
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	1 A53920	scavenger receptor
2	2424	90.4	529	1 JC5533	scavenger receptor
3	2236	83.4	509	1 A48528	membrane glycoprot
4	752.5	28.1	478	1 A56325	lysosomal integral
5	739	27.6	478	2 JC5670	lysosomal membrane
6	738	27.5	478	1 JH0241	85K lysosomal memb
7	692	25.8	472	1 A54870	cell adhesion rece
8	678	25.3	472	2 I49590	CD36 antigen - mou
9	673	25.1	472	1 A47402	fatty acid binding
10	600	22.4	519	1 S38957	epithelial membran
11	597	22.3	457	1 S43137	D-CD36 protein - f
12	483	18.0	525	2 A59259	sensory neuron mem
13	481.5	18.0	534	2 T27054	hypothetical prote
14	412	15.4	536	2 T24000	hypothetical prote
15	377.5	14.1	531	2 T20763	hypothetical prote
16	369	13.8	590	2 T20537	hypothetical prote
17	353.5	13.2	552	2 T27424	hypothetical prote
18	344	12.8	562	2 T15396	hypothetical prote
19	113	4.2	901	2 T03726	capsid polypeptide
20	101	3.8	1589	2 T22668	hypothetical prote
21	100.5	3.7	557	2 T50788	ubiquitin specific
22	100.5	3.7	1573	2 T50113	3-dehydroquinase s
23	100	3.7	896	2 T07408	lipoxigenase (EC 1
24	99.5	3.7	451	2 F97230	probable maltodext
25	98.5	3.7	427	2 C87232	probable integral
26	98.5	3.7	448	2 T44869	probable membrane
27	98.5	3.7	3036	2 T18995	hypothetical prote
28	98	3.7	398	2 S74347	hypothetical prote
29	97	3.6	1026	2 T18220	chitin synthase (E

phospho-n-acetylmu
PTS system mannose
PTS system mannose
hypothetical prote
hypothetical prote
phosphotransferase
PTS system, mannos
htra-like serine p
pilin longus precu
probable nucleotid
uncharacterized pr
cellulose synthase
hypothetical prote
prostaglandin-endo
acetylornithine tr
viron protein - hu

30 96.5 3.6 361 2 E71664
31 95 3.5 303 2 AC1087
32 95 3.5 303 2 AB1451
33 94.5 3.5 756 2 C84682
34 94 3.5 828 2 G87584
35 93 3.5 303 2 C97304
36 93 3.5 303 2 C95033
37 92.5 3.5 433 2 H97199
38 92 3.4 238 2 I41148
39 92 3.4 369 2 S33518
40 92 3.4 2817 2 B97033
41 91.5 3.4 1081 2 T05351
42 91 3.4 350 2 C70561
43 91 3.4 603 2 JC5063
44 90.5 3.4 423 2 S61868
45 90 3.4 554 2 T41952

scavenger receptor SR-BI - Chinese hamster
N/Alternate names: CD36-related class B scavenger receptor
C/Species: Cricetulus griseus (Chinese hamster)
C/Date: 28-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: A53920
R/Acton, S.L.; Scherer, P.E.; Lodish, H.F.; Krieger, M.
J. Biol. Chem. 269, 21003-21009, 1994
A/Title: Expression cloning of SR-BI, a CD36-related class B scavenger receptor.
A/Reference number: A53920; MUID:94342261; PMID:7520436
A/Accession: A53920
A/Molecule type: mRNA
A/Residues: 1-509 <ACT>
A/Cross-references: UNIPROT:Q60417; UNIPARC:UPI00000E7766; GB:U11453; MID:9562021; PIDN:7766
C/Function:
A/Description: mediates the endocytosis of modified lipoproteins such as oxidized or acetylated lipoproteins
C/Superfamily: lysosomal integral membrane protein II
C/Keywords: glycoprotein; transmembrane protein
F/2-8/Domain: intracellular #status predicted <CYT1>
F/9-33/Domain: transmembrane #status predicted <TM1>
F/34-442/Domain: extracellular #status predicted <EXT>
F/443-464/Domain: transmembrane #status predicted <TM2>
F/465-509/Domain: intracellular #status predicted <CYT2>
F/102,108,173,212,227,255,310,330/Binding site: carbohydrate (Asn) (covalent) #status pre

ALIGNMENTS

RESULT 1

A53920
scavenger receptor SR-BI - Chinese hamster
N/Alternate names: CD36-related class B scavenger receptor
C/Species: Cricetulus griseus (Chinese hamster)
C/Date: 28-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: A53920
R/Acton, S.L.; Scherer, P.E.; Lodish, H.F.; Krieger, M.
J. Biol. Chem. 269, 21003-21009, 1994
A/Title: Expression cloning of SR-BI, a CD36-related class B scavenger receptor.
A/Reference number: A53920; MUID:94342261; PMID:7520436
A/Accession: A53920
A/Molecule type: mRNA
A/Residues: 1-509 <ACT>
A/Cross-references: UNIPROT:Q60417; UNIPARC:UPI00000E7766; GB:U11453; MID:9562021; PIDN:7766
C/Function:
A/Description: mediates the endocytosis of modified lipoproteins such as oxidized or acetylated lipoproteins
C/Superfamily: lysosomal integral membrane protein II
C/Keywords: glycoprotein; transmembrane protein
F/2-8/Domain: intracellular #status predicted <CYT1>
F/9-33/Domain: transmembrane #status predicted <TM1>
F/34-442/Domain: extracellular #status predicted <EXT>
F/443-464/Domain: transmembrane #status predicted <TM2>
F/465-509/Domain: intracellular #status predicted <CYT2>
F/102,108,173,212,227,255,310,330/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 6.5e-210;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSARWVAVGLGVVGLLCAVLGVVMTLVMPSLIKQOVLKNVRIDPSSLSPAMWKEIP 60
Db 1 MGSSARWVAVGLGVVGLLCAVLGVVMTLVMPSLIKQOVLKNVRIDPSSLSPAMWKEIP 60

Qy 61 VPFYLSVYFEVVPSPSEILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSVFVHSLH 120
Db 61 VPFYLSVYFEVVPSPSEILKGEKPVVRERGPVYVREFRHKANITFNDNDTVSVFVHSLH 120

Qy 121 FQDRSHGESDYIILPNILVLGGAVMMESKSAAGLKLMMTLGLATLQRAFMNRTVGEIL 180
Db 121 FQDRSHGESDYIILPNILVLGGAVMMESKSAAGLKLMMTLGLATLQRAFMNRTVGEIL 180

Qy 181 WGYDEPFVNFINKYLPDMRPIKGFGLFVEMNNSDGLFTVFTGVGNFSKIHLDVRNGL 240
Db 181 WGYDEPFVNFINKYLPDMRPIKGFGLFVEMNNSDGLFTVFTGVGNFSKIHLDVRNGL 240

Qy 241 SKVNYWHSEQCMMINGTSGQWAPFMTPOSSLEFFPEACRSKMLTYHDSGVGEPIPTYR 300
Db 241 SKVNYWHSEQCMMINGTSGQWAPFMTPOSSLEFFPEACRSKMLTYHDSGVGEPIPTYR 300

Qy 301 FTAPKTLFANGSVYPNNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNAADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPNNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYNAADPVLSEAVLG 360

Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYTNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKIGTGQTKIEPVVLLPFWQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKIGTGQTKIEPVVLLPFWQSG 420
Qy 421 AMGGEPLNTFYTLQVLMPOVQLVQVYVLLGLGGLLLIPVYIQLRQOEKCFLEWGSKKG 480
Db 421 AMGGEPLNTFYTLQVLMPOVQLVQVYVLLGLGGLLLIPVYIQLRQOEKCFLEWGSKKG 480
Qy 481 SQKEAIQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SQKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 2
JC5533
scavenger receptor class B type I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5533
R;Mizutani, T.; Sonoda, Y.; Minegishi, T.; Wakabayashi, K.; Miyamoto, K.
Biochem. Biophys. Res. Commun. 234, 499-505, 1997
A;Title: Cloning, characterization, and cellular distribution of rat scavenger receptor
A;Reference number: JC5533; MUID: 97320450; PMID: 9177301
A;Accession: JC5533
A;Molecule type: mRNA
A;Residues: 1-529 <MIZ>
A;Cross-references: UNIPROT:P97943; UNIPARC:UPI0000177A34
A;Experimental source: ovary
C;Comment: This protein is a specific receptor for high density lipoprotein. It plays a
to ovarian theca interna cells or to corpus luteum.
C;Genetics:
A;Gene: srbi
C;Superfamily: lysosomal integral membrane protein II
F;1-25/Domain: signal sequence #status predicted <SIG>
F;466-482/Domain: transmembrane #status predicted <TM>

Query Match 90.4%; Score 2424; DB 2; Length 529;
Best Local Similarity 85.6%; Pred. No. 5.2e-189;
Matches 453; Conservative 31; Mismatches 25; Indels 20; Gaps 1;

Qy 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGVSRRARWALGLVGLLCAALGVIMILVPSLIKQVLKNVRIDPSSLSFGMKKEIP 60
Qy 61 VPFLSYVFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
Db 61 VPFLSYVFEVNVNPSVLNGQKPVVRERGYPVYRFRHKANITFNDNDTVSIENRSLR 120
Qy 121 FQDRSHGSESVDYIILPNILVLGGAVMMESKSLGLMTLGLATLGQRAFMNRTVGEIL 180
Db 121 FQDRSQGSESVDYVLPNILVLGGAVNMEDKPTSLKILMTLGLVGTGQRAFMNRTVGEIL 180
Qy 181 WGYEDPPVNFINKYLPDMFPIKGKFGFLFVEMNNSDGLFTVFTGVQNFSLHLDVKNGL 240
Db 181 WGYEDPPVNFILSKYFPDMFPIKGKFGFLVGNNDSSGVFTVFTGVQNFSLHLDVKNGL 240
Qy 241 SKVNYHSEQCNNINGTSGQWAPFMTPOSSEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SEVNYHSEQCNNINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYTNADPVLSEAVLG 360
Db 301 FTAPDPTLFANGSVYPPNEGFCPCRESIGQNVSTCRFGAPLFLSQPHFYTNADPVLSEAVLG 360
Qy 361 -----LNPDPREHSLFLDIHPVTGILNPDPEKHSFLDIHPVTGIPMNCVKQLQISLYIKAVKI 400
Db 361 LNPDPEKHSFLDIHPVTGILNPDPEKHSFLDIHPVTGIPMNCVKVQQLSLIKSVKGV 420
Qy 401 GQTKIEPVVLLPFWQSGAMGEPNTFYTLQVLMPOVQLVQVYVLLGLGGLLLIPV 460
Db 421 GQTKIEPVVLLPFWQSGMMGKTLNTFYTLQVLMPOVQLVQVYVLLGLGGLLLIPV 480

Qy 461 IYQLRSOEKCFLEWGSKKGSDKEAIOAYSESLSMPAAKGTVLQEAKL 509
Db 481 IYQLRSOEKCFLEWGSKKGSDKEAIOAYSESLSMPAAKGTVLQEAKL 529

RESULT 3
A48528
membrane glycoprotein CLA-1 protein long form precursor - human
N;Alternate names: CD36 and LIMP-II analogous-1 (CLA-1)
N;Contains: membrane glycoprotein CLA-1, short splice form
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S36656; A48528
R;Vega, M.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36656
A;Accession: S36656
A;Molecule type: mRNA
A;Residues: 1-509 <VEG>
A;Cross-references: UNIPROT:Q8WTV0; UNIPARC:UPI0000073A04; EMBL:Z22555; NID:g397606; PID:
A;Note: this sequence report represents the long form
R;Calvo, D.; Vega, M.A.
J. Biol. Chem. 268, 18929-18935, 1993
A;Title: Identification, primary structure, and distribution of CLA-1, a novel member of
A;Reference number: A48528; MUID: 93366811; PMID: 7689561
A;Accession: A48528
A;Molecule type: mRNA
A;Residues: 1-42,143-509 <CAL>
A;Cross-references: UNIPARC:UPI0000174241; GB:Z22555
A;Note: this sequence report represents the short form; the long form was also sequenced
C;Genetics:
A;Gene: GDB:CD3611
A;Cross-references: GDB:228074
A;Map position: 12pter-12qter
C;Superfamily: lysosomal integral membrane protein II
C;Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; myristyle
F;2-509/Product: membrane glycoprotein CLA-1, long splice form #status predicted <LMAT>
F;2-42,143-509/Product: membrane glycoprotein CLA-1, short splice form #status predicted
F;2-8/Domain: intracellular #status predicted <CYT1>
F;9-33/Domain: transmembrane #status predicted <TM1>
F;34-442/Domain: extracellular #status predicted <EXT>
F;443-464/Domain: transmembrane #status predicted <TM2>
F;465-509/Domain: intracellular #status predicted <CYT2>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;102,108,173,212,227,255,310,330/Binding site: carbohydate (Asn) (covalent) #status pre

Query Match 83.4%; Score 2236; DB 1; Length 509;
Best Local Similarity 81.3%; Pred. No. 9.5e-174;
Matches 414; Conservative 46; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MGSSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGCSAKARWAAAGALGVAGLLCAVLGAVMIIVMPSLIKQVLKNVRIDPSSLSFNMWKEIP 60
Qy 61 VPFLSYVFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
Db 61 IPFLSYVFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFLEYRTFQ 120
Qy 121 FQDRSHGSESVDYIILPNILVLGGAVMMESKSLGLMTLGLATLGQRAFMNRTVGEIL 180
Db 121 FQDSKSHGSESVDYVNPILVLGGAVMMENKPTLKLIMTLAFTLGERAFMNTVGEIM 180
Qy 181 WGYEDPPVNFINKYLPDMFPIKGKFGFLFVEMNNSDGLFTVFTGVQNFSLHLDVKNGL 240
Db 181 WGYKDPVLNINKYPCGMFFPKDKFGLFAELNNSDGLFTVFTGVQNFSLHLDVKNGL 240
Qy 241 SKVNYHSEQCNNINGTSGQWAPFMTPOSSEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVDFHSDQCNNINGTSGQWAPFMTPESSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYTNADPVLSEAVLG 360

Db 301 FVAPKTLFANGSIYPPNEGFCPCLESGLQNVSTCRFAPLFLSHPHFLNADPVLAEAVTG 360
 Qy 361 LNPDPREHSLDHPVGTGPMNCSVKLQISLYIKAVKGIGQTKIBPVVPLPILWPEQSG 420
 Db 361 LHPNQEAHSLFDHPVGTGPMNCSVKLQISLYIKAVKGIGQTKIBPVVPLPILWPEQSG 420
 Qy 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLPVVYIQLRSEKCFELFWSGSKKG 480
 Db 421 AMEGTHTFTQVLMPQVLYQVYVLLGLGGLLLPVVYIQLRSEKCFELFWSGSKKG 480
 Qy 481 SODKEALQAYSESLSMPAAKGTVLQEAEL 509
 Db 481 SKOKEALQAYSESLSMTAPKGSVLQEAEL 509

RESULT 4
 A56525
 N;Alternate names: Igp85; Limp II; lysosomal membrane 85K sialoglycoprotein
 C;Species: Homo sapiens (man)
 C;Date: 19-Oct-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
 C;Accession: A56525; JQ1523
 R;Calvo, D.; Dopazo, J.; Vega, M.A.
 Genomics 25, 100-106, 1995
 A;Title: The CD36, CLA-1 (CD36L1), and LIMPII (CD36L2) gene family: cellular distribution
 A;Reference number: A56525; MUID:95293360; PMID:7539776
 A;Accession: A56525
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-478 <CAL>
 A;Cross-references: UNIPROT:Q14108; UNIPARC:UPI000017423A
 R;Fujita, H.; Takata, Y.; Kono, A.; Tanaka, Y.; Takahashi, T.; Himeno, M.; Kato, K.
 Biochem. Biophys. Res. Commun. 184, 604-611, 1992
 A;Title: Isolation and sequencing of a cDNA clone encoding the 85KDa human lysosomal sial
 A;Reference number: JQ1523; MUID:92246940; PMID:11374238
 A;Accession: JQ1523
 A;Molecule type: mRNA
 A;Residues: 1-83,'E',85-478 <FUJ>
 A;Cross-references: UNIPARC:UPI000032D38; GB:DL2676; NID:g219702; PIDN:BAA02177.1; PID:
 A;Experimental source: Pancreatic islet
 R;Sandoval, I.V.; Arredondo, J.J.; Alcalde, J.; Noriega, A.G.; Vandekerckhove, J.; Jimer
 J. Biol. Chem. 269, 6622-6631, 1994
 A;Title: The residues Leu(1le) (475)-Ile(Leu, Val, Ala) (476), contained in the extended c
 some.
 A;Reference number: A57905; MUID:94165051; PMID:7509809
 A;Contents: annotation; sorting signal
 C;Genetics:
 A;Gene: CD36L2
 A;Cross-references: GDB:383649
 A;Map position: 4pter-4qter
 C;Superfamily: lysosomal integral membrane protein II
 C;Keywords: glycoprotein; lysosome; transmembrane protein
 F;2-478/Product: lysosomal membrane 85K sialoglycoprotein #status predicted <LVS>
 F;2-3/Domain: intracellular #status predicted <CYR1>
 F;4-26/Domain: transmembrane #status predicted <TR1>
 F;27-432/Domain: lysosomal luminal #status predicted <LLUM>
 F;433-458/Domain: transmembrane #status predicted <TR2>
 F;459-478/Domain: intracellular #status predicted <CYR2>
 F;475-476/Region: endosomal/lysosomal sorting signal
 F;475,68,105,206,224,249,304,325,412,430/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 28.1%; Score 752.5; DB 1; Length 478;
 Best Local Similarity 33.9%; Pred. No. 3.2e-53;
 Matches 162; Conservative 100; Mismatches 187; Indels 29; Gaps 9;

Qy 15 GVVGLLCAVLGVVMIIL--VMPSLIKQVLLKNVRIDPSSLSPFAMWKEIPVPFYLVSVPFEV 72
 Db 10 GTLSLLLVTSVTLVAVRFQKAVDQTIKQVNLQNGTKVFNSEKPPPLPVYIQTFYFN 69

Qy 73 VNPSEILKGEKPVVREPGVYVREFRUKANITFNDN-DTVSFVHEHSLHFPQDRSHGS 131
 Db 70 TNPSEILQGEIPLLEBVGPTVYRELKANKIQSGENGTTISAVTNKAYVPERQSVGDPN 129

Qy 132 -DYIILPNILVLGGAVNMESKAGLKLMMTLGLATLGQRAFPMNRTVGEILWGYEDPVPNF 190
 Db 130 VDLIRTNIPLL--TVVDLAQLTLLRELIEAMKAYQKQLFVTHVTHVHLLWGYKDEILSL 187

Qy 191 INKYLDPMPPIKGRGLFVEMNNSDSGLFTVTVGVQNFPSKIHLDVDRWGLSKVNYWHSEQ 250
 Db 188 VHLFKPDVSP--NFGLFYERNGTNDGEVFLTGEDNYLNFSKIVWNGKTSLDWMWTTDT 244

Qy 251 CNMNGTSGQMAFPPTQSSLEFFSPACRSKMLTYHDSGVPEGIPTYRFTAPKTLFAN 310
 Db 245 CNMNGTGDGSPHPLSKDEVLVLPFSDLCRSVHITFSSFENVEGLPAFRYKVPAILAN 304

Qy 311 GSVYPPNEGFC----PCLSSGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLGLNDPDR 366
 Db 305 TS---ENAGFCIPEGNCLGSGVLNVSICKNGAPIMSFPHFYQADBERFVSAIEGMHNPQE 361

Qy 131 SDYIIIPNIIIVLGGAVNMESKAGLKLMMTLGLATLGQRAFPMNRTVGEILWGYEDPVPNF 190
 Db 130 IDLIRTNIPVL--TVIEWQVHFLREIEAMKAYQKQLFVTHVTHVHLLWGYKDEILSL 187

Qy 191 INKYLDPMPPIKGRGLFVEMNNSDSGLFTVTVGVQNFPSKIHLDVDRWGLSKVNYWHSEQ 250
 Db 188 IHVFRPDISY---FGLFYEKNGTNDGDYVFLTGEDSYLNFTKIVWNGKTSLDWMWTTDK 244

Qy 251 CNMNGTSGQMAFPPTQSSLEFFSPACRSKMLTYHDSGVPEGIPTYRFTAPKTLFAN 310
 Db 245 CNMNGTGDGSPHPLTKDEVLVLPFSDLCRSVHITFSDYESVQGLPAFRYKVPAILAN 304

Qy 311 GSVYPPNEGFC----PCLSSGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLGLNDPDR 366
 Db 305 TS---DNAGFCIPEGNCLGSGVLNVSICKNGAPIMSFPHFYQADBERFVSAIEGMHNPQE 361

Qy 367 EHSFLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLPILWPEQSGAMGEP 426
 Db 362 DHETFDVINPLTGIILKAARKFQINIYVKLDDFVETGDIRTMVFPVYMLNESVHIDKTL 421

Qy 427 LNTFTQVLMPQVLYQVYVLLGLGGLLLPVVYIQLRSEKCFELFWSGSKGSODK 484
 Db 422 ASRL-KSMNTTLLIITNIPYIIMALGVFFGLV-----FTWLACKGQSSMDE 466

RESULT 5
 JC5670
 N;Alternate names: 85K glycoprotein precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
 C;Accession: JC5670
 R;Tabuchi, N.; Akasaki, K.; Sasaki, T.; Kanda, N.; Tsuji, H.
 J. Biochem. 122, 756-763, 1997
 A;Title: Identification and characterization of a major lysosomal membrane glycoprotein,
 A;Reference number: JC5670; MUID:98060500; PMID:9399579
 A;Accession: JC5670
 A;Molecule type: mRNA
 A;Residues: 1-478 <TAB>
 A;Cross-references: UNIPROT:Q35114; UNIPARC:UPI0000231D6; GB:AB008553; NID:g2618485; PII
 C;Superfamily: lysosomal integral membrane protein II
 F;1-26/Domain: signal sequence #status predicted <SIG>
 F;433-458/Domain: transmembrane #status predicted <TM>
 F;474-475/Region: endosomal/lysosomal sorting signal

Query Match 27.6%; Score 739; DB 2; Length 478;
 Best Local Similarity 32.9%; Pred. No. 4e-52;
 Matches 158; Conservative 103; Mismatches 195; Indels 24; Gaps 9;

Qy 15 GVVGLLCAVLGVVMIIL--VMPSLIKQVLLKNVRIDPSSLSPFAMWKEIPVPFYLVSVPFEV 72
 Db 10 GTLSLLLVTSVTLVAVRFQKAVDQTIKQVNLQNGTKVFNSEKPPPLPVYIQTFYFN 69

Qy 73 VNPSEILKGEKPVVREPGVYVREFRUKANITFNDN-DTVSFVHEHSLHFPQDRSHGS 131
 Db 70 TNPSEILQGEIPLLEBVGPTVYRELKANKIQSGENGTTISAVTNKAYVPERQSVGDPN 129

Qy 132 -DYIILPNILVLGGAVNMESKAGLKLMMTLGLATLGQRAFPMNRTVGEILWGYEDPVPNF 190
 Db 130 VDLIRTNIPLL--TVVDLAQLTLLRELIEAMKAYQKQLFVTHVTHVHLLWGYKDEILSL 187

Qy 191 INKYLDPMPPIKGRGLFVEMNNSDSGLFTVTVGVQNFPSKIHLDVDRWGLSKVNYWHSEQ 250
 Db 188 VHLFKPDVSP--NFGLFYERNGTNDGEVFLTGEDNYLNFSKIVWNGKTSLDWMWTTDT 244

Qy 251 CNMNGTSGQMAFPPTQSSLEFFSPACRSKMLTYHDSGVPEGIPTYRFTAPKTLFAN 310
 Db 245 CNMNGTGDGSPHPLSKDEVLVLPFSDLCRSVHITFSSFENVEGLPAFRYKVPAILAN 304

Qy 311 GSVYPPNEGFC----PCLSSGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLGLNDPDR 366
 Db 305 TS---ENAGFCIPEGNCLGSGVLNVSICKNGAPIMSFPHFYQADBERFVSAIEGMHNPKE 361

Db 191 -----PVPVTTTVGLFPYNNATDGVYKFNKGKONISKVAIDITYGKRNLSYWS- HCD 244
 Qy 253 MINGTSGOMWAFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYRTAPTAKTLTFANGS 312
 Db 245 MINGTDAASFPFPFVEKSQVLQFFSSDICRSIYAVPESDVNLKGIPVYRVLVPSKAFASPV 304
 Qy 313 VYPNVEGFCP-----CLESGIQNVSTCRGAPLFLSHPHYPNADPVLSEAVLGLNPPD 365
 Db 305 ENPDNYCFCTEKIKISKNCTSYGVLDISCKEGRPVYISLPHFLYASPDVSEPIDGLNPNE 364
 Qy 366 REHSLFDIDHPVTGIPMNCYSVKLQISLIVKAVKGIQGTGKIE-PVVLPLLWFEQSGAMGG 424
 Db 365 EEHRTYLDIEPIGTFTQFARKLQVNLVKPSEKIQVLKNKNTIVPILWLNETGTIGD 424
 Qy 425 EPLNTFTQLVLMPOVLQYQVYVLLGLGLLLPVI 461
 Db 425 EKANMFSQVTGKINLLGLIEMLLSVGVVMFVAFMI 461

 RESULT 8
 I49590
 CD36 antigen - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49590
 R:Endmann, G.; Stanton, L.W.; Madden, K.S.; Bryant, C.M.; White, R.T.; Protte
 J. Biol. Chem. 268, 11811-11816, 1993
 A:Title: CD36 is a receptor for oxidized low density lipoprotein.
 A:Reference number: I49590; MUID:93280144; PMID:7685021
 A:Accession: I49590
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-472 <RES>
 A:Cross-references: UNIPROT:Q08857; UNIPARC:UPI00000018D7; GB:L23108; NID:G567
 C:Superfamily: lysosomal integral membrane protein II

 Query Match 25.3%; Score 678; DB 2; Length 472;
 Best Local Similarity 30.4%; pred. No. 3.6e-47;
 Matches 143; Conservative 102; Mismatches 178; Indels 48; Gaps 9

 Qy 16 VVGLLCAVLGVMVLLVMPSLIKQVLKNVRIDPSLSFAMKKEIPVPVLSVYFVEVNP 75
 Db 14 VIGAVLAVFGGILMPVGDMLIEKIKREVLEEGTAFKNVKTGTITTYRQFPIFDVQNP 73
 Qy 76 SEILKGEKPV-VREGRGVYVR-EPRHKANITFNDN-TVSVFEHSLHFQDPSRSHGSESD 132
 Db 74 DDVAKNSKKVKQRGPTTYRVRVLAKENITQDPEDHTVSPQNGALFEPSSLVSGTDED 133
 Qy 133 YIILPNILVLG-----GAVMMESKSAGLKLMMTLGLATLGQRAFNMRTVGE 178
 Db 134 NFTVLNLAVAAAPHIYQNSFQVVVLSLKKSKS-----MFQTRSLKE 177
 Qy 179 ILNGYEDPFVNFINKYLPDMFPIKGKGLFVEMNNSDGLTFTVTGVQNFKSHLAVDRWN 238
 Db 178 LLNGYKDPFLSLV-----PYPISITTVGVFPYNDTVGVYKVFNGKDNISKVAIESYK 231
 Qy 239 GLSKVNYHSEQNMINGTSGQWAPWMTQSSLEFFSPESACRSKMLTYHDSGVFEGIPT 298
 Db 232 GKNLSYWS-YCDMINGTDAASFPFVEKSRTLRFFSSDICRSIYAVFGSEIDLKGPV 290
 Qy 299 YRTAPAKTLFANGSVYPNVEGFCP-----CLESGIQNVSTCRGAPLFLSHPHFYNA 351
 Db 291 YRVFLPANAFAPLQNDNHCFCTEKVISNCTSYGVLDIGCKEGRPVYISLPHFLHAS 350
 Qy 352 PVLSEAVLGLNPPPREHSLFLDHPVTGIPMNCYSVKLQISLIVKAVKGIQGTGKIE-PV 410
 Db 351 PDVSEPIEGLHPNEDEHRTYLDVEPIGTFTQFARKLQVNLVKPARKIEALKRKRPVI 410
 Qy 411 LPLLWFEQSGAMGGEPLNTFTQLVLMPOVLQYQVYVLLGLGLLLPVI 461
 Db 411 VPTLWLNETGTIGDKAEKMFQTVTGKIKLGMVEMALLGIVGVVMFVAFMI 461

RESULT 9

A47402
fatty acid binding/transport protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A47402
R;Abumrad, N.A.; El-Maghrabi, M.R.; Amri, E.Z.; Lopez, E.; Grimaldi, P.A.
J. Biol. Chem. 268, 17665-17668, 1993
A;Title: Cloning of a rat adipocyte membrane protein implicated in binding or transport
A;Reference number: A47402; MUID:93352566; PMID:7688729
A;Accession: A47402

A;Molecule type: mRNA
A;Residues: 1-472 <ABU>

A;Cross-references: UNIPROT:Q07969; UNIPARC:UPI0000155E68; GB:L19658; NID:g310112; PIDN:

C;Superfamily: lysosomal integral membrane protein II
C;Keywords: glycoprotein; transmembrane protein

F;2-6/Domain: intracellular #status predicted <CYT1>
F;7-30/Domain: transmembrane #status predicted <TM1>
F;31-439/Domain: extracellular #status predicted <EXT>

F;440-466/Domain: transmembrane #status predicted <TM2>
F;467-472/Domain: intracellular #status predicted <CYT2>
F;79,102,134,205,220,235,247,417/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 25.1%; Score 673; DB 1; Length 472;
Best Local Similarity 31.0%; Pred. No. 9.2e-47;
Matches 146; Conservative 95; Mismatches 182; Indels 48; Gaps 9;

QY 16 VGLLCVAVGLVWMLVMPSLIKQVLLKVRIDPSSLSFAMWKEIPVFLSYVFFEVNVP 75
DB 14 VIGAVLAVFGGILMPVGDLLIETIKREVLEEGTAFKQNVKTGTVTYRQFVWFVQNP 73

QY 76 SEILKGKPV-VRRGPPVYR-BFRHKANITFNDND-TVSFVHRSLHFOPDRSHGESD 132
DB 74 EVAKNSKIKVQRGPYTRVRYLAKENITQPKOSTVSVQNGAIFPSLSVGTEND 133

QY 133 YIILPNILVLG-----GAVMMESKAGLKLMMTLGLATLGLQAFMNRVTGE 178
DB 134 NFTVLNLAVAAPHIYNTSFQGVLSNLKKS-----MFQTRSLKE 177

QY 179 ILWGYPDFVNFNKLPMFPPIKGKGLFVEMNNSDGLFTVFTGVQNFSLHLDVRWN 238
DB 178 LLMGYKDPFSLV-----PYPISTTVGVFPYNNYTDVGYVNSGKDNISKVAIIDTYK 231

QY 239 GLSKVNYHSEQCNMINGTSGQWAPMTFQSSLEFPSPACRSMKLTYHDSGVFEGIPT 298
DB 232 GKRNLSWES-YCDMNGTDAASPPLGKSRTRLRFSSDICHSIYAVFSEVNLKGIPIV 290

QY 299 YRFTAPKTLFANGSVYPPNFGCP-----CLESIGQNVSTCRFGAPLFLSHPHFYNAD 351
DB 291 YRFVLPANAFASPLQPNPDNHCFCCTEKVSNNTSYGVLDIGCKEKGKFPVNSLPHFLHAS 350

QY 352 PVLSEAVLGNPDPREHSLFDTHPTGIPMNCVKLOISLYIKAVKGIQGTGKIB-PVV 410
DB 351 PDVSEPIEGLNPTDEHRTYLDVEPIGTFTLOFSKRLQVNLVKPARKIKALNKLKRPYI 410

QY 411 LPLWFQSGAMGGEPLNTFTVLVLMPOVLQVQVLLGLGGLLLVLPVI 461
DB 411 VPILWLNMTETIGDEKAEKMFNRNQTKIKLLGLVEMVLLGVGVVNFVAFMI 461

RESULT 10
S38957
epithelial membrane protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S38957

R;Hart, K.; Wilcox, M.
J. Mol. Biol. 234, 249-253, 1993

A;Title: A Drosophila gene encoding an epithelial membrane protein with homology to CD36
A;Reference number: S38957; MUID:94047068; PMID:7693949

A;Accession: S38957
A;Molecule type: mRNA
A;Residues: 1-519 <HAR>

A;Cross-references: UNIPROT:Q24336; UNIPARC:UPI00000774AD; EMBL:X73332; NID:g429163; PIDN:

C;Genetics:
A;Gene: FlyBase:emp

A;Cross-references: FlyBase:FBgn0010435
C;Superfamily: lysosomal integral membrane protein II
C;Keywords: transmembrane protein

F;2-19/Domain: intracellular #status predicted <CYT1>
F;20-39/Domain: transmembrane #status predicted <TM1>
F;460-482/Domain: transmembrane #status predicted <TM2>

F;483-519/Domain: intracellular #status predicted <CYT2>

Query Match 22.4%; Score 600; DB 1; Length 519;
Best Local Similarity 30.3%; Pred. No. 8.9e-41;
Matches 155; Conservative 88; Mismatches 224; Indels 44; Gaps 12;

QY 6 RARWAVGLGVVGLLCAVLGVVMIIVMPSLIKQVLLKVRIDPSSLSFAMWKEIPVFL 65
DB 18 RKWWTI-----VVAALIIIGGIIVVACEFTVLIDAVVDRMVVALRPGKATFGWAKAPVPEPI 74

QY 66 SVYFFEVNPSIL-KGEKPVVRRGPPVYVRRFRHKANITFNDNDTVSFVHRSLHFQPD 124
DB 75 SLIYVNTVADDFLSNGSKAIVDEVGPPYVSETWEKVNIVENDNGTLSYNLRKIYSFRED 134

QY 125 RHGSESDYIILPNILVLGAVMMESKAGLKLMMTLGLATLGLQAFMNRVTGEILWYGE 184
DB 135 LSVGPEDDVVIVENIPMLSATSQSKHAARFLRLAMASIMDLKIKPFVQVSVGQLLWGYE 194

QY 185 DPFVNFINKYLDMPPIKQK-----FGLFVEMNNSDGLFTVFTGVQNFSLHLDVRWN 239
DB 195 DPLL-----KLAKDVVPKEQKLYEFGLLYGKNGTSSDRVTVTNTGVDDIRRYGIDNFG 250

QY 240 LSKVNYHSEQCNMINGTSGQWAPMTFQSSLEFPSPACRSMKLTYHDSGVFEG-IPT 298
DB 251 RTHLPHTWTDACNTLAGTDSIFPPHIDHRLHLYVDKDLCLLLPLVFEKEVMTSNEVFG 310

QY 299 YRFTAPKTLFANGSVYPPN-----GFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADP 352
DB 311 YRFTTRVGRRCGQ--PPGQHVLLSRGKPCSPNGLFNVSLCQYDSPIMLSPPHFYLADE 368

QY 353 VLSEAVLGNPDPRE-HSLFLDIHPVTGIPMNCVKLOISLYIKAVKGIQGTGKIBPVVL 411
DB 369 SLRTQVEGISPPMKEKHQFFFDVQPKMGTTLRVARIQINLAVSQVFDIKQVANFPDIIF 428

QY 412 LPLWFQSGAMGGEPLNTFTVLV-----LMPQVLQVQVQVLLGLGGLLLVLPVIYQLR- 465
DB 429 PILWFE-----GIDNLPDEVLTALMRFAEQVPKIRVALIVGLCALGVILLLLSTFCILRN 484

QY 466 SQEKCFLFWSGS-----KKGSDQKE 485
DB 485 SHRQSTLHLEGSNYLATAQVDMNKKQNKQ 515

RESULT 11
S43137
D-CD36 protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S43137; S43136

R;Franc, N.; Dimarcq, J.; Hoffmann, J.; Lagueux, M.
submitted to the EMBL Data Library, March 1994

A;Description: d-CD36 : a second Drosophila gene related to the CD36 family of cell adhe

A;Reference number: S43136
A;Accession: S43137
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-457 <FRA>

A;Cross-references: UNIPROT:Q27367; UNIPARC:UPI000016BB39; EMBL:Z31583; NID:g468537; PIDN:

C;Genetics:
A;Gene: FlyBase:croquemort

A;Cross-references: FlyBase:FBgn0015924
C;Superfamily: lysosomal integral membrane protein II

Query Match 22.3%; Score 597; DB 1; Length 457;

Db	170	KDVFRLRVKAMDIMFRGIINCDRTFPAKCACTMKKDAVTGVYIYBPNQFRFSUGTGN	229
QY	213	NS--DSGLFTFTVGTQVNSKHLVDRMNGLSKVNYHSEOCNMINGTSGOMWAFPMTPQSS	271
Db	230	NTVPDPVTVYRGKINIMDVQVVALNGKQIDIR-DHCNEPQSGTGTGVFPFPLTYKDR	288
QY	272	LEFFSPACRSKMLTYHDSGVFGFIPTFTAPKTLFANGSVYPPNEGFC----PCLESG	327
Db	289	LQSPFSLDCRSFKAWFOKKTSGYKIKTNRYIANVGDFAND---PELQCFCDPTDECLPKG	345
QY	328	IQNVSTCRFGAPLFLSHPHFNADPVLSEAVILGNDDPREHSLFLDIHPVTGIPMNCVK	387
Db	346	IMDRKC-LKVPMTVSLPHLETDTSVTNQVKGTLDPDNEHGIADFEPLSGTLMDAKOR	404
QY	388	LQISLIVKAVGIGQTKGIEPVPVLLPWPQSGAMGGEPLNTFYTLVLMPOVLQVQVY	447
Db	405	MOYNIKLLRTDKIAIFKDLPSIVPCFVWHEGILLNKTFFVKMLKHQLFIPKRIVGVIWM	464
QY	448	LLIGLGLLLLLVPVIYQIURSEKCPFLFWSGS-----KGSQDKAEIAQVSESLMP	497
Db	465	MVSLGLIAVLAVGMVHFKN---IMGWAAKGESTTAKVNPEDSGNQGVSVIGQDREPP	521
RESULT 13			
T27054			
hypothetical protein Y49E10.20 - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004			
C:Accession: T27054			
R:Barlow, K.			
submitted to the EMBL Data Library, August 1997			
A:Reference number: Z20303			
A:Accession: T27054			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-534 <WIL>			
A:Cross-references: UNIPROT:Q9XTT3; UNIPARC:UPI0000083B4E; EMBL:Z98866; PIDN:CI			
A:Experimental source: clone Y49E10			
C:Genetics:			
A:Gene: CESP:Y49E10.20			
A:Map position: 3			
A:Insertion: 42/3; 105/2; 188/3; 231/3; 359/1; 440/2; 505/3			
C:Superfamily: lysosomal integral membrane protein II			
Query Match 18.0%; Score 481.5; DB 2; Length 534;			
Best Local Similarity 27.7%; Pred. No. 4e-31;			
Matches 150; Conservative 102; Mismatches 201; Indels 89; Gaps 23			
QY	16	VVGLCAVLGVYMLVMP--SLIKQQVLKNVRIDPSSLSP-----AMWKEIIPV 62	
Db	14	ILGLLLAAAGVLLIGIPIDRIVNRQV----IDQDFLGYTRDENGTEVNPAMTKSWLKP 68	
QY	63	PY---LSVYFEVNPSEILK-GEKPVRRGYPVYREFRHKANITFNDDNTVSFVHEHS 118	
Db	69	LYAMQLANIMFNVTNVDGILKRHEKPNLHIEGIFVFEVQEKYVYHRFADNTRVFYKOK 128	
QY	119	L-HFQPDPS----HGSSESDVILLPNLIV--LGAVNMVESKAGLKLMMTLLGATLQORAF 171	
Db	129	LYHFNKNASCPTCHDNK--VTIPNIVFQKLIDAADVTTFGVRIKFAISVLKMWSEAPY 186	
QY	172	MNRTVGEILM-GYEDDPFVNFINK-----YLPDMFFPIKGKFLGVEMNNNSDGLFTVFTGV 225	
Db	187	ITVKVSDALPGYEDPIIDIVCKNKLILQFLCETNSLQRRVGFYQNGTTDGIYEVDAGV 246	
QY	226	QNFSKIHLVDRWGLSKV--NYHSEOCNMINGTSGOMWAFPMTPQSSLEFFSPACRSNM 283	
Db	247	PSPSKIGHLYTWNNTNTEMPGSDTDTKYARMINGTDGQLFSPMLKREDRLTIFVFPQICRSI 306	
QY	284	KLTYHDSGVFGIPTYFTAPKTLFANGSVYPPNEGFC-----PCLES 326	
Db	307	QWEYTKQVAVNGVPSWYAPPLDLY--DPALPQNRAPCNKNGMPRVFDTNNTVOIENCLPA 364	

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:35:04 ; Search time 147.5 Seconds
(without alignments)
2434.671.Million cell updates/sec

Title: US-08-765-108-4

Perfect score: 2881

Sequence: 1 MGSGARARWAVGLGVVGLL.....YBSLMSPAKGTVLQBAKL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	1	Q60417 cricetus
2	2447	91.3	509	1	Q61009 mus musculus
3	2447	91.3	509	2	Q4FK30 mouse
4	2444	91.2	509	1	Q61009 mus musculus
5	2430	90.6	509	2	Q85548 rat
6	2424	90.4	509	2	Q85548 rat
7	2260	84.3	509	2	Q85548 rat
8	2244	83.7	509	2	Q85548 rat
9	2227	83.1	509	2	Q85548 rat
10	2215	82.6	506	2	Q85548 rat
11	2215	82.6	509	1	Q85548 rat
12	2158	80.5	509	1	Q85548 rat
13	2066	77.1	552	1	Q85548 rat
14	2066	77.1	552	1	Q85548 rat
15	2049	76.4	501	2	Q85548 rat
16	1415	52.8	460	2	Q85548 rat
17	1303	48.6	457	2	Q85548 rat
18	797	29.7	2096	2	Q85548 rat
19	772	28.8	532	2	Q85548 rat
20	751	28.0	477	1	Q85548 rat
21	751	28.0	478	2	Q85548 rat
22	740	27.6	531	2	Q85548 rat
23	739	27.6	477	1	Q85548 rat
24	738	27.5	477	1	Q85548 rat
25	735	27.4	483	2	Q85548 rat
26	728	27.2	465	2	Q85548 rat
27	709	26.5	484	2	Q85548 rat
28	709	26.4	472	2	Q85548 rat
29	707	26.4	471	2	Q85548 rat
30	702	26.2	472	2	Q85548 rat
31	699	26.1	472	2	Q85548 rat

32	696	26.0	472	2	Q35754 rat
33	692	25.8	471	1	Q35754 rat
34	688	25.7	522	2	Q7Q950 anoga
35	686	25.6	472	2	Q6J512 macaca mula
36	685	25.6	472	2	Q4R6B4 macaca fabc
37	685	25.6	471	1	Q70110 mesocricetu
38	683	25.5	460	2	Q4SACL tetng
39	678	25.3	471	1	Q356 mouse
40	675	25.2	472	2	Q8C6Z4 mouse
41	673	25.1	471	1	Q356 rat
42	657	24.5	471	1	Q356 bovin
43	649.5	24.2	601	2	Q8IGF0 drome
44	647.5	24.2	520	2	Q7KVF1 drome
45	647.5	24.2	551	2	Q9W0X0 drome

ALIGNMENTS

RESULT 1

ID	SCRB1 CRIGR	STANDARD;	PRT;	509 AA.
AC	Q60417;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DB	Scavenger receptor class B member 1 (SRB1) (SR-BI) (HaSR-BI).			
GN	Name:SCARB1;			
OS	Cricetulus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Cricetidae; Cricetinae; Cricetulus.			
OX	NCBI_TaxID=10029;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Ovarian carcinoma;			
RX	MEDLINE=94342261; PubMed=7520436;			
RA	Acton S.L., Scherer P.E., Lodish H.P., Krieger M.;			
RT	"Expression cloning of SR-BI, a CD36-related class B scavenger receptor.";			
RL	J. Biol. Chem. 269:21003-21009(1994).			

CC - FUNCTION: Receptor for different ligands such as phospholipids, cholesterol ester, lipoproteins, phosphatidylserine and apoptotic cells. Probable receptor for HDL, located in particular region of the plasma membrane, called caveolae. Facilitates the flux of free and esterified cholesterol between the cell surface and extracellular donors and acceptors, such as HDL and to a lesser extent, apoB-containing lipoproteins and modified lipoproteins. Probably involved in the phagocytosis of apoptotic cells, via its phosphatidylserine binding activity (By similarity).

CC - SUBCELLULAR LOCATION: Integral membrane protein. Predominantly localized to cholesterol and sphingomyelin-enriched domains within the plasma membrane, called caveolae (By similarity).

CC - PTM: N-glycosylated (By similarity).

CC - SIMILARITY: Belongs to the CD36 family.

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DR EMBL: U11453; AAA61572.1; -; mRNA.

DR PIR: A53920; A53920.

DR InterPro: IPR002159; CD36.

DR InterPro: IPR005428; CD36 antigen.

DR PANTHER: PTHR11923; CD36; 1.

DR Pfam: PF01130; CD36; 1.

DR PRINTS: PR01610; CD36ANTIGEN.

DR PRINTS: PR01609; CD36FAMILY.

KW Glycoprotein; Receptor; Transmembrane.

FT TOPO_DOM 1 11 Cytoplasmic (Potential).

FT TRANSMEM 12 32 Potential.

steroidogenic tissues.
 -!- PTM: N-glycosylated (By similarity).
 -!- SIMILARITY: Belongs to the CD36 family.

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 EMBL: U37799; AAC52378.1; -; mRNA.
 DR EMBL; AK010622; BAB27068.1; -; mRNA.
 DR EMBL; AK028191; BAC25802.1; -; mRNA.
 DR EMBL; AK033114; BAC28157.1; -; mRNA.
 DR EMBL; BC004656; AA04656.1; -; mRNA.
 DR Ensembl; ENSMUSG00000037936; Mus musculus.
 DR MGI; MGI:893578; Scarbl.

GO: GO:0016599; C:cytosolic membrane; IDA.
 DR GO; GO:0002399; C:integral to membrane of membrane fraction; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR InterPro; IPR002159; CD36.
 DR InterPro; IPR005428; CD36 antigen.
 DR PANTHER; PTHR11923; CD36; 1.
 DR Pfam; PF01130; CD36; 1.
 DR PRINTS; PR01610; CD36ANTIGEN.
 DR PRINTS; PR01609; CD36FAMILY.
 DR Glycoprotein; Receptor; Transmembrane.
 KW TOPO_DOM 1 11
 FT Transmem 12 32
 FT Transmem 33 440
 FT TOPO_DOM 441 461
 FT Transmem 462 509
 FT CARBOHYD 102 108
 FT CARBOHYD 108 108
 FT CARBOHYD 116 116
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 FT CARBOHYD 173 173
 FT CARBOHYD 212 212
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 FT CARBOHYD 255 255
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 FT CARBOHYD 383 383
 FT CARBOHYD 396 396
 FT CONFLICT 396 396
 FT CONFLICT 468 509

EC: EC:FLWGSKSGSODKEAIOAYSESLSMPAAKGTVLQEAQ
 S -> F (in Ref. 2; BAB27068).
 L -> GPEDTTSPPNLIAWSDPPSPYTPLEDSLSQPTSS
 AMA (in Ref. 2; BAB27068).
 5CFCD62DD6ECB1C CRC64;

Query Match 91.3%; Score 2447; DB 1; Length 509;
 Best Local Similarity 89.0%; Pred. No. 1.7e-182;
 Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSARARWAVGLGVVGLLCVGLVGMVILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 DB 1 MGSRRARWALGALGALGALLFAALGVVMIILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60

QY 61 VPFYLSVYFPEVNVNPSSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
 DB 61 VPFYLSVYFPEVNVNPSSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120

QY 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKMNTLGLATLQORAFMNRVTGVEIL 180
 DB 121 FQPKSHGSESDYIILPNILVLGSLMESKPSVLKLMNTLGLATLQORAFMNRVTGVEIL 180

QY 181 WGYEDPFWNFINKYLPDMPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
 DB 181 WGYDDPFWHFLNTYLPDMLPIKKGKGLFVGMNNSGVTFTVFTGVQNFSKIHLVDKRWGL 240

QY 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPFACRSKMLTVDHSGVFEIGPTYR 300
 DB 241 SKIDYWHSEOCNMINGTSGQWAPFMTPESSLEFFSPFACRSKMLTYNESRVEIGPTYR 300

QY 301 FTAPKTLFANGSVYYPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 DB 301 FTAPDTLFGANGSVYYPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360

QY 361 LNPDPREHSLFLDIHPVTGTPMNCVKLQISLYIKAVKGIGQTKIEPVPVLLPWFQSG 420
 DB 361 LNPNPKHSLFLDIHPVTGTPMNCVKLQISLYIKAVKGIGQTKIEPVPVLLPWFQSG 420

RESULT 3

Q4FK30_MOUSE
 ID Q4FK30_MOUSE PRELIMINARY; PRT; 509 AA.
 AC Q4FK30;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Scarbl protein.
 GN Name=Scarbl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Wuenstmann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.;
 RA "Cloning of mouse full open reading frames in Gateway(R) system entry
 RT vector (pDONR201).";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CTO10222; CAJ18430.1; -; mRNA.
 SQ SEQUENCE 509 AA; 56754 MW; 5CFCD62DD6ECB1C CRC64;

Query Match 91.3%; Score 2447; DB 2; Length 509;
 Best Local Similarity 89.0%; Pred. No. 1.7e-182;
 Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSARARWAVGLGVVGLLCVGLVGMVILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 DB 1 MGSRRARWALGALGALGALLFAALGVVMIILVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60

QY 61 VPFYLSVYFPEVNVNPSSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
 DB 61 VPFYLSVYFPEVNVNPSSEILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120

QY 121 FQDRSHGSESDYIILPNILVLGAVVMESKSLAGLKMNTLGLATLQORAFMNRVTGVEIL 180
 DB 121 FQPKSHGSESDYIILPNILVLGSLMESKPSVLKLMNTLGLATLQORAFMNRVTGVEIL 180

QY 181 WGYEDPFWNFINKYLPDMPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
 DB 181 WGYDDPFWHFLNTYLPDMLPIKKGKGLFVGMNNSGVTFTVFTGVQNFSKIHLVDKRWGL 240

QY 241 SKVNYWHSEOCNMINGTSGQWAPFMTPOSSLEFFSPFACRSKMLTVDHSGVFEIGPTYR 300
 DB 241 SKIDYWHSEOCNMINGTSGQWAPFMTPESSLEFFSPFACRSKMLTYNESRVEIGPTYR 300

QY 301 FTAPKTLFANGSVYYPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 DB 301 FTAPDTLFGANGSVYYPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360

QY 361 LNPDPREHSLFLDIHPVTGTPMNCVKLQISLYIKAVKGIGQTKIEPVPVLLPWFQSG 420
 DB 361 LNPNPKHSLFLDIHPVTGTPMNCVKLQISLYIKAVKGIGQTKIEPVPVLLPWFQSG 420


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QY 481 SODKEALQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAMQAYSESLSMPAAKGTVVQEAKL 509

RESULT 6
Q6SR89 RAT
ID Q6SR89 RAT PRELIMINARY; PRT; 509 AA.
AC Q6SR89;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Scavenger receptor class B type 1.
GN Name-Scarbl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RX MEDLINE=99236778; PubMed=10221589; DOI=10.1385/ENDO.9:3:243;
RA McLean M.P., Sandhoff T.W.;
RT "Expression and hormonal regulation of the high-density lipoprotein
RT (HDL) receptor scavenger receptor class B type I messenger ribonucleic
RT acid in the rat ovary.";
RL Endocrine 9:243-252(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RX MEDLINE=20043932; PubMed=10579331; DOI=10.1210/en.140.12.5669;
RA Lopez D., McLean M.P.;
RT "Sterol regulatory element-binding protein-la binds to cis elements in
RT the promoter of the rat high density lipoprotein receptor SR-BI
RT gene.";
RL Endocrinology 140:5669-5681(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RA McLean M.P., Sandhoff T.W., Lopez D.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451993; AAR18387.1; -; mRNA.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004872; F.receptor activity; IEA.
DR GO; GO:0007155; P.cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 56859 MW; EA0A76ECD207706C CRC64;

Query Match 90.4%; Score 2424; DB 2; Length 509;
Best Local Similarity 88.4%; Pred. No. 1.1e-180;
Matches 450; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGSSARARVAVGLGVVGLLCVGLVVMILVWPSLIKQVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGVSSEARVVALGLVGLLCVGLVVMILVWPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPPYLSVYFFVFNVPSEILKGEKPVVRERGYPVYRFRUKANITFNDNDTVSFVHRSLH 120
Db 61 VPPYLSVYFFVFNVPSEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVPIENRSLR 120
QY 121 FQPDRRSHGESDYIILPNLIVLGGAVMMESKAGLKLMTGLATIGQAFNMRTVGEIL 180
Db 121 FQPDROQGESDYIVLPNLIVLGGAVMMEDKPTSLKLLMTGLVLTWQGAQFMNRTVGEIL 180
QY 181 WGYEDPFPVNFINKYLPDMFPFIKGKFLGFVEMNNSDGLFTFTVGQNFQSKIHVLDRWNGL 240

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Db 181 WGYEDPFFVNFSLKYFPGMPFIKGRGFLVGMNDSSGVFTVTCGVNQFSKIHLVDKWNGL 240
Qy 241 SKNYWHSEOCNMINGTSCQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SEVNYWHSEOCNMINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQBSRVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCRESIQNVSTCRFGAPLFLSQPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDLHPVTGIPMNCVKQLSLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPKEHSLFDLHPVTGIPMNCVKQLSLYIKSVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLVPVLYOLRSQKCFLWSSKKG 480
Db 421 MMGKTLNTFYTLVLMPOVLQVYVLLGLGGLLVPVLYOLRSQKCFLWSSKKG 480
Qy 481 SODKEAIQAYSESLSMSPAAGTGLVLEAKL 509
Db 481 SODKEAMQAYSESLSMSPAAGTGLVLEAKL 509

RESULT 7
Q6T8F1 TUPGB PRELIMINARY; PRT; 509 AA.
AC Q6T8F1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scavenger receptor class B member 1.
GN Name=SCARB1;
OS Tupaia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaiia.
OC NCBI_TaxID=37347;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Barth H., Cerino R., Arcuri M., Hoffmann M., Schurmann P., Adah M.I.,
RA Giesler B., Zhao X., Ghisetti V., Lavezzo B., Blum H.E.,
RA von Weizsacker F., Vitelli A., Scarselli E., Baumert T.F.;
RT "Scavenger Receptor Class B Type I and Hepatitis C Virus Infection of
RT Primary Tupaia Hepatocytes.";
RL J. Virol. 79:5774-5785(2005);
DR EMBL; AY28553; ARL2144.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 57369 MW; FOA3FBB1431FFB18 CRC64;

Query Match 84.3%; Score 2260; DB 2; Length 509;
Best Local Similarity 81.3%; Pred. No. 6.9e-168;
Matches 414; Conservative 49; Mismatches 46; Indels 0; Gaps 0;

Qy 1 MGGSARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQOVLKVRIDPSSLSFAMWKEIP 60
Db 1 MGGRRARWAVAVGVVGLLCVAVGVVMIIVMPSLIKQOVLKVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFVFNPNPSEILKGEKPVVRGPGYVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPFYLSVYFVFNPNPSEILKGEKPVVRGPGYVYRFRHKSNITFNDNDTVSYLVSFR 120
Qy 121 FQDRSHGSSDYIILPNILVILGAVNMESKAGLKLMTLGLATLGCQAFMRTVCEIL 180
Db 121 FQPARGLGSSDYIIVMPNILVILGAAIMNKNPMSLKLMTLAFSTLGERAFMRTVAEIM 180
Qy 181 WGYEDPFFVNFINKYLPDMFPIKGRGFLVGMNDSGLFTVTCGVNQFSKIHLVDKWNGL 240
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Db 181 WGYEDPVLVINKYFDPMLPFKGFGLPAELNNSGLFTVTCGVKDFQRIHLVDKWNGL 240
Qy 241 SKNYWHSEOCNMINGTSCQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNFHSDQCNMINGTSCQWAPFMTPESSLEFFSPACRSKMLTYQBSRVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDLHPVTGIPMNCVKQLSLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LHPNQEHSLFDLHPVTGIPMNCVKQLSLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLVPVLYOLRSQKCFLWSSKKG 480
Db 421 AMEGETLRTFYTLVLLPAVLHYAQVYVLLALGCLLLVPVHHIRSQEKCYLFWSSKKG 480
Qy 481 SODKEAIQAYSESLSMSPAAGTGLVLEAKL 509
Db 481 PKDKEAIQAYSESLSMTPAPRGIVLQEARL 509

RESULT 8
Q52LZ5 HUMAN
ID Q52LZ5_HUMAN PRELIMINARY; PRT; 509 AA.
AC Q52LZ5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Scavenger receptor class B, member 1.
GN Name=SCARB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RS MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones J.E., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RS TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC093732; AAH93732.1; -; mRNA.
KW Receptor.
SQ SEQUENCE 509 AA; 56973 MW; 0184AE9CEC595374 CRC64;

Query Match 83.7%; Score 2244; DB 2; Length 509;
Best Local Similarity 81.5%; Pred. No. 1.2e-166;
```

Matches 415; Conservative 46; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MGGSARARVAVGLGVGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 Db 1 MGCSAKARWAAGALGVAGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 Qy 61 VPFLSVYVFEVWNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSILH 120
 Db 61 IPFLSVYVFDVWNPSEILKGEKQVVRERGYPVYVREFRHKSNITFNNNDTVSFLEYRTFQ 120
 Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180
 Db 121 FQPSKSHGSESDYIIVMNLVLGAVMENKFWILKLIMTLAFTLGERAFMNRVTGGEIM 180
 Qy 181 WGYEDPFFNFKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYKDPVLNLYKFPFGPFKDFGLFAELNNSDGLFTVFTGVQNISRIHLVDKWNGL 240
 Qy 241 SKVNYHSEOCNMINGTSGQWAPFMTQSSLEFSPSEACSMKLYTHDSGVFEGIPTYR 300
 Db 241 SKVDFWSDQCNMNGTSGQWAPFMTQSSLEFSPSEACSMKLYTHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FVAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFNADPVLSEAVTG 360
 Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVLPLWFQSG 420
 Db 361 LHPNQEAHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVLPLWFQSG 420
 Qy 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPIYQIRSOEKCFLFWSGSKG 480
 Db 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPIYQIRSOEKCFLFWSGSKG 480
 Qy 481 SODKEAIOAYSESLMSPAAGKTVLQEAKL 509
 Db 481 SKDKEAIOAYSESLMTAPKGSVLQEAKL 509

RESULT 9

Q6WIW9_RABIT PRELIMINARY; PRT; 509 AA.

AC Q6WIW9_RABIT PRELIMINARY; PRT; 509 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Scavenger receptor class B type I.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RP PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;

RA Ritsch A., Tancevski I., Schoger W., Pfeifhofer C., Gander R.,
 RA Eller P., Foeger B., Stanzl U., Patsch J.R.;

RT "Molecular characterization of rabbit scavenger receptor class B types
 RT I and II: portal to central vein gradient of expression in the
 RT liver".

RL J. Lipid Res. 45:214-222(2004).

DR EMBL; AY283277; AAP40266.1; -; mRNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR002159; CD36.

DR InterPro; IPR005428; CD36_antigen.

DR Pfam; PF01130; CD36; 1.

DR PRINTS; PR01610; CD36ANTIGEN.

DR PRINTS; PR01609; CD36FAMILY.

KW Receptor.

SQ SEQUENCE 509 AA; 57052 MW; 00DD47F1AF2DB4E0 CRC64;

Query Match 83.1%; Score 2227; DB 2; Length 509;

Best Local Similarity 80.4%; Pred. No. 2.6e-165;
 Matches 409; Conservative 48; Mismatches 52; Indels 0; Gaps 0;

Qy 1 MGGSARARVAVGLGVGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 Db 1 MGGRARARRAAGLGVVGLCAVLGVVMIWVPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
 Qy 61 VPFLSVYVFEVWNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVHRSILH 120
 Db 61 APFLSVYVFDVWNPSEILKGEKQVVRERGYPVYVREFRHKANITFNDNDTVSFLEHRSFQ 120
 Qy 121 FQDRSHGSESDYIILPNILVLGAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180
 Db 121 FQDPKSGSESDYIVIPNLVLAASFMEHHRPMSLKLIMTLAFTLQORAFMNRVTGGEIM 180
 Qy 181 WGYEDPFFNFKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Db 181 WGYEDPPLNLYKFPFGPFKDFGLFAEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
 Qy 241 SKVNYHSEOCNMINGTSGQWAPFMTQSSLEFSPSEACSMKLYTHDSGVFEGIPTYR 300
 Db 241 SKVNFHSDQCNMNGTSGQWAPFMTQSSLEFSPSEACSMKLYTHDSGVFEGIPTYR 300
 Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Db 301 FVAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVLPLWFQSG 420
 Db 361 LHPNEEHALFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVLPLWFQSG 420
 Qy 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPIYQIRSOEKCFLFWSGSKG 480
 Db 421 AMGEPLNTFTQVLMPQVLYQVYVLLGLGGLLLVPIYQIRSOEKCFLFWSGSKG 480
 Qy 481 SODKEAIOAYSESLMSPAAGKTVLQEAKL 509
 Db 481 SKDKEAIOAYSESLMTAPKGSVLQEAKL 509

RESULT 10

Q6B4I7_RAT PRELIMINARY; PRT; 506 AA.

AC Q6B4I7_RAT PRELIMINARY; PRT; 506 AA.

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Scavenger receptor class B type 2.

GN Names=Scarb2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.

OX NCBI_TaxID=101116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RP STRAIN=Sprague-Dawley;

RA Lopez D., Rubin D., McLean M.P.;

RT "Regulation of the Rat SR-B Isoforms";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY682847; AAT85567.1; -; mRNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR002159; CD36.

DR InterPro; IPR005428; CD36_antigen.

DR Pfam; PF01130; CD36; 1.

DR PRINTS; PR01610; CD36ANTIGEN.

DR PRINTS; PR01609; CD36FAMILY.

KW Receptor.

SQ SEQUENCE 506 AA; 56342 MW; 6FDBE25301320E2E CRC64;

RESULT 12
ID SCRB1_BOVIN STANDARD; PRT; 509 AA.

AC O18824;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
GN Name=SCARB1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Corpus luteum;
RX MEDLINE=98068685; PubMed=9406850; DOI=10.1016/S0303-7207(97)00173-1;
RA Rajapaksha W.R.A.K.J.S., McBride M., Robertson L., O'Shaughnessy P.J.;
RT "Sequence of the bovine HDL-receptor (SR-BI) cDNA and changes in
RT receptor mRNA expression during granulosa cell luteinization in vivo
RT and in vitro.";
RL Mol. Cell. Endocrinol. 134:59-67 (1997).

CC -I- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apolipoprotein
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apolipoprotein lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae (By similarity).
CC -I- PTM: N-glycosylated (By similarity).
CC -I- SIMILARITY: Belongs to the CD36 family.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; AF019384; AAB70920.1; -; mRNA.
CC InterPro; IPR002159; CD36.
CC InterPro; IPR005428; CD36 antigen.
CC PANTHER; PTHR11923; CD36; 1.
CC Pfam; PF01130; CD36; 1.
CC PRINTS; PR01610; CD36ANTIGEN.
CC PRINTS; PR01609; CD36FAMILY.
CC KW Glycoprotein; Receptor; Transmembrane.
CC TOPO_DOM 1 11 Cytoplasmic (Potential).
CC TRANSHEM 12 32 Potential.
CC TOPO_DOM 33 440 Extracellular (Potential).
CC TRANSHEM 441 461 Potential.
CC TOPO_DOM 462 509 Cytoplasmic (Potential).
CC CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
CC SQ SEQUENCE 509 AA; B3B7FD368C22C12F CRC64;

Query Match 80.5%; Score 2158; DB 1; Length 509;
Best Local Similarity 76.6%; Pred. No. 6.5e-160;
Matches 390; Conservative 63; Mismatches 56; Indels 0; Gaps 0;

QY 1 MGSARARWVAVGLGVVGLLCAVLGVVIMLWPSLIKQVVKVIRIDPSSLSFAMWKEIP 60
DB 1 MGNLSRARRVTAALGFIQLLFAVLGIIMVWPSIIKQVVKVIRIDPSSLSFAMWKEIP 60
QY 61 VPYLSVYFPEVNVSEILKGEKPVYRERGPYVYRFRHKKANITENDNDTVSFVHRSLSH 120
DB 61 VPFYLSVYFNFIVNPEGIIQKQKQVQOEHPYVYRFRHKKSNITFNNDTVSFLEYSYQ 120
QY 121 FQDRSHGESDYIIILPNILVLGAVWMSKSLAGLKLMTLGLATLQRAFMRNRTVGEIL 180
DB 121 FQDKSRGQESDYIIVNPNILVLSASMMENRPGLLKMTLAFSTLQRAFMRNRTVGEIM 180
QY 181 WGYEDPFVNFINKYLPDMFPKIGKFGLVFEMNNSDGLFTVFTGVQNFSKIHLVDWNGL 240
DB 181 WGYDDPLIHLINQYFFNPLSPFKGKFGFAELNNSDGLFTVFTGVKNFSRIHLVDWNGV 240
QY 241 SKYNYHSEOCNMGNTSGOMWAPFMTPOSSLFPPSPACRSKMLTYHDSGVVEGITYR 300
DB 241 SKYNYHSDQCNMGNTSGOMWAPFMTPESSLFYSPACRSKMLTYKQGVFGGIFTFR 300
QY 301 FTAPKTLFANGSVYVNEGFCPCLESGIQNVSTCRFCAPLFLSHPHFYFNADPVLSEAVLG 360
DB 301 FVAPSTLFANGSVYVNEGFCPCRESGIQNVSTCRFNAPLFLSHPHFYFNADPVLSEAVS 360
QY 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKIGQTKIEPVPVPLLMFQSG 420
DB 361 LHPNPKHSLFLDIHPVTGIPMNCVSKLQISLVKSVKIGQTKIPIQVPLLMFQSG 420
QY 421 AMGGEPLNFTYOLVLMPOVLQVQVYVLLGLGLLLLPVYIYQIRSQEKCFLFWSGSKG 480
DB 421 AMEGTLETFTYIQLVLMPKVLYHAQVLLALGCVLLIPIIYQIRSQEKCFLFWISPKKG 480
QY 481 SODKEAIOAYSESLMSPAAGTGLQBAKL 509
DB 481 SKDKEAVQAYSEFLMTSAPKGTGLQEARL 509

RESULT 13
ID SCRB1_HUMAN STANDARD; PRT; 552 AA.
AC QSWTV0; Q14016; Q6KFX4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI) (CD36 antigen-like
DE 1) (CD36 and LIMP2 analogous 1) (CLA-1) (Collagen type I receptor,
DE thrombospondin receptor-like 1).
DE Name=SCARB1; Synonyms=CD36L1, CLA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Promyelocyte;
RX MEDLINE=93366811; PubMed=7689561;
RA Calvo D., Vega M.;
RT "Identification, primary structure and distribution of CLA-1, a novel
RT member of the CD36/LIMP2 gene family.";
RN J. Biol. Chem. 268:18929-18935 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RC Hirano K.-I., Yamashita S., Matsuzawa Y.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Slatkine M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [4]
RN FUNCTION.
RX MEDLINE=22244044; PubMed=12356718; DOI=10.1093/emboj/cdf529;
RX Scarselli E., Anselmi H., Cerino R., Roccaecceca R.M., Acali S.,
RA Filocane G., Traboni C., Nicosia A., Cortese R., Vitelli A.;
RT "The human scavenger receptor class B type I is a novel candidate
RT receptor for the hepatitis C virus";
RL EMBO J. 21:5017-5025(2002).
RN [5]
RN GLYCOSYLATION.
RX MEDLINE=22128898; PubMed=12016218; DOI=10.1074/jbc.M202879200;
RX Kawasaki Y., Nakagawa A., Nagao K., Shiratsuchi A., Nakanishi Y.;
RT "Phosphatidylserine binding of class B scavenger receptor type I, a
RT phagocytosis receptor of testicular Sertoli cells";
RN J. Biol. Chem. 277:27559-27566(2002).
RN [6]
RN INTERACTION WITH HCV E1/E2 ENVELOPE HETERODIMER.
RX MEDLINE=22928133; PubMed=12913001; DOI=10.1074/jbc.M305289200;
RX Bartosch B., Vitelli A., Granier C., Goujon C., Dubuisson J.,
RA Pascale S., Scarselli E., Cortese R., Nicosia A., Cosset F.-L.;
RT "Cell entry of hepatitis C virus requires a set of co-receptors that
RT include the CD81 tetraspanin and the SR-B1 scavenger receptor";
RL J. Biol. Chem. 278:41624-41630(2003).
RN [7]
RN VARIANT SER-2.
RX MEDLINE=22407477; PubMed=12519372;
RX DOI=10.1034/j.1399-0004.2003.630108.x;
RX Tai E.S., Adiconis X., Ordovas J.M., Carmena-Ramon R., Real J.,
RA Corella D., Ascascas J., Carmena R.;
RT "Polymorphisms at the SRB1 locus are associated with lipoprotein
RT levels in subjects with heterozygous familial hypercholesterolemia";
RL Clin. Genet. 63:53-58(2003).
RN [8]
RN VARIANTS SER-2; ILE-135 AND SER-167.
RX PubMed=12966036; DOI=10.1093/hmg/ddg314;
RX Morabia A., Cayanis E., Costanza M.C., Ross B.M., Flaherty M.S.,
RA Alvin G.B., Day K., Gilliam T.C.;
RT "Association of extreme blood lipid profile phenotypic variation with
RT 11 reverse cholesterol transport genes and 10 non-genetic
RT cardiovascular disease risk factors";
RL Hum. Mol. Genet. 12:2733-2743(2003).
CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apob-containing lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity. Receptor for hepatitis C
CC virus glycoprotein E2. Binding between SCARB1 and E2 was found to
CC be independent of the genotype of the viral isolate.
CC -1- SUBUNIT: Plays a critical role in HCV attachment and/or cell entry
CC by interacting with HCV E1/E2 glycoproteins heterodimer. The C-
CC terminal region binds to PDZK1 (By similarity).
CC -1- INTERACTION:

CC P55345:HRMTLL; NDBExp=1; IntAct=EBI-78657, EBI-78458;
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=3;
CC IsoId=Q8WTV0-1; Sequences=Displayed;
CC Notes=May be due to a competing donor splice site. No
CC experimental confirmation available;
CC Name=1; Synonyms=SR-B1;
CC IsoId=Q8WTV0-2; Sequences=VSP_008554;
CC Name=2; Synonyms=SR-BII;
CC IsoId=Q8WTV0-3; Sequences=VSP_008553, VSP_008554;
CC Name=4; Synonyms=SR-BIII;
CC IsoId=Q8WTV0-4; Sequences=VSP_011037, VSP_008554;
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- FTM: N-glycosylated.
CC -1- POLYMORPHISM: The Ser-2 variant is associated with higher plasma
CC triglyceride concentration in subjects with heterozygous familial
CC hypercholesterolemia.
CC -1- SIMILARITY: Belongs to the CD36 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; Z22555; CA80277.1; -; mRNA.
CC EMBL; AF515445; AAQ08185.1; -; mRNA.
CC EMBL; BC022087; -; NOT ANNOTATED CDS; mRNA.
CC EMBL; BC080647; AAH80647.1; -; mRNA.
CC FIR; S36566; A48528.
CC IntAct; Q8WTV0; -;
CC Ensembl; ENSG00000073060; Homo sapiens.
CC HGNC; HGNC:1664; SCARB1.
CC MIM; 601040; -;
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC GO; GO:0005215; F:transporter activity; TAS.
CC GO; GO:0008203; P:cholesterol metabolism; TAS.
CC GO; GO:0006810; P:transport; TAS.
CC InterPro; IPR002159; CD36.
CC InterPro; IPR005428; CD36 antigen.
CC PANTHER; PTHR11923; CD36; 1.
CC Pfam; PF01130; CD36; 1.
CC PRINTS; PR01610; CD36ANTIGEN.
CC PRINTS; PR01609; CD36FAMILY.
CC KW Alternative splicing; Glycoprotein; Polymorphism; Receptor;
KW Transmembrane.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 443 Extracellular (Potential).
FT TRANSMEM 444 464 Potential.
FT TOPO_DOM 465 552 Cytoplasmic (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 1 42 MGCSKARWAAGALGAGLCAVIGAVIMVWVPSLIKQQL
FT Missing (in isoform 4).
FT FTID=VSP_011037.
FT Missing (in isoform 2).
FT FTID=VSP_008553.
FT VARSPLIC 468 552 VGAGQARADSHSLACWKGASDRILWPTAASPPPAVL
FT RLCRSGSGHCWGUHURSLKSLACWKGASDRILWPTAASPPPAVL
FT TGS -> EKCYLFWSSSKSGSKDEAIQAYSESLMTSAPKG

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FT SVLQBAKL (in isoform 1, isoform 2 and
FT isoform 4).
FT /FTid=VSP_008554.
FT G -> S (in dbSNP:4238001).
FT /FTid=VAR_017098.
FT V -> I.
FT /FTid=VAR_017099.
FT G -> S.
FT /FTid=VAR_017100.
FT S -> G (in dbSNP:10396213).
FT /FTid=VAR_019507.
FT C -> R (in dbSNP:2293440).
FT /FTid=VAR_017101.
FT F -> L (in Ref. 2).
FT F -> S (in Ref. 1).
FT CONFLICT 70 70
FT CONFLICT 97 97
SQ SEQUENCE 552 AA; 60878 MW; 06B0BD771FEA284F CRC64;

Query Match 77.1%; Score 2066.5; DB 1; Length 552;
Best Local Similarity 76.5%; Pred. No. 1e-152;
Matches 385; Conservative 49; Mismatches 60; Indels 9; Gaps 2;

Qy 1 MGSARARWAVAGLVGVVGLLCVAVGLVGMVILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGCSAKARWAAGLVAGLVGLVAVGLVGMVILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFVFNVPNSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLSH 120
Db 61 IPFYLSVYFVFNVPNSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLSH 120
Qy 121 FQDRSHGSESDYILNPILVILGAVNMESKAGLKLMTLGLATLQRAFMRNRTVGEIL 180
Db 121 FQPSKSHGSESDYIVMPNIIIVLGAAMVNMENKPMTLKIMTLAFTLGERAFMRNRTVGEIM 180
Qy 181 WGYEDPFVNFINKYLPDMFPPIKGKGLFVEMNNSDSGLFTVFTGVQNFSLHLDVNRNGL 240
Db 181 WGYKDPVLNINKYLPDMFPPIKGKGLFVEMNNSDSGLFTVFTGVQNFSLHLDVNRNGL 240
Qy 241 SKVNYHSEQCNNINGTSGQWMAFPMTPOSSLEFFSPSEACRSMKLTVDHSGVFEIGIPTYR 300
Db 241 SKVDFHSDQCNMINTSGQWMAFPMTPOSSLEFFSPSEACRSMKLTVDHSGVFEIGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVLPVLLWFEQSG 420
Db 361 LHPNQEASLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFTQLVLMPOVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKKG 480
Db 421 AMEGETLHTFTQLVLMPOVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKKG 480
Qy 481 SQDKAEATQAY-----SESLSMPAA 499
Db 476 RADSHSLACWKGASDRTLMPTA 498

RESULT 14
Q59FM4 HUMAN PRELIMINARY; PRT; 581 AA.
AC Q59FM4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Scavenger receptor class B member 1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209436; BAD92673.1; -, mRNA.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 581 AA; 64186 MW; 795810C1C2FA75A3 CRC64;

Query Match 77.1%; Score 2066.5; DB 2; Length 581;
Best Local Similarity 76.5%; Pred. No. 1e-152;
Matches 385; Conservative 49; Mismatches 60; Indels 9; Gaps 2;

Qy 1 MGSARARWAVAGLVGVVGLLCVAVGLVGMVILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 29 MGCSAKARWAAGLVAGLVGLVAVGLVGMVILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 88
Qy 61 VPFYLSVYFVFNVPNSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLSH 120
Db 89 IPFYLSVYFVFNVPNSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLSH 148
Qy 121 FQDRSHGSESDYILNPILVILGAVNMESKAGLKLMTLGLATLQRAFMRNRTVGEIL 180
Db 149 FQPSKSHGSESDYIVMPNIIIVLGAAMVNMENKPMTLKIMTLAFTLGERAFMRNRTVGEIM 208
Qy 181 WGYEDPFVNFINKYLPDMFPPIKGKGLFVEMNNSDSGLFTVFTGVQNFSLHLDVNRNGL 240
Db 209 WGYKDPVLNINKYLPDMFPPIKGKGLFVEMNNSDSGLFTVFTGVQNFSLHLDVNRNGL 268
Qy 241 SKVNYHSEQCNNINGTSGQWMAFPMTPOSSLEFFSPSEACRSMKLTVDHSGVFEIGIPTYR 300
Db 269 SKVDFHSDQCNMINTSGQWMAFPMTPOSSLEFFSPSEACRSMKLTVDHSGVFEIGIPTYR 328
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360
Db 329 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHYNADPVLSEAVLG 388
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVLPVLLWFEQSG 420
Db 389 LHPNQEASLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVLPVLLWFEQSG 448
Qy 421 AMGGEPLNTFTQLVLMPOVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKKG 480
Db 449 AMEGETLHTFTQLVLMPOVLYVQVYVLLGLGGLLLVPVYIQLRSQEKCFLFWSGSKKG 503
Qy 481 SQDKAEATQAY-----SESLSMPAA 499
Db 504 RADSHSLACWKGASDRTLMPTA 526

RESULT 15
Q6WIW8 RABIT PRELIMINARY; PRT; 501 AA.
AC Q6WIW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Scavenger receptor class B type II.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
RA Ritsch A., Tancevski I., Schgoer W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Patsch J.R.;
RT "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RL J. Lipid Res. 45:214-222(2004).
```


DR EMBL; AY283278; AAP40267.1; -; mRNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 501 AA; 55675 MW; 9A839B31C49F4C71 CRC64;

Query Match 76.4%; Score 2049; DB 2; Length 501;
Best Local Similarity 80.3%; Pred. No. 2.le-151;
Matches 375; Conservative 44; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MGSARARWAVGLGVVGLLCVAVGLVVMILVMPSLIKQVLLKNVRIDPSSLSPAMWKEIP 60
Db 1 MGRARARRAAAGLVVGLLCVAVGLVIAAVPPLIRQVVLKNVRIDPNSLSFNMWKEIP 60

Qy 61 VPFYLSVYFPEVNPSPILKEKRPVVRERGPYVYRERHKANITFNDNDTVSFVHRSLH 120
Db 61 APFYLSVYFVNVNPNILKEKRPQVRERGPYVYRERHKANITFNDNDTVSFLEHRSFQ 120

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Db 121 FQDKSRGSESDYIVINILVLAASFMEHRPMSLKLIMTLAFSALQORAFMNRVTGEIM 180

Qy 181 WGYEDPFVNFINKYLPDMFPIKGKGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNL 240
Db 181 WGYEDPLMLINKYLPGVFPFKDKGLFAEMNDSGCVFTVFTGVKDFSRHLVDKWNGL 240

Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTQSSLEFPSPACRSMKLITYHDSGVFEGIPTYR 300
Db 241 SKVNFHSDQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLIYQKPGVFGGIPTYR 300

Qy 301 FTAPKTLFANGSVYPPNEGFCPLGSIQNVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSMYPPNEGFCPLDSDGIQNVSTCRFCGAPFLSHPHFYNADPVLAEAVLG 360

Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKIGQTKIEBPVVLPLLWFEQSG 420
Db 361 LHPNEEEHALFLDIHPVTGIPMNCVKQLQISLYMKAIRGIGQTKIEBPVVLPLMWFCESG 420

Qy 421 AMGEPLNTFYTLVLMPOVLQVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 467
Db 421 AMGETLSTFYTLVLLPNVLQVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 467

Search completed: February 23, 2006, 12:45:05
Job time : 150.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:45:24 ; Search time 34 Seconds
(without alignments)
1237.704 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2881
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2681	100.0	509	2	US-08-032-894-4
6	2681	100.0	509	2	US-09-031-626-4
7	2681	100.0	509	2	US-09-241-581B-4
8	2681	100.0	509	2	US-08-285-428-4
9	2681	100.0	509	2	US-09-385-799-2
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27	572	21.3	412	2	US-09-949-016-11488

28 455 17.0 310 2 US-09-270-542-90 Sequence 90, Appl
29 398 14.8 458 2 US-09-270-767-43768 Sequence 43768, A
30 353 13.2 332 2 US-09-270-767-46306 Sequence 46306, A
31 301 11.2 462 2 US-09-270-767-45262 Sequence 45262, A
32 277 10.3 158 2 US-09-270-767-61875 Sequence 61875, A
33 227 8.5 248 2 US-09-270-767-59167 Sequence 59167, A
34 221 8.2 301 2 US-09-270-767-33112 Sequence 33112, A
35 221 8.2 301 2 US-09-270-767-48329 Sequence 48329, A
36 199 7.4 74 2 US-09-513-999C-65328 Sequence 65328, Ap
37 177.5 6.6 181 2 US-09-270-767-42865 Sequence 42865, A
38 110.5 4.1 172 2 US-09-270-767-60022 Sequence 60022, A
39 110.5 4.1 205 2 US-09-270-767-44571 Sequence 44571, A
40 103.5 3.9 45 2 US-09-161-939A-4 Sequence 4, Appl
41 99.5 3.7 45 2 US-09-161-939A-21 Sequence 21, Appl
42 98.5 3.7 45 2 US-09-161-939A-19 Sequence 19, Appl
43 96 3.6 320 2 US-09-134-000C-4950 Sequence 4950, Ap
44 93.5 3.5 383 2 US-09-638-937-15 Sequence 15, Appl
45 93 3.5 261 2 US-09-107-532A-6012 Sequence 6012, Ap

ALIGNMENTS

RESULT 1
US-08-559-505-2
; Sequence 2, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Langshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
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; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."

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; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175,
; OTHER INFORMATION: 213-214, 227-229, 255-257, 310-312, 330-332 and 383-385 repre
; OTHER INFORMATION: N-linked glycosylation sites."
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21, 251,
; OTHER INFORMATION: 280, 321, 323, 334, 384 and 470 represent potential disulfide
US-08-559-505-2

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARVAVGLGVVGLLCVILGVVMTILVMPSLIKQVLKNVRIDPSLSFAMKEIP 60
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Db 481 SQDKEATQAYSSELSMSPAAGTVLQEAKL 509

RESULT 2
US-08-749-907-2
; Sequence 2, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlanta Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA

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RESULT 3
US-08-980-980-4
; Sequence 4, Application US/08890980
; Patent No. 5998141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-980-980-4

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-08-980-979-4
; Sequence 4, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordoval, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-980-979-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-032-894-4
; Sequence 4, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.0
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; TYPE: PRT
; ORGANISM: Human
US-09-032-894-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 AMGGEPLNTFYTLVLMPOVLQVYVLLGLGGLLLPVVIYQLRQSEKCF 480
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RESULT 6
US-09-031-626-4
; Sequence 4, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-031-626-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,428
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..509
OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger"
FEATURE:
NAME/KEY: Domain
LOCATION: 9..32
OTHER INFORMATION: /note= "Putative transmembrane"
OTHER INFORMATION: domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 440..464
OTHER INFORMATION: /note= "Putative transmembrane"
OTHER INFORMATION: domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..385
OTHER INFORMATION: /note= "Positions 102-104, 108-110,
OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257,310-312,
OTHER INFORMATION: 330-332 and 383-385 represent potential N-linked glycosylation"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..470
OTHER INFORMATION: /note= "The cysteines at positions
OTHER INFORMATION: 21, 251, 280, 321, 323, 334, 384 and 470 represent
OTHER INFORMATION: potential disulfide linkages."
US-08-265-428-4
Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSARARWAVGLGVVGLLCAVLGVVMIIVMSLIHQQLKQVKNRIPDPSLSFAMWKEIP 60
Db 1 MGSARARWAVGLGVVGLLCAVLGVVMIIVMSLIHQQLKQVKNRIPDPSLSFAMWKEIP 60
Qy 61 VPFLSVYFEVNVNPSILGKGPVVRGPGYVYRPRHKANITFNDNDTVSVFVHRSLH 120
Db 61 VPFLSVYFEVNVNPSILGKGPVVRGPGYVYRPRHKANITFNDNDTVSVFVHRSLH 120
Qy 121 FQDRSHGSESDYIILNPIVLGVAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180
Db 121 FQDRSHGSESDYIILNPIVLGVAVNMESKAGLKLMTLGLATLQORAFMNRVTGGEIL 180
Qy 181 WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Db 181 WGEDPFPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKNYWHSEQCNMINGTSGQWAPFMTPOSLEFPSPACRSKMLTYHDSGVPEGIPTYR 300
Db 241 SKNYWHSEQCNMINGTSGQWAPFMTPOSLEFPSPACRSKMLTYHDSGVPEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360

Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISYIKAVKGIGOTGKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLOISYIKAVKGIGOTGKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGPELNTFYTLVLMPOVLQVVOYVLLGIGLGLLLVPVIYQLRSQEKCFLFWSGSKG 480
Db 421 AMGGPELNTFYTLVLMPOVLQVVOYVLLGIGLGLLLVPVIYQLRSQEKCFLFWSGSKG 480
Qy 481 SQDKEAIQAYSESLMSPAAGKTVLQEAKL 509
Db 481 SQDKEAIQAYSESLMSPAAGKTVLQEAKL 509
RESULT 9
US-09-385-799-2
Sequence 2, Application US/09385799
Patent No. 6962688
GENERAL INFORMATION:
APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,799
FILING DATE: 30-Aug-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,907
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..509
OTHER INFORMATION: /function= "Amino acid sequence for the
Hamster Scavenger Receptor Class B-I."
FEATURE:
NAME/KEY: Domain
LOCATION: 9..32
OTHER INFORMATION: /note= "Putative transmembrane domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 440..464
OTHER INFORMATION: /note= "Putative transmembrane domain."
FEATURE:


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; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
;
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
US-09-385-799-2
Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSARARWAVAGLVGVVGLLCVAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGSSARARWAVAGLVGVVGLLCVAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Db 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Qy 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Qy 181 WGYEDPFPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
Db 181 WGYEDPFPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
Qy 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNYHSEOCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
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Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQVSTCRFCGAPFLSHPHFYNDPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDHPVTGTPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFPQSG 420
Db 361 LNPDPREHSLFLDHPVTGTPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFPQSG 420
Qy 421 AMGCEPLNTFTQVLTAMPQVLYQVYVLLGLGGLLAVPVYIYQLRSQEKCFLWSGSKG 480
Db 421 AMGCEPLNTFTQVLTAMPQVLYQVYVLLGLGGLLAVPVYIYQLRSQEKCFLWSGSKG 480
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Db 481 SQDKEALQAYSESLSMPAAKGTVLQEA 509

RESULT 10
PCT-US95-07721-4
; Sequence 4, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-1."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257,
; OTHER INFORMATION: 310-312, 330-332 and 383-385 represent
; OTHER INFORMATION: potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions
; OTHER INFORMATION: 21, 251, 280, 321, 323, 334, 384 and
; OTHER INFORMATION: 470 represent potential disulfide
; OTHER INFORMATION: linkages."
;
PCT-US95-07721-4
Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-285;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSARARWAVAGLVGVVGLLCVAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGSSARARWAVAGLVGVVGLLCVAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Db 61 VPFLSVYFPEVVPNPSEILKGEKPVVRERGYPVYVREFRHKANITFNDNDTVSFVEHRS 120
Qy 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGGAVMMESKAGLKMVMTLGLATLQORAFMNRVTGVEIL 180
Qy 181 WGYEDPFPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
Db 181 WGYEDPFPVNFINKYLPDMFPPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRW 240
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Db 241 SKVNYHSEOCNMGNTSGOMWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
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Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVQVYLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
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Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509

RESULT 11
US-08-559-505-4
; Sequence 4, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; OTHER INFORMATION: murine Scavenger Receptor Class BI."
US-08-559-505-4

Query Match 91.3%; Score 2447; DB 1; Length 509;
Beat Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
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pb 1 MGGSSRRWVWALGLGALGLLPAALGVVMILWPSLKKQVLKNVRIDPSSLSFGMWKEIP 60

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Db 61 VPFYLSVYFEFVNPSIILKGKPPVVRGPPVYREFRHKAMITFNDNDTVSFEHRSILH 120
Qy 121 FQDRSHGSESIIILPNLVLGGAVMMESKAGLMMTLGLATLQORAFMNRVTYGEIL 180
Db 121 FQDRSHGSESIIILPNLVLGGAVMMESKAGLMMTLGLATLQORAFMNRVTYGEIL 180
Qy 181 WGYEDPFVNFINKYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFHSKIHLDVWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMFPIKKGKGLFVEMNNSDGLFTVFTGVQNFHSKIHLDVWNGL 240
Qy 241 SKVNYHSEOCNMGNTSGOMWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKIDYHSEOCNMGNTSGOMWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPPNEGFCPCRESGIQNVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLMPOVLQVQVYLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQVQVYLLGLGGLLLVPPVYIQLRSQEKCFLEWSSGSKG 480
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Db 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509

RESULT 12
US-08-749-907-4
; Sequence 4, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

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; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class BI."
US-08-749-907-4

Query Match      91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSSARARVAVGLGVVGLCAVLGVVMIILVPSLIIKQVILKVRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARVAVGLGVVGLCAVLGVVMIILVPSLIIKQVILKVRIDPSSLSFAMWKEIP 60

QY 61 VPYLSVYFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
DB 61 VPYLSVYFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120

QY 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180

QY 181 WGYEDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYEDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240

QY 241 SKVNYHSEQCINMNGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKVNYHSEQCINMNGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300

QY 301 FTAPKTLFANGSVYPPNEGCPCEGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGCPCEGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360

QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLSLYIKAVKGIQGTGKIEPPVPLLLWFEQSG 420
DB 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLSLYIKAVKGIQGTGKIEPPVPLLLWFEQSG 420

QY 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVVIYQLRSQEKCFLWMSGKKG 480
DB 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVVIYQLRSQEKCFLWMSGKKG 480

QY 481 SQDKEAIQAYSESLSMSPAAGTGLVQEA 509
DB 481 SQDKEAIQAYSESLSMSPAAGTGLVQEA 509

RESULT 13
US-09-241-581B-8
; Sequence 8, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for
; the murine Scavenger Receptor Class BI."
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-241-581B-8

Query Match      91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSSARARVAVGLGVVGLCAVLGVVMIILVPSLIIKQVILKVRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARVAVGLGVVGLCAVLGVVMIILVPSLIIKQVILKVRIDPSSLSFAMWKEIP 60

QY 61 VPYLSVYFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120
DB 61 VPYLSVYFEVNVNPSILKGEKPVVRERGYPVYRFRHKANITFNDNDTVSFVHRSLSH 120

QY 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180

QY 181 WGYEDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
DB 181 WGYEDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240

QY 241 SKVNYHSEQCINMNGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKVNYHSEQCINMNGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300

QY 301 FTAPKTLFANGSVYPPNEGCPCEGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGCPCEGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360

QY 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLSLYIKAVKGIQGTGKIEPPVPLLLWFEQSG 420
DB 361 LNPDPRHSLFLDIHPVTGIPMNCVKQLSLYIKAVKGIQGTGKIEPPVPLLLWFEQSG 420

QY 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVVIYQLRSQEKCFLWMSGKKG 480
DB 421 AMGGEPLNTFYTLVLMPOVLQVQVYVLLGLGGLLLVPVVIYQLRSQEKCFLWMSGKKG 480

QY 481 SQDKEAIQAYSESLSMSPAAGTGLVQEA 509
DB 481 SQDKEAIQAYSESLSMSPAAGTGLVQEA 509

RESULT 14
US-09-385-799-4
; Sequence 4, Application US/09385799
; Patent No. 6962688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: 1201 West Peachtree Street
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QY 481 SODKEAIQAYSESLMSPAAKGTVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAKGTVLQEA 509

RESULT 15
PCT-US95-07721-8
; Sequence 8, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class B1 and C1 Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-385-799-4

Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSSARARVAVGLGVVGLLCVAVGVVMIILVPSLIIKQVLLKQVLRIDPSSLSFAMWKEIP 60
Db 1 MGSSARARVAVGLGVVGLLCVAVGVVMIILVPSLIIKQVLLKQVLRIDPSSLSFAMWKEIP 60

QY 61 VPFLSVYFPEVNPSEILKGEKPVVRERGYPYVYRFRHKKANITFNDNDTVSFVEHSLH 120
Db 61 VPFLSVYFPEVNPSEILKGEKPVVRERGYPYVYRFRHKKANITFNDNDTVSFVEHSLH 120

QY 121 FQDRSHGSESDYIILPNILVLGAVNMESKSLAGLKLMTLGLATLQORAFMNRVTGGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGAVNMESKSLAGLKLMTLGLATLQORAFMNRVTGGEIL 180

QY 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
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QY 481 SODKEAIQAYSESLMSPAAKGTVLQEA 509
Db 481 SODKEAIQAYSESLMSPAAKGTVLQEA 509

RESULT 15
PCT-US95-07721-8
; Sequence 8, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class B1 and C1 Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
PCT-US95-07721-8

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.7e-260;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSSARARVAVGLGVVGLLCVAVGVVMIILVPSLIIKQVLLKQVLRIDPSSLSFAMWKEIP 60
Db 1 MGSSARARVAVGLGVVGLLCVAVGVVMIILVPSLIIKQVLLKQVLRIDPSSLSFAMWKEIP 60

QY 61 VPFLSVYFPEVNPSEILKGEKPVVRERGYPYVYRFRHKKANITFNDNDTVSFVEHSLH 120
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QY 181 WGYEDPPVNFINKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKRWGL 240
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Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVVKLQISLYIKAVKGIGGTGKIHPVVLPLLWFEQSG 420
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Qy 421 AMGGEPLNTFYTLVLMPOVLQYVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480
Db 421 AMGGEPLNTFYTLVLMPOVLQYVYVLLGLGGLLLVPVIYQLRSQEKCFLWMSGKKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLOEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLOEAKL 509

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Search completed: February 23, 2006, 12:47:15
Job time : 36 secs

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LOCATION: (310)..(312)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (330)..(332)
OTHER INFORMATION: Potential
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NAME/KEY: CARBOHYD
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NAME/KEY: DISULFID
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OTHER INFORMATION: Potential
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NAME/KEY: DISULFID
LOCATION: (470)
OTHER INFORMATION: Potential
US-09-148-012-2

Query Match 100.0%; Score 2681; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSARARWAVAGLVGVLCAVLGVVMILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVLCAVLGVVMILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Qy 61 VPYLSVYFPEVVPNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPYLSVYFPEVVPNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Qy 121 FQDRSHGSESDYIILPNILVLCGAVMMESKAGLKMMTLGLATLQRAFPMNRTVGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLCGAVMMESKAGLKMMTLGLATLQRAFPMNRTVGEIL 180
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Db 181 WGYEDDPVFNKYLPMDFPIKGFGLFVEMNNSDSLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMKLT.YHDSGVFEGIPTYR 300
Db 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMKLT.YHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVVLP.LLWFQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVVLP.LLWFQSG 420
Qy 421 AMGEPLNTFYTQLVLMPOVLQVYVLLGLGGLLLLPVVIYQLRSQEKCF.LFWSGSKG 480
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Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVVLP.LLWFQSG 420
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Qy 421 AMGEPLNTFYTQLVLMPOVLQVYVLLGLGGLLLLPVVIYQLRSQEKCF.LFWSGSKG 480
Db 421 AMGEPLNTFYTQLVLMPOVLQVYVLLGLGGLLLLPVVIYQLRSQEKCF.LFWSGSKG 480
Qy 481 SODKEAIQAYSESIMSPAAGT.VLQBAKL 509
Db 481 SODKEAIQAYSESIMSPAAGT.VLQBAKL 509
RESULT 2
US-09-779-152-4
; Sequence 4, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779,152
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890,979
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-779-152-4

Query Match 100.0%; Score 2681; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSARARWAVAGLVGVLCAVLGVVMILVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
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Qy 61 VPYLSVYFPEVVPNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPYLSVYFPEVVPNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Qy 121 FQDRSHGSESDYIILPNILVLCGAVMMESKAGLKMMTLGLATLQRAFPMNRTVGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLCGAVMMESKAGLKMMTLGLATLQRAFPMNRTVGEIL 180
Qy 181 WGYEDDPVFNKYLPMDFPIKGFGLFVEMNNSDSLFTVFTGVQNFSKIHLVDRWNGL 240
Db 181 WGYEDDPVFNKYLPMDFPIKGFGLFVEMNNSDSLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSMKLT.YHDSGVFEGIPTYR 300
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Db 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVVLP.LLWFQSG 420
Db 361 LNPDPREHSLFLDIHPVTGIPMNCVKLQISLYIKAVKGIGQTKIEPVVLP.LLWFQSG 420
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Qy 481 SODKEATQAYSESLMSPAAGTGLVLEAKL 509
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RESULT 3
US-10-023-610-4
; Sequence 4, Application US/10023610
; Publication No. US20030023059A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/10/023.610
; CURRENT FILING DATE: 2001-12-17
; EARLIER APPLICATION NUMBER: 09/686,106
; EARLIER FILING DATE: 2000-10-10
; EARLIER APPLICATION NUMBER: 09/032,894
; EARLIER FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-10-023-610-4

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 SKVNYHSEOCNMINGTSGOWWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVPEGIPTYR 300
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Qy 361 LNPDPREHSLFLDHPVTGIPMNCVKQLISLYIKAVKGIGQTKIEPVLPLLPFQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVKQLISLYIKAVKGIGQTKIEPVLPLLPFQSG 420

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Db 421 AMGGEPLNTFTQLVLPQVLYQYVYLLGLGGLLLVPVIYQLRSQEKCFPLFWSGSKG 480

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Db 481 SODKEATQAYSESLMSPAAGTGLVLEAKL 509

RESULT 4
US-10-178-611-2

; Sequence 2, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
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; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-178-611-2

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.le-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 481 SODKEATQAYSESLSMSPAAGTIVLQEAKL 509

RESULT 5
US-10-164-863-2
; Sequence 2, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Cricetus griseus
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; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
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; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
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; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
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; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
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; LOCATION: (227)..(229)
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; LOCATION: (310)..(312)
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; NAME/KEY: CARBOHYD
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; NAME/KEY: CARBOHYD
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; NAME/KEY: DISULFID
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; OTHER INFORMATION: Potential
US-10-164-863-2

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.1e-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVVGLLCAVLGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSYFPEVNVNPSILKGEKPVVRERGYPVYVFRHKANITFNDNDTVSFVHRSLH 120
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Db 61 VPFYLSVYFVFNPSBILKGEKPVVRERGPTVYRFRHKANITFNDNDTVSFVHRSLSH 120
Qy 121 FOPDRSHGSESDYIILPNILVILGAVNMESKAGIKLMMTILGLATLQRAFMRNRTVGEIL 180
Db 121 FOPDRSHGSESDYIILPNILVILGAVNMESKAGIKLMMTILGLATLQRAFMRNRTVGEIL 180
Qy 181 WGYEDPPFNFKINKLPDMFPPIKGRFGLFVENWNSDGLFTVFTGVQNFSKIHLVDRNGL 240
Db 181 WGYEDPPFNFKINKLPDMFPPIKGRFGLFVENWNSDGLFTVFTGVQNFSKIHLVDRNGL 240
Qy 241 SKVNYHSEQCNMINGTSGQWMAFMTPOSSLEFPSPACRSMKLTTHDSGVFEGIPTYR 300
Db 241 SKVNYHSEQCNMINGTSGQWMAFMTPOSSLEFPSPACRSMKLTTHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVVPPNEGFCPCLESIGIQNVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVVPPNEGFCPCLESIGIQNVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVPLLLWFQSG 420
Db 361 LNPDPREHSLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVPLLLWFQSG 420
Qy 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLLPVLYQLRSQEKCFLWSSGSKG 480
Db 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLLPVLYQLRSQEKCFLWSSGSKG 480
Qy 481 SODKEATQAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEATQAYSESLMSPAAGTIVLQEA 509

RESULT 6
US-10-212-848-4
; Sequence 4, Application US/10212848
; Publication No. US2004002222EA1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Jeanette
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RISK FACTORS
; TITLE OF INVENTION: FOR ABNORMAL LIPID LEVELS AND THE DISEASES AND DISORDERS
; TITLE OF INVENTION: ASSOCIATED THEREWITH
; FILE REFERENCE: WMI-012
; CURRENT APPLICATION NUMBER: US/10/212,848
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-848-4

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.1e-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVLCAVLGVNMLWPSLIXQOVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVLCAVLGVNMLWPSLIXQOVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFVFNPSBILKGEKPVVRERGPTVYRFRHKANITFNDNDTVSFVHRSLSH 120
Db 61 VPFYLSVYFVFNPSBILKGEKPVVRERGPTVYRFRHKANITFNDNDTVSFVHRSLSH 120
Qy 121 FOPDRSHGSESDYIILPNILVILGAVNMESKAGIKLMMTILGLATLQRAFMRNRTVGEIL 180
Db 121 FOPDRSHGSESDYIILPNILVILGAVNMESKAGIKLMMTILGLATLQRAFMRNRTVGEIL 180
Qy 181 WGYEDPPFNFKINKLPDMFPPIKGRFGLFVENWNSDGLFTVFTGVQNFSKIHLVDRNGL 240
Db 181 WGYEDPPFNFKINKLPDMFPPIKGRFGLFVENWNSDGLFTVFTGVQNFSKIHLVDRNGL 240
Qy 241 SKVNYHSEQCNMINGTSGQWMAFMTPOSSLEFPSPACRSMKLTTHDSGVFEGIPTYR 300

Db 241 SKVNYHSEQCNMINGTSGQWMAFMTPOSSLEFPSPACRSMKLTTHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVVPPNEGFCPCLESIGIQNVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVVPPNEGFCPCLESIGIQNVSTCRFCGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPREHSLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVPLLLWFQSG 420
Db 361 LNPDPREHSLFDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIBPVVPLLLWFQSG 420
Qy 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLLPVLYQLRSQEKCFLWSSGSKG 480
Db 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGGLLLLPVLYQLRSQEKCFLWSSGSKG 480
Qy 481 SODKEATQAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEATQAYSESLMSPAAGTIVLQEA 509

RESULT 7
US-10-706-073-2
; Sequence 2, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10/706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
; OTHER INFORMATION: Potential
; FEATURE:

NAME/KEY: CARBOHYD
LOCATION: (310)..(312)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (330)..(332)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (383)..(385)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (21)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (251)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (280)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (321)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (323)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (334)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (384)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (470)
OTHER INFORMATION: Potential
US-10-706-073-2

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 4.1e-258;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGVGVVGLLCVAVGVVMIIVMPSLIKQOVLKNVRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFFEVNPNPSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLH 120
Db 61 VPFLSVYFFEVNPNPSILKGEKPVVRERGPYVYRFRHKANITFDNDTVSFVHRSLH 120
Qy 121 FQDRSHGSESDYIILPNILVLGAVVMESKAGLKMVTLGLATLQRAFMRNTVGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGAVVMESKAGLKMVTLGLATLQRAFMRNTVGEIL 180
Qy 181 WGYEDPFVNFINKYLPDMFPIKGKFGFLFVEMNNSDSLFTVFTGVQNFSLHLDVRWNL 240
Db 181 WGYEDPFVNFINKYLPDMFPIKGKFGFLFVEMNNSDSLFTVFTGVQNFSLHLDVRWNL 240
Qy 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESIGIONVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGIONVSTCRFGAPLFLSHPHYNADPVLSEAVLG 360

Qy 361 LNPDPREHSLFDIHPVTGIPMNCVVKLQISLYIKAVKGIGTGKIEPVVLPILLWFEQSG 420
Db 361 LNPDPREHSLFDIHPVTGIPMNCVVKLQISLYIKAVKGIGTGKIEPVVLPILLWFEQSG 420
Qy 421 AMGGEPLNTFYTLVLPQVQLVQVYVLLGLGGLLLLVPIYQLRSQEKCFLFWSGSKG 480
Db 421 AMGGEPLNTFYTLVLPQVQLVQVYVLLGLGGLLLLVPIYQLRSQEKCFLFWSGSKG 480
Qy 481 SODKEAIQAYSESLMSPAKGTVLQEAKL 509
Db 481 SODKEAIQAYSESLMSPAKGTVLQEAKL 509
RESULT 8
US-10-933-037-2
Sequence 2, Application US/10933037
Publication No. US20050136005A1
GENERAL INFORMATION:
APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/933,037
FILING DATE: 02-Sep-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT7538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..509
OTHER INFORMATION: /function= "Amino acid sequence for the
Hamster Scavenger Receptor Class B-I."
FEATURE:
NAME/KEY: Domain
LOCATION: 9..32
OTHER INFORMATION: /note= "Putative transmembrane domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 440..464
OTHER INFORMATION: /note= "Putative transmembrane domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..385
OTHER INFORMATION: /note= "Positions 102-104, 108-110,
173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
potential N-linked glycosylation sites."
FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: 21...470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-933-037-2

Query Match
Best Local Similarity 100.0%; Score 2681; DB 5; Length 509;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVLLCAVLGVVMIILVPSLIKQVVKVRIIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVLLCAVLGVVMIILVPSLIKQVVKVRIIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFVFNVPNSBILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPFYLSVYFVFNVPNSBILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Qy 121 FQDRSHGSESDYIILPNILVGVAVNMESKAGLKLMMTLGLATLQRAFPMNRTVGEIL 180
Db 121 FQDRSHGSESDYIILPNILVGVAVNMESKAGLKLMMTLGLATLQRAFPMNRTVGEIL 180
Qy 181 WGYEDPFPNFKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Db 181 WGYEDPFPNFKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPRHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLIWFQSG 420
Db 361 LNPDPRHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLIWFQSG 420
Qy 421 AMGGEPLNTFTQLVMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLFWSGSKG 480
Db 421 AMGGEPLNTFTQLVMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLFWSGSKG 480
Qy 481 SQKEAIOAYSLSMSPAAGTVLQEA 509
Db 481 SQKEAIOAYSLSMSPAAGTVLQEA 509

RESULT 10
US-10-178-611-4
; Sequence 4, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795

```

```

; NAME/KEY: Modified-site
; LOCATION: 21...470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-933-037-2

Query Match
Best Local Similarity 100.0%; Score 2681; DB 5; Length 509;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSARARWAVAGLVGVLLCAVLGVVMIILVPSLIKQVVKVRIIDPSSLSFAMWKEIP 60
Db 1 MGSARARWAVAGLVGVLLCAVLGVVMIILVPSLIKQVVKVRIIDPSSLSFAMWKEIP 60
Qy 61 VPFYLSVYFVFNVPNSBILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Db 61 VPFYLSVYFVFNVPNSBILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
Qy 121 FQDRSHGSESDYIILPNILVGVAVNMESKAGLKLMMTLGLATLQRAFPMNRTVGEIL 180
Db 121 FQDRSHGSESDYIILPNILVGVAVNMESKAGLKLMMTLGLATLQRAFPMNRTVGEIL 180
Qy 181 WGYEDPFPNFKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Db 181 WGYEDPFPNFKYLPDMFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDRWNGL 240
Qy 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKVNYHSEOCNMGTSQGWAPFMTQSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVVYPNNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDPRHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLIWFQSG 420
Db 361 LNPDPRHSLFLDIHPVTGIPMNCVSKLQISLYIKAVKGIGQTKIEPVVPLIWFQSG 420
Qy 421 AMGGEPLNTFTQLVMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLFWSGSKG 480
Db 421 AMGGEPLNTFTQLVMPQVLYQVYVLLGLGILLVPIVYQIORSQEKCFLFWSGSKG 480
Qy 481 SQKEAIOAYSLSMSPAAGTVLQEA 509
Db 481 SQKEAIOAYSLSMSPAAGTVLQEA 509

RESULT 9
US-09-148-012-4
; Sequence 4, Application US/09148012
; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-09-148-012-4

Query Match
Best Local Similarity 91.3%; Score 2447; DB 3; Length 509;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 509 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
;   NAME/KEY: misc. feature
;   LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
;   murine Scavenger Receptor Class BI."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-178-611-4

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSRRARWAVAGLVGVGLLCAVLGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSRRARWALGLGALGLLFAALGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYREFRHKANITFNDNDTVSFVHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYREFRHKANITFNDNDTVSFVHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 WGYEDDPVNFINKYLPDMPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 WGYEDDPVNFINKYLPDMPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 SKVNYHSEQCNNINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPTYR 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 SKIDYHSEQCNNINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPTYR 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 FTAPKTLFANGSVYPNEGFCPCLESQINVTCTRCGAPLFLSHPHFYNADPVLSEAVLG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 FTAPDTLFANGSVYPNEGFCPCRESQINVTCTRCGAPLFLSHPHFYNADPVLSEAVLG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 LNPDPREHSLFDLHPVTGIPMNCVKQLSIYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 LNPDPREHSLFDLHPVTGIPMNCVKQLSIYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 421 AMGGEPLNTFYTLVLPQVLYVQVYVLLGLGGLLLVPVYQLRSQEKCFLEWSGSKG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 AMGGEPLNTFYTLVLPQVLYVQVYVLLGLGGLLLVPVYQLRSQEKCFLEWSGSKG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 481 SODKEATQAYSESLSMSPAAGTGLQEA 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 481 SODKEATQAYSESLSMSPAAGTGLQEA 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-10-164-863-4
; Sequence 4, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4

;
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
;
Query Match          89.0%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

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; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-164-863-4

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGSRRARWAVAGLVGVGLLCAVLGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSRRARWALGLGALGLLFAALGVVMIIVMPSLIKQVLRIDPSSLSFAMWKEIP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYREFRHKANITFNDNDTVSFVHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VPFYLSVYFEVVPNPSEILKGEKPVVRERGYPVYREFRHKANITFNDNDTVSFVHRS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 FQDRSHGSESDYIILPNILVGLGAVMMESKAGLKLMMTLGLATLQRAFNRVTVEIL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 WGYEDDPVNFINKYLPDMPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 WGYEDDPVNFINKYLPDMPIKGFGLFVGMNNSDGLFTVFTGVQNFSKIHLVDRW 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 SKVNYHSEQCNNINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPTYR 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 SKIDYHSEQCNNINGTSGQWAPFMTPOSSLEFFSPACRSKMLTYHDSGVPEGIPTYR 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 FTAPKTLFANGSVYPNEGFCPCLESQINVTCTRCGAPLFLSHPHFYNADPVLSEAVLG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 FTAPDTLFANGSVYPNEGFCPCRESQINVTCTRCGAPLFLSHPHFYNADPVLSEAVLG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 LNPDPREHSLFDLHPVTGIPMNCVKQLSIYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 LNPDPREHSLFDLHPVTGIPMNCVKQLSIYIKAVKGIGQTKIEPVVLPVLLWFEQSG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 421 AMGGEPLNTFYTLVLPQVLYVQVYVLLGLGGLLLVPVYQLRSQEKCFLEWSGSKG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 AMGGEPLNTFYTLVLPQVLYVQVYVLLGLGGLLLVPVYQLRSQEKCFLEWSGSKG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 481 SODKEATQAYSESLSMSPAAGTGLQEA 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 481 SODKEATQAYSESLSMSPAAGTGLQEA 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-10-706-073-4
; Sequence 4, Application US/10706073
; Publication No. US2004007526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10/706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
;
Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

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QY 1 MGSSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARWVGLGALGALLFAALGVVMIILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
QY 61 VPFLSYVFPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPFLSYVFPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVILGAVVMSKSLKLMNTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVILGAVVMSKSLKLMNTLGLATLQORAFMNRVTGEIL 180
QY 181 WGYDDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
DB 181 WGYDDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
QY 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
QY 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVLPLWFEQSG 420
DB 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVLPLWFEQSG 420
QY 421 AMGGEPLNTFYTLVLMPOVLYVYVLLGLGGLLLVPIICQLRSQEKCFLWMSGKKG 480
DB 421 AMGGEPLNTFYTLVLMPOVLYVYVLLGLGGLLLVPIICQLRSQEKCFLWMSGKKG 480
QY 481 SQDKEAIQAYSESLMSPAAGTGLVQEA 509
DB 481 SQDKEAIQAYSESLMSPAAGTGLVQEA 509

RESULT 13

US-10-933-037-4
; Sequence 4, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-933-037-4
Query Match 91.3%; Score 2447; DB 5; Length 509;
Best Local Similarity 89.0%; Pred. No. 9.3e-235;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSSARARWAVGLGVVGLLCAVLGVVMIILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
DB 1 MGSSARARWVGLGALGALLFAALGVVMIILVPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
QY 61 VPFLSYVFPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
DB 61 VPFLSYVFPVNPSEILKGEKPVVRERGPYVYRFRHKANITFNDNDTVSFVHRSLH 120
QY 121 FQDRSHGSESDYIILPNILVILGAVVMSKSLKLMNTLGLATLQORAFMNRVTGEIL 180
DB 121 FQDRSHGSESDYIILPNILVILGAVVMSKSLKLMNTLGLATLQORAFMNRVTGEIL 180
QY 181 WGYDDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
DB 181 WGYDDPVPFINKYLPDMPIKGFGLFVEMNNSDGLFTVFTGVQNFSLHLDVDRWNL 240
QY 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300
DB 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFPSPACRSKMLTYHDSGVFEGIPTYR 300
QY 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
DB 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPFLSHPHFYNDPVLSEAVLG 360
QY 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVLPLWFEQSG 420
DB 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIGQTKIEPVLPLWFEQSG 420
QY 421 AMGGEPLNTFYTLVLMPOVLYVYVLLGLGGLLLVPIICQLRSQEKCFLWMSGKKG 480
DB 421 AMGGEPLNTFYTLVLMPOVLYVYVLLGLGGLLLVPIICQLRSQEKCFLWMSGKKG 480
QY 481 SQDKEAIQAYSESLMSPAAGTGLVQEA 509
DB 481 SQDKEAIQAYSESLMSPAAGTGLVQEA 509

RESULT 14

US-10-322-281-565
; Sequence 565, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-565

Query Match 88.5%; Score 2374; DB 4; Length 513;
Best Local Similarity 87.6%; Pred. No. 1.8e-227;
Matches 446; Conservative 34; Mismatches 23; Indels 6; Gaps 3;

Qy	1	MGSSRARVAVGLGVGLCAVLGVVILVWPSLIKQOVLKNVRIDPSSLSFAMWKPEIP	60
Db	11	MGSSRARV - VGLGALGILLFAALGVVILVWPSLIKQOVLKNVRIDPSSLSFAMWKPEIP	68
Qy	61	VPPYLSVYEFVNVNSEILKGEKPVVERGPPVYREPRHKANITFNDNDTVSFVEHRSILH	120
Db	69	VPPYLSVYEFVNVNSEVLNGQKPVVERGPPVYREPRQVNTFNDNDTVSFVENRSILH	128
Qy	121	FOPDRSHGSESDEYIILPNILVLGGAVMMESKAGLKMNTLGLATLQRAFNMRTVGEIL	180
Db	129	FQPKDSHGSESDEYIILPNILVLGGSILMESKPVSLKLMNTLAVTWQRAFNMRTVGEIL	188
Qy	181	WGYEDDPVNFINKYLPDMPPKIGKFGLEVENNSDSGLFTVTVGVQVNFSKIHLVDRWGL	240
Db	189	WGYDDDPVHFLNTYLPDMLPIKGKFGLEVGWNNNSGVTFTVTVGVQVNFSLIHLVDXWGL	248
Qy	241	SKVNVHSSQCNMINGTSQMWAPMPTPOSSLEFFSPACRSMKLTVHDSGVGPEGIPTVYR	300
Db	249	SKIDYHSSQCNMINGTSQMWAPMPTPESSLEFFSPACRSMKLTVNESRVEGIP--Y	306
Qy	301	FTAPKTLFANGSVYPPNBSGFCPLBSGIONYSTCRFGAPLFLSHPHYPNADPVLSEAVLG	360
Db	307	FTAPDTLFGANGSVYPPNEBSGFCPCEBSGIONYSTCRFGAPLFLSHPHYPNADPVLSEAV--	364
Qy	361	LAMPDPREHSLFLDIHPVTGIPMNCSSVKLQISLYITKAVKGIGOTCKTEBPVVLPLLWFEQSG	420
Db	365	LQNPKEHSLFLDIHPVTGIPMNCSSVRKQLSLYITKSVKGIQGTGKTEBPVVLPLLWFEQSG	424
Qy	421	AMGGEPLNTFYQLVMPQOVLYVYLLGJGLLLLPVVIYQLRSOEKCFLEWSSKKG	480
Db	425	AMGGEPLNTFYQLVLMQVLYVYLLGJGLLLLPVVIICQLRSOEKCFLEWSSKKG	484
Qy	481	SQKEAIQAYSLSLMSPAKGTVLOEAKL	509
Db	485	SQKEAIQAYSLSLMSPAKGTVLOEAKL	513

RESULT 15

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RESUL1 IS
US-09-779-152-2
; Sequence 2, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-172CP2
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US/09/779,152
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-779-152-2

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Query Match	83.7%	Score 2244;	DB 3;	Length 509;
Best Local Similarity	81.5%;	pred. No. 1.7e-214;		
Matches 415;	Conservative 46;	Mismatches 48;	Indels 0;	Gaps 0;

Qy	121	FQDRSHGSESDYIILPNIIVLGVANVMSKSAGLKMMTLUGLATLGORAFNMRVTVGELL	180
Db	121	FQPSKSHGSESDYIVMPNIILVGAAVNMENKPMTKLIIMTIAFTTTLGERRAFNMRVTGEM	180
Qy	181	WGYEDDPVFNTKYLPMDFPIKGKFGLFVMNNNSDSLFTVPTGVQNFSKTHLVDRWNGL	240
Db	181	WGYPDPLVNLIKPYPPWFPPDKFGGLFAELUNNSDSGLFTVTVGNISRIHLVDKNWGL	240
Qy	241	SKVNYHSEOCNMINGTSGOWAPFMTPQSLEFPFSPEACRSMKLYTHDSGVFEGITPYR	300
Db	241	SKYDFWHSDQCNMINGTSGOWPFFMTPPESSELFYFSPACRSMKYKESGVFEGITPYR	300
Qy	301	FTPAKTLFANGSVYPPNEGPCPLESGIQNVSTCRFGAPLFIHHPHFYNADPVLGEAVLG	360
Db	301	FVAPAKTLFANGSIYPPNEGPCPLESGIQNVSTCRFGAPLFLSHPHFNLADPVLAEAVTG	360
Qy	361	LNPDPREHSLFDITHPTVGIIPMNCVKLOISLYIKAVKIGIGOTGKIIEPVLPPLLWFEOSG	420
Db	361	LHPNQEAHSFLDITHPTVGIIPMNCVSKQLSLYMKSVAGIGOTGKIEBPVPJLLWFAESG	420
Qy	421	AMGGEPLNTFTQLVLMPOVLQVYYVYVLLGLGGILLVLPVITYQRUSQBCKCFLFWSSKKKG	480
Db	421	AMEGETLHTFTQLVLMPKVHWHAQYVLLALGCVVLLVPVICQIESQEKCXYLFWSSKKKG	480
Qy	481	SQKKEATOAYSSESLSMSPAAGTVLQEAKL	509
Db	481	SKQKEATOAYSSESLSMTSPKGSVLQEAKL	509

Search completed: February 23, 2006, 12:51:23
Job time : 122 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:47:29 ; Search time 11.5 Seconds
(without alignments)
658.923 Million cell updates/sec

Title: US-08-765-108-4
Perfect score: 2681
Sequence: 1 MGSSARWVAVGLGVVGLL.....YSESLMSPAAGTIVLQEAFL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2236	83.4	509	7 US-11-055-309A-12	Sequence 12, Appl
2	2236	83.4	509	7 US-11-072-175-219	Sequence 219, App
3	2236	83.4	532	6 US-10-821-234-918	Sequence 918, App
4	97	3.6	1075	7 US-11-098-686-10295	Sequence 10295, A
5	91.5	3.4	1081	7 US-11-142-700-23	Sequence 23, Appl
6	89.5	3.3	441	6 US-10-753-537-20	Sequence 20, Appl
7	89.5	3.3	458	7 US-11-077-550-114	Sequence 114, App
8	89.5	3.3	548	7 US-11-077-550-24	Sequence 24, Appl
9	89.5	3.3	610	7 US-11-142-700-16	Sequence 16, Appl
10	89.5	3.3	858	7 US-11-077-550-22	Sequence 22, Appl
11	89.5	3.3	860	7 US-11-077-550-175	Sequence 175, App
12	89.5	3.3	862	7 US-11-077-550-94	Sequence 94, Appl
13	89.5	3.3	862	7 US-11-077-550-171	Sequence 171, App
14	89.5	3.3	864	7 US-11-077-550-102	Sequence 102, App
15	89.5	3.3	865	7 US-11-077-550-100	Sequence 100, App
16	89.5	3.3	866	7 US-11-077-550-88	Sequence 88, Appl
17	89.5	3.3	866	7 US-11-077-550-104	Sequence 104, App
18	89.5	3.3	867	7 US-11-077-550-80	Sequence 80, Appl
19	89.5	3.3	867	7 US-11-077-550-96	Sequence 96, Appl
20	89.5	3.3	867	7 US-11-077-550-98	Sequence 98, Appl
21	89.5	3.3	870	7 US-11-077-550-92	Sequence 92, Appl
22	89.5	3.3	871	7 US-11-077-550-84	Sequence 84, Appl
23	89.5	3.3	871	7 US-11-077-550-86	Sequence 86, Appl
24	89.5	3.3	871	7 US-11-077-550-90	Sequence 90, Appl
25	89.5	3.3	876	7 US-11-077-550-82	Sequence 82, Appl

26	89.5	3.3	876	7 US-11-077-550-106	Sequence 106, App
27	89.5	3.3	876	7 US-11-077-550-108	Sequence 108, App
28	89.5	3.3	888	7 US-11-077-550-112	Sequence 112, App
29	89.5	3.3	1169	7 US-11-077-550-20	Sequence 20, Appl
30	89.5	3.3	1420	7 US-11-077-550-110	Sequence 110, App
31	89	3.3	947	6 US-10-453-372-1010	Sequence 1010, App
32	89	3.3	962	6 US-10-453-372-1042	Sequence 1042, App
33	88	3.3	951	6 US-10-453-372-1012	Sequence 1012, App
34	88	3.3	2515	7 US-11-113-424-53	Sequence 53, Appl
35	86	3.2	1138	7 US-11-049-536-2	Sequence 2, Appli
36	86	3.2	6738	6 US-10-922-232B-56	Sequence 56, Appl
37	85.5	3.2	302	6 US-10-926-709-8	Sequence 8, Appli
38	85.5	3.2	304	7 US-11-142-700-2	Sequence 2, Appli
39	85.5	3.2	2399	7 US-11-052-554A-92	Sequence 92, Appl
40	85	3.2	477	7 US-11-186-284-127	Sequence 127, App
41	85	3.2	477	7 US-11-043-788-243	Sequence 243, App
42	85	3.2	1086	7 US-11-142-700-10	Sequence 10, Appl
43	84.5	3.2	459	6 US-10-453-372-1046	Sequence 1046, Ap
44	84.5	3.2	729	7 US-11-130-821-4	Sequence 4, Appli
45	84	3.1	385	7 US-11-202-731-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-11-055-309A-12
; Publication 12, Application US/11055309A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: Treatment for Dark Adaptation
; FILE REFERENCE: HO-P02351US
; CURRENT APPLICATION NUMBER: US/11/055,309A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 509
; TYPE: PRT
; ORGANISM: HUMAN
US-11-055-309A-12

Query Match	83.4%	Score 2236;	DB 7;	Length 509;
Best Local Similarity	81.3%	Pred. No. 3e-205;		
Matches 414;	Conservative 46;	Mismatches 49;	Indels 0;	Gaps 0;
Qy	1	MGSSARWVAVGLGVVGLLCAVLGVVMIIVMPSLIKQVLKXVRIDPSSLSFAMWKEIP	60	
Db	1	MGSSAKARWAAGALGVAGLLCAVLGAVIIVVPSLIKQVLKXVRIDPSSLSFAMWKEIP	60	
Qy	61	VPVLSVYFPEVYVNPSEILKGEKPVYRERGYPYVYRERKXANITFNDNDTVSPVHRSLH	120	
Db	61	IPFVLSYFPEVYVNPSEILKGEKPVYRERGYPYVYRERKXANITFNDNDTVSPVHRSLH	120	
Qy	121	FQDRGHGSSDYIILPNILVLGAVVMESKAGLLMTLGLATLQORAFMNRVTGEIL	180	
Db	121	FQSKGHGSSDYIIVPNILVLGAAVMENKPMTLKIMTLAFTTLGERAFMNRVTGEIM	180	
Qy	181	WGYEDPFVNFINKYLPDMFPFKGKFLFVEMNNSDGLFTVFTGVQNFSKIHILVDWNGL	240	

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Db 181 WGYKDPVLNLINKYFGMPFPKDKFGLFAELNNSDGLFTVFTGVQNIIRHLVDKWNGL 240
Qy 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKYDFWHSDDCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLYKESGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLSEAVTG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Db 361 LHPNQEAHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKSVAGIGQGTGKIEPVVLPVLLWFAESG 420
Qy 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
Db 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
Qy 481 SQKKEAIQAYSESLMSPAAGTGLVQEAKL 509
Db 481 SKDKEAIQAYSESLMTSAPKGSVLQEAKL 509

RESULT 2
US-11-072-175-219
; Sequence 219, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-219

Query Match 83.4%; Score 2236; DB 7; Length 509;
Best Local Similarity 81.3%; Pred. No. 3e-205;
Matches 414; Conservative 46; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MGCSARARWAVAGLVGVLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 1 MGCSAKARWAAGALGVAGLLCAVLGAVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Qy 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRSLSH 120
Db 61 IPFLSVYFPEVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFLEVRTFQ 120
Qy 121 FQDRSHGSESDYIILPNILVLGGAVMNESKAGLKMVTLGLATLGQAFMNRVTGVEIL 180
Db 121 FQPSKSHGSESDYIVMNPILVLGAAVMNENKPMVTLKIMTLAFTTIGERAFMNRVTGVEIM 180
Qy 181 WGYEDPVPVFNKYLPMDFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKWNGL 240
Db 181 WGYKDPVLNLINKYFGMPFPKDKFGLFAELNNSDGLFTVFTGVQNIIRHLVDKWNGL 240
Qy 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 241 SKYDFWHSDDCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLYKESGVFEGIPTYR 300
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLSEAVTG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Db 361 LHPNQEAHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKSVAGIGQGTGKIEPVVLPVLLWFAESG 420
Qy 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
Db 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
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Db 301 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLSEAVTG 360
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Db 361 LHPNQEAHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKSVAGIGQGTGKIEPVVLPVLLWFAESG 420
Qy 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
Db 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
Qy 481 SQKKEAIQAYSESLMSPAAGTGLVQEAKL 509
Db 481 SKDKEAIQAYSESLMTSAPKGSVLQEAKL 509

RESULT 3
US-10-821-234-918
; Sequence 918, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 918
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-918

Query Match 83.4%; Score 2236; DB 6; Length 532;
Best Local Similarity 81.3%; Pred. No. 3.2e-205;
Matches 414; Conservative 46; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MGCSARARWAVAGLVGVLLCAVLGVVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 60
Db 24 MGCSAKARWAAGALGVAGLLCAVLGAVMIIVMPSLIKQVVKVNRIDPSSLSFAMWKEIP 83
Qy 61 VPFLSVYFPEVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFVHRSLSH 120
Db 84 IPFLSVYFPEVNVNPSILKGEKPVVRERGPVYVREPRHKANITFNDNDTVSFLEVRTFQ 143
Qy 121 FQDRSHGSESDYIILPNILVLGGAVMNESKAGLKMVTLGLATLGQAFMNRVTGVEIL 180
Db 144 FQPSKSHGSESDYIVMNPILVLGAAVMNENKPMVTLKIMTLAFTTIGERAFMNRVTGVEIM 203
Qy 181 WGYEDPVPVFNKYLPMDFPIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDKWNGL 240
Db 204 WGYKDPVLNLINKYFGMPFPKDKFGLFAELNNSDGLFTVFTGVQNIIRHLVDKWNGL 263
Qy 241 SKVNYHSEOCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLTYHDSGVFEGIPTYR 300
Db 264 SKYDFWHSDDCNMGNTSGQWAPFMTPOSSLEFFSPEACRSKMLYKESGVFEGIPTYR 323
Qy 301 FTAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 324 FVAPKTLFANGSVYPPNEGFCPCLESGIQNVSTCRFSAPLFLSHPHFLNADPVLSEAVTG 383
Qy 361 LNPDPREHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKGIQGTGKIEPVVLPVLLWFEQSG 420
Db 384 LHPNQEAHSLFLDIHPVTGIPMNCVKQLQISLYIKAVKSVAGIGQGTGKIEPVVLPVLLWFAESG 443
Qy 421 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 480
Db 444 AMGEPLNTFTYQTLVLMPOVQVYVLLGLGLLLVPIYQVLRQSKCFLFWSSGSKG 503
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Qy 481 SODKEATQAYSESLSPAAGKTVLQEAAL 509
Db 504 SKDKEAIQAYSESLMTAPKGVQLQEAAL 532

RESULT 4

US-11-098-686-10295
; Sequence 10295, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10295
; LENGTH: 1075
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10295

Query Match 3.6%; Score 97; DB 7; Length 1075;
Best Local Similarity 20.2%; Pred. No. 0.87;
Matches 81; Conservative 64; Mismatches 140; Indels 116; Gaps 21;

Qy 31 VMPSLIKQVQLKNRVIDPSSLSFAMWKEIPV-PYL----- 65
Db 38 ILSTISQ--LKDTISANSIGFHI---VFPKLYLTNVLQTKGTTHIKECLTPKI 92
Qy 66 -----SVYFVFNVP--SEILKGB-KPVVRERGPVYRFRHKKANITFNDNDTVSFV 114
Db 93 TNLISGNISIVSEVIOPIASIIILQNEQKNSKTTGVAIPKQVSHLQLI---TDSKLI 149
Qy 115 EHRSLHQPDRSHGSESDYIILPNILVGLNAV-MWESKSAGLKLMTLGLATLQORAPMN 173
Db 150 ENGSIPTQ-----NNDYCF--KIINGKIGVSKLTLSLKL----- 184
Qy 174 RTVGEILGWYEDPPVN-----FINKYLPDMFPKKGKGLFVEMNNSDSLFTVFT 223
Db 185 -TADLIWEIMNTVSNNSSTAQKSEIKVQLHIDM-PYKINTALL-----HDTSLYDLFT 238
Qy 224 GVQNFS-----KHLVDRWNL-----SKVNYWHSEQNM-----INGT--SGQ----- 260
Db 239 NTKKTFKVSAGIPTTNTANNITPDTFTKLEKNSDKLTWHGQLHIEGTLPGNNTSIPIL 298
Qy 261 MWAPFMTQOS-SLEFFSPACRSKMLYHDSGVFEGIPTRVPTAPKTLFANGSV----- 313
Db 299 LSVFPTTSSSEDMTHFPFLIKNSKLLFDKTHIDLHGTIKNYDTLSNLFFDGTMDVKNFS 358
Qy 314 YPNNEGCPCLSEGIQNVSTCRFCAPLFLSHPHFYNADPVL 354
Db 359 FPVWTFARQLPNGIQHALNQLSGEIKFTLSPPQVNAQKII 399

RESULT 5

US-11-142-700-23
; Sequence 23, Application US/11142700
; Publication No. US20060026721A1
; GENERAL INFORMATION:
; APPLICANT: Stephen M. Allen
; APPLICANT: Gary M. Fader
; APPLICANT: Saverio Carl Falco
; APPLICANT: Anthony J. Kinney
; APPLICANT: Jonathan E. Lightner
; APPLICANT: Guo-Hua Miao

; APPLICANT: J. Antoni Rafaleki
; APPLICANT: Catherine J. Thorpe
; TITLE OF INVENTION: Plant Cellulose Synthases
; FILE REFERENCE: BB-1170
; CURRENT APPLICATION NUMBER: US/11/142,700
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/09/720,383
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/092,844
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 1081
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-142-700-23

Query Match 3.4%; Score 91.5; DB 7; Length 1081;
Best Local Similarity 23.4%; Pred. No. 2.9;
Matches 71; Conservative 45; Mismatches 120; Indels 67; Gaps 16;

Qy 62 PFYLSVYFEP-----VNPSEILKGEKPVV-----BERGPVYRFRHKKANIT 104
Db 726 PVFIATFMEQGGIPPTTNPATLLKRAIHVISCYEDKTEWKEIG-WIY-----GSVT 778
Qy 105 FNDNDTVSFVEHR---SLHFQPDGRSHGSESDYIILPNIL-----VLGGAVMMESKSG 154
Db 779 --EDILTGFMHARGWISIVCNPRPAKSPINLSRLNOVLWALSGSIEILLRHP 836
Qy 155 LKMLMTGLATLQORAPMNTVGEILGWYEDFPVFNINKYLPDMFPKKGKGLFVEMNNS 214
Db 837 IWYGYHGLRLLBRIAYINTIVPIT---SIPLIAYC--ILPAFCLITDRF-IIPEISNY 890
Qy 215 DSGLFTVF-----TGQNFPSKHLVDRWNLGSKVNYWHSEQNMINGTSGQWAPFMT 268
Db 891 ASIWFIILLFISIAVTGI-----LELRMSGVSIEDWNRNEQFWVIGTSAHLFAVFOGL 943
Qy 269 QSSLEFFSPACRSKMLTYHDSGVFEGIPTRFTA-----PKT-LFAN-----GSVYPPN 317
Db 944 LKVLAGIDINTVTSKATDED-GDFAELIYFKTKTALLIPTTVLLVNLGIVAGSVAVN 1002
Qy 318 EGF 320
Db 1003 SGY 1005

RESULT 6

US-10-753-537-20
; Sequence 20, Application US/10753537
; Publication No. US20050260230A1
; GENERAL INFORMATION:
; APPLICANT: STEWARD, LANCE E
; APPLICANT: FERNANDEZ-SALAS, ESTER
; APPLICANT: HERRINGTON, TODD M
; APPLICANT: AOKI, KEI R
; TITLE OF INVENTION: Leucine-based motif and clostridial neurotoxins
; FILE REFERENCE: D-2885CJP
; CURRENT APPLICATION NUMBER: US/10/753,537
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US/09/910,346C
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/620,840
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-753-537-20

Query Match 3.3%; Score 89.5; DB 6; Length 441;

Query Match 3.3%; Score 89.5; DB 7; Length 858;


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; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-11-077-550-102

Query Match          3.3%; Score 89.5; DB 7; Length 864;
Best Local Similarity 18.7%; Pred. No. 3.3;
Matches 91; Conservative 67; Mismatches 146; Indels 183; Gaps 23;

QY 73 VNPSEILKGEKPVVRERGYPVYREFRHKANI-----TF-----NNDTVSFVEHRSLS-- 119
DB 20 IDNNNIIMPEPPFARGTGRY-YKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCE 78
QY 120 HFQPDRESHSESYYIILPNILVLGGAVMMESKAGLKL--MWTGLATLGQRAF-----MN 173
DB 79 YYPDYLTNDKKNIFLQTMIKLFNRI--KSKPLGKLEMIINGIPYLGDRVRVPLEEFN 136
QY 174 RTVGEILGWEDPPVNFINKYLPDMPPIKGFGLFVE-----MNSDSGLFTVFTG 224
DB 137 TNIASVT-----VNKLISNPGEVERKKGIFANLIIFGPGVNLNENE-----TIDIG 182
QY 225 VQNFSKHLVDRWNGLSKVNYHSEQCNMINGTSGQMWAPFMTTPQSSLEFFSPEACRSKM 284
DB 183 IQN-----HFASR-----EGFGGIM-----QMK 200
QY 285 LTYHDSGVFEGIPYRTAPKTLFANGSVYPPNEGFCPCLESIGIONVSTCRFGAPLPLSH 344
DB 201 -----FCPEYVSFVNNVQENK-GASIFNRR 224
QY 345 PHFYNDAPVLSEAVLGLNPDPRHSLFLDHPVTGIPMNCVSKLQISLYIKAVKGIGQTG 404
DB 225 GYP--SDPAL--IL-----MHLEIHLVHLGLYGI-----248
QY 405 KIEPVVLPPL-----WFEQSGAMGGEPLNTF-----YTQLVLMQVLYQVQYVL 448
DB 249 KVDD--LPVINEKFFMQSDTAIQABELYTFGGQDPSIITPSTDKSIYDKVLQNRGIV 306
QY 449 LGLGGLLLLP-----VIYQLRSQEKCFLFWSGSKGQDKEAIQAYSESLMSPAAGT 502
DB 307 DRLMKVLVCISDPNININIKYKFKYFVESEGKYSIDVESFDKLYKSLMFGFTETN 366
QY 503 VLQEAKL 509
DB 367 IAENYKI 373

RESULT 15
US-11-077-550-100
; Sequence 100, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
```

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; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-11-077-550-100

Query Match          3.3%; Score 89.5; DB 7; Length 865;
Best Local Similarity 18.7%; Pred. No. 3.3;
Matches 91; Conservative 67; Mismatches 146; Indels 183; Gaps 23;

QY 73 VNPSEILKGEKPVVRERGYPVYREFRHKANI-----TF-----NNDTVSFVEHRSLS-- 119
DB 20 IDNNNIIMPEPPFARGTGRY-YKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCE 78
QY 120 HFQPDRESHSESYYIILPNILVLGGAVMMESKAGLKL--MWTGLATLGQRAF-----MN 173
DB 79 YYPDYLTNDKKNIFLQTMIKLFNRI--KSKPLGKLEMIINGIPYLGDRVRVPLEEFN 136
QY 174 RTVGEILGWEDPPVNFINKYLPDMPPIKGFGLFVE-----MNSDSGLFTVFTG 224
DB 137 TNIASVT-----VNKLISNPGEVERKKGIFANLIIFGPGVNLNENE-----TIDIG 182
QY 225 VQNFSKHLVDRWNGLSKVNYHSEQCNMINGTSGQMWAPFMTTPQSSLEFFSPEACRSKM 284
DB 183 IQN-----HFASR-----EGFGGIM-----QMK 200
QY 285 LTYHDSGVFEGIPYRTAPKTLFANGSVYPPNEGFCPCLESIGIONVSTCRFGAPLPLSH 344
DB 201 -----FCPEYVSFVNNVQENK-GASIFNRR 224
QY 345 PHFYNDAPVLSEAVLGLNPDPRHSLFLDHPVTGIPMNCVSKLQISLYIKAVKGIGQTG 404
DB 225 GYP--SDPAL--IL-----MHLEIHLVHLGLYGI-----248
QY 405 KIEPVVLPPL-----WFEQSGAMGGEPLNTF-----YTQLVLMQVLYQVQYVL 448
DB 249 KVDD--LPVINEKFFMQSDTAIQABELYTFGGQDPSIITPSTDKSIYDKVLQNRGIV 306
QY 449 LGLGGLLLLP-----VIYQLRSQEKCFLFWSGSKGQDKEAIQAYSESLMSPAAGT 502
DB 307 DRLMKVLVCISDPNININIKYKFKYFVESEGKYSIDVESFDKLYKSLMFGFTETN 366
QY 503 VLQEAKL 509
DB 367 IAENYKI 373

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Job time : 12.5 secs
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GenCore version 5.1.7
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Perfect score: 1785
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: gb_on.*
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6: gb_pat.*
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8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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1	1785	100.0 1785 6 AR078245	AR078245 Sequence
2	1785	100.0 1785 6 AR195310	AR195310 Sequence
3	1785	100.0 1785 6 AX305450	AX305450 Sequence
4	1785	100.0 1785 9 MMU37799	MMU37799 Mus musculus
5	1785	100.0 2496 6 CQ868666	CQ868666 Sequence
6	1785	100.0 2512 9 BC004656	BC004656 Mus muscu
7	1607	90.0 1607 6 AX419948	AX419948 Sequence
8	1530	85.7 1530 9 CT010222	CT010222 Mus muscu
9	1460.6	81.8 2392 9 D89655	D89655 Rattus norv
10	1459.4	81.8 2408 9 BC078504	BC078504 Rattus no
11	1459.4	81.8 2497 9 AB002151	AB002151 Rattus no
12	1452.6	81.4 2401 9 AY451993	AY451993 Rattus no
13	1426	79.9 1674 9 RNU76205	RNU76205 Rattus norv
14	1396.2	78.2 1825 6 AR091980	AR091980 Sequence
15	1396.2	78.2 1825 6 AR112115	AR112115 Sequence
16	1396.2	78.2 1825 6 AR149157	AR149157 Sequence
17	1369.8	76.7 1788 6 AR078244	AR078244 Sequence
18	1369.8	76.7 1788 6 AR195308	AR195308 Sequence

19	1369.8	76.7	1788	6	AR222273	AR222273 Sequence
20	1369.8	76.7	1788	9	CGU11453	U11453 Cricetus
21	1342	75.2	1590	9	AF071495	AF071495 Rattus no
22	1215.2	68.1	2272	9	AY682847	AY682847 Rattus no
23	1144.2	64.1	2622	8	EC080647	EC080647 Homo sapi
24	1142.6	64.0	2630	6	AR091979	AR091979 Sequence
25	1142.6	64.0	2630	6	AR112114	AR112114 Sequence
26	1142.6	64.0	2630	6	AR149156	AR149156 Sequence
27	1141	63.9	2566	6	AR261646	AR261646 Sequence
28	1141	63.9	2566	6	AR474634	AR474634 Sequence
29	1141	63.9	2566	6	AR635204	AR635204 Sequence
30	1141	63.9	2566	8	HSCLAIGNA	Z22555 H.sapiens e
31	1127.8	63.2	3144	6	CQ868669	CQ868669 Sequence
32	1117.4	62.6	2670	4	AF467889	AF467889 Sus scrofa
33	1115.8	62.5	1681	8	BC093732	BC093732 Homo sapi
34	1103.6	61.8	2598	4	AF019384	AF019384 Bos tauru
35	1073.6	60.1	2400	4	AY283277	AY283277 Oryctolag
36	1072.4	60.1	1530	4	AY428553	AY428553 Tupaia be
37	1047.6	58.7	1527	6	AX763178	AX763178 Sequence
38	966.6	54.2	1845	8	AF515445	AF515445 Homo sapi
39	959	53.7	4391	8	AB209436	AB209436 Homo sapi
40	947.6	53.1	1659	11	AY892789	AY892789 Synthetic
41	947.6	53.1	1659	11	BT008093	BT008093 Synthetic
42	936.8	52.5	2271	4	AY283278	AY283278 Oryctolag
43	866.2	48.5	2347	6	CQ842792	CQ842792 Sequence
44	866.2	48.5	2347	8	AK124112	AK124112 Homo sapi
45	765.4	42.9	1440	6	CQ722206	CQ722206 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR078245 1785 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 3 from patent US 5962322.
ACCESSION AR078245
VERSION AR078245.1 GI:10004991
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Kozarsky,K., Rigotti,A. and Krieger,M.
TITLE Methods for modulation of cholesterol transport
JOURNAL Patent: US 5962322-A 3 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..1785
organism="unknown"
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Qy	61	GCTCCAGGCGCGCTGGGTGGCCCTTTGGGGTTGGGGCTCTGTTTCTGCTGCGC	120
Db	61	GCTCCAGGCGCGCTGGGTGGCCCTTTGGGGTTGGGGCTCTGTTTCTGCTGCGC	120
Qy	121	TCGGCGTTGTCATGATCTCATGTCGCCCTCCCTCATCAAGCAGCGAGTCTCAAGAATG	180
Db	121	TCGGCGTTGTCATGATCTCATGTCGCCCTCCCTCATCAAGCAGCGAGTCTCAAGAATG	180
Qy	181	TCGCATAGACCCGAGCAGCGCTCTCTTCGGGATGGAAGGAGATCCCGTCCCTTCT	240
Db	181	TCGCATAGACCCGAGCAGCGCTCTCTTCGGGATGGAAGGAGATCCCGTCCCTTCT	240
Qy	241	ACTTGTCTGTCTACTTCTTCAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAGC	300

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Db	1381	CGCAGTATGTCTGCTGGGGCTTTGGAGGCCTCCTGTTGCTGGTGGCCCATCATCTGCCAAC	1440
Qy	1441	TGCGCAGCCAGGAGAAATGCTTTTGTGTTGGAGTGTGTAGTAAAGGGCTCCGAGATA	1500
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Qy	1501	AGGAGGCATTCAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGGCACGGTGC	1560
Db	1501	AGGAGGCATTCAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGGCACGGTGC	1560
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Db	1621	GGTCAGACCAAGCCAGTCCCTACACCCCGCTTTTGAGGACTCTCTCAGCGGACAGC	1680
Qy	1681	CCACAGTGCATGGCTGAGCCCCCAGATGTACACCTGTCCGACGCAACGACATGG	1740
Db	1681	CCACAGTGCATGGCTGAGCCCCCAGATGTACACCTGTCCGACGCAACGACATGG	1740
Qy	1741	ATGCCACGATGTGCAAAACAACTCAGGACCCAGGACAGACC	1785
Db	1741	ATGCCACGATGTGCAAAACAACTCAGGACCCAGGACAGACC	1785
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LOCUS	AR195310	1785 bp	DNA linear PAT 20-APR-2002
DEFINITION	Sequence 7 from patent US 6350859.		
ACCESSION	AR195310		
VERSION	AR195310.1 GI:20244747		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1785)		
AUTHORS	Krieger,M., Acton,S.L. and Rigotti,A.		
TITLE	Class BI and CI scavenger receptors		
JOURNAL	Patent: US 6350859-A 7 26-FEB-2002;		
FEATURES	Location/Qualifiers		
source	1..1785		
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Best Local Similarity	100.0%;	Prod. No. 0;	
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Db	61	GCTCCAGGGCGCGCTGGGTGGCTTGGGGTTGGGGCCCTGGGGCTCTGTTTGTCTGCGC	120
Qy	121	TCGGCGTTGTATGATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180
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Db	181	TCGCATAGACCCGAGCAGCTGTCTTCGGGATGTGGAAGGAGATCCCGTCCCTTTCT	240
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RESULT 3
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LOCUS 1785 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 201 from Patent WO0188188.
ACCESSION AX305450
VERSION AX305450.1 GI:17644972
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Ishikawa, K., Asai, S., Takahashi, Y., Nagata, T. and Ishii, Y.
TITLE Method for examining ischemic conditions
JOURNAL Patent: WO 0188188-A 201 22-NOV-2001;
School Juridical Person Nihon University (JP)
FEATURES
Location/Qualifiers
1. 1785
/organism="Mus musculus"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Mus musculus scavenger receptor class B type I (msr-BI) mRNA,
DEFINITION complete cds.
ACCESSION U37799
VERSION U37799.1 GI:1167551
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Acton,S., Rigotti,A., Landschulz,K.T., Xu,S., Hobbs,H.H. and
Krieger,M.
TITLE Identification of scavenger receptor SR-BI as a high density
lipoprotein receptor
JOURNAL Science 271 (5248), 518-520 (1996)
PUBMED 8560269
REFERENCE 2 (bases 1 to 1785)
AUTHORS Acton,S. and Krieger,M.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1995) Susan L. Acton, Biology, MIT, 77
Massachusetts Ave., Cambridge, MA 02139, USA
FEATURES
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PEACRSKMLTVNESRVEGIPVTPFTAPDPLPANGSVYPNEGFCPCRESGIQNVSTC
RFGAPLFLSHPHFVADPVLSEAVLGLNPNPKHSLFDLHPVTGIPMNSVQQLSL
YIKSVKIGTGKKEIPVVLPLLMFEQSGMGKPLSTFYTLQVLMPOVLHYAQVLLG
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L"

ORIGIN

Query Match		100.0%;	Score 1785;	DB 9;	Length 1785;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1785;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCGTCCTCTTCAGGTCTCAGGCGCCGAGAGCCCTTCGCGCAGCGGACATGCGCGCA	60		
Db	1	CCGTCCTCTTCAGGTCTCAGGCGCCGAGAGCCCTTCGCGCAGCGGACATGCGCGCA	60		
Qy	61	GCTCCAGGCGCGCTGGGTGGCTTGGGGTTGGCGCCCTGGGGCTGCTGTTTCTGCGC	120		
Db	61	GCTCCAGGCGCGCTGGGTGGCTTGGGGTTGGCGCCCTGGGGCTGCTGTTTCTGCGC	120		
Qy	121	TCGCGCTGTGATCATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG	180		
Db	121	TCGCGCTGTGATCATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG	180		
Qy	181	TCGCGATAGACCCGAGCAGCTGCTTCCGGATGTGGAAGGAGATCCCGTCCCTTTCT	240		
Db	181	TCGCGATAGACCCGAGCAGCTGCTTCCGGATGTGGAAGGAGATCCCGTCCCTTTCT	240		
Qy	241	ACTTGTCTGTCTACTTCTTCAAGTGTCAACCCAAACGAGGTCTCAACGCGCCAGAACG	300		
Db	241	ACTTGTCTGTCTACTTCTTCAAGTGTCAACCCAAACGAGGTCTCAACGCGCCAGAACG	300		
Qy	301	CAGTAGTCCGGAGCGTGAGCCCTATGTCTACAGGGAGTTTCAGACAAAGGTCAACATCA	360		
Db	301	CAGTAGTCCGGAGCGTGAGCCCTATGTCTACAGGGAGTTTCAGACAAAGGTCAACATCA	360		
Qy	361	CTTTCATGACACAGCAGCAGCTGCTTCCGGAGAACCCGAGCTCCATTTCCAGCCTG	420		
Db	361	CTTTCATGACACAGCAGCAGCTGCTTCCGGAGAACCCGAGCTCCATTTCCAGCCTG	420		
Qy	421	ACAAGTCGCTATGCTCAGAGAGTCACTATGTACTGTCTTAACTCTTGTCTCTGGGG	480		
Db	421	ACAAGTCGCTATGCTCAGAGAGTCACTATGTACTGTCTTAACTCTTGTCTCTGGGG	480		
Qy	481	GCTCGATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGACCTTTGGCGCTGG	540		
Db	481	GCTCGATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGACCTTTGGCGCTGG	540		
Qy	541	TCACCATGGGCGCAGCTGCTTTATGAAACCGCAGTGTGTGAGATCTGTGGGGCTATG	600		
Db	541	TCACCATGGGCGCAGCTGCTTTATGAAACCGCAGTGTGTGAGATCTGTGGGGCTATG	600		
Qy	601	ACGATCCCTTCTGTCATTTCTCAACAGCTACCTCCAGACATGCTTCCCATAAAGGCA	660		
Db	601	ACGATCCCTTCTGTCATTTCTCAACAGCTACCTCCAGACATGCTTCCCATAAAGGCA	660		
Qy	661	AATTTGGCCTGTTTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCACGG	720		
Db	661	AATTTGGCCTGTTTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCACGG	720		
Qy	721	CGCTCCAGAAATTTACAGAGATCTCATCTGTGGGCAAAATGGAACGAGCTCAGCAAGATCG	780		
Db	721	CGCTCCAGAAATTTACAGAGATCTCATCTGTGGGCAAAATGGAACGAGCTCAGCAAGATCG	780		
Qy	781	ATTATTGGCAATTCAGACAGTGTAAATGATGATGAGTCTCCGCGCAGATGTGGGCAC	840		
Db	781	ATTATTGGCAATTCAGACAGTGTAAATGATGATGAGTCTCCGCGCAGATGTGGGCAC	840		
Qy	841	CCTTTCATGACACCCGAATCTCTCGCTGGAAATTTCTTCAGCCCGGAGGATGCGAGTCCATGA	900		

RESULT 5
CQ868666
LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism

CQ868666
Sequence 78 from Patent WO2004074321.
CQ868666
CQ868666.1 GI:51998641
Mus musculus (house mouse)

2496 bp DNA linear

PAT 13-SEP-2004

Db	841	CTTTCATGACACCCGAATCTCTCGCTGGAAATTTCTTCAGCCCGGAGGATGCGAGTCCATGA	900
Qy	901	AGCTGACCTCAACAGGAATCAAGGGTGTTCAGAGGCATTCCTCCAGTATCGCTTTCACGGCCC	960
Db	901	AGCTGACCTCAACAGGAATCAAGGGTGTTCAGAGGCATTCCTCCAGTATCGCTTTCACGGCCC	960
Qy	961	CCGATACTCTGTTTGGCAACCGGGTCCGTCTACCCACCCAAACGAAAGGCTTCTGCCCATGCC	1020
Db	961	CCGATACTCTGTTTGGCAACCGGGTCCGTCTACCCACCCAAACGAAAGGCTTCTGCCCATGCC	1020
Qy	1021	GAGAGTCTGCAATTCAGAAATGTGAGACCTTCGAGGTTTGGTGGCTCTCTGTTCTCTCCC	1080
Db	1021	GAGAGTCTGCAATTCAGAAATGTGAGACCTTCGAGGTTTGGTGGCTCTCTGTTCTCTCCC	1080
Qy	1081	ACCCCACTTTTACACCGCGAGCCTGTGTGTGTCAGAAAGTGTTCCTGGTCTGAACCCCTA	1140
Db	1081	ACCCCACTTTTACACCGCGAGCCTGTGTGTGTCAGAAAGTGTTCCTGGTCTGAACCCCTA	1140
Qy	1141	ACCCAAAGGAGCAATCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCATGAACCT	1200
Db	1141	ACCCAAAGGAGCAATCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCATGAACCT	1200
Qy	1201	GTTCTGTGAAGATGCGAGCTGAGCCTCTATCATCAAAATCTGTCAAGGGCATCGGGCAACAG	1260
Db	1201	GTTCTGTGAAGATGCGAGCTGAGCCTCTATCATCAAAATCTGTCAAGGGCATCGGGCAACAG	1260
Qy	1261	GGAAGATCGAGCAGTAGTTCGCGCTGCTGTGTCGAGTTCGAAACAGAGCGGAGCAATGGGTG	1320
Db	1261	GGAAGATCGAGCAGTAGTTCGCGCTGCTGTGTCGAGTTCGAAACAGAGCGGAGCAATGGGTG	1320
Qy	1321	GCAAGCCCTTGACAGCAGTTCCTACACGAGCTGTGTGCTGATGCCCCAGGTTCTTCACTACG	1380
Db	1321	GCAAGCCCTTGACAGCAGTTCCTACACGAGCTGTGTGCTGATGCCCCAGGTTCTTCACTACG	1380
Qy	1381	CGCAGTATGTGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGTGGTCCCATCATCTGCCAAC	1440
Db	1381	CGCAGTATGTGCTGCTGGGGCTTGGAGGCTCTCTGTTGCTGTGGTCCCATCATCTGCCAAC	1440
Qy	1441	TGCGCAGCCAGGAGAAATGCTTTTCTGTTGGAGTGTGTAGTAAAGGGCTCCCGAGATA	1500
Db	1441	TGCGCAGCCAGGAGAAATGCTTTTCTGTTGGAGTGTGTAGTAAAGGGCTCCCGAGATA	1500
Qy	1501	AGGAGGCCAATTCAGGCTTCTCTGAGTCTCTGATGTCCAGCTGCCCAGGCGACCGGTGC	1560
Db	1501	AGGAGGCCAATTCAGGCTTCTCTGAGTCTCTGATGTCCAGCTGCCCAGGCGACCGGTGC	1560
Qy	1561	TGCAAGAGCCAAAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCCTGATAGCTT	1620
Db	1561	TGCAAGAGCCAAAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCCTGATAGCTT	1620
Qy	1621	GGTCCAGCCAGCCACCCAGTCCCTTACACCCGCTTCTTGAGGACTCTCTCAGCGGACAGC	1680
Db	1621	GGTCCAGCCAGCCACCCAGTCCCTTACACCCGCTTCTTGAGGACTCTCTCAGCGGACAGC	1680
Qy	1681	CCACCAAGTCCATGGCTGAGCCGCCAGATGTCAACCTGTGCGCAGCAGCAGCATGG	1740
Db	1681	CCACCAAGTCCATGGCTGAGCCGCCAGATGTCAACCTGTGCGCAGCAGCAGCATGG	1740
Qy	1741	ATGCCCAAGCATGTGCAAAACAACTCAGGGACCCAGGACAGACC	1785
Db	1741	ATGCCCAAGCATGTGCAAAACAACTCAGGGACCCAGGACAGACC	1785

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
REFERENCE	1 Morris, D.W. and Malandro, M.S.								
AUTHORS	Novel therapeutic gpcr targets in cancer								
TITLE	Patent: WO 2004074321-A 78 02-SEP-2004;								
JOURNAL	Sagres Discovery, Inc. (US)								
FEATURES	Location/Qualifiers								
	1..2496								
source	/organism="Mus musculus"								
ORIGIN	/mol_type="unassigned DNA"								
	/db_xref="taxon:10090"								
	Query Match 100.0%; Score 1785; DB 6; Length 2496;								
	Best Local Similarity 100.0%; Pred. No. 0;								
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0									
Qy	1	CCGTCCTCTTCAGGTCTGAGCCCGGAGAGCCCTTCCGGCGCAGCGGACATGGCGGCA	60						
Db	143	CGGTCTCTTCAGGTCTGAGCCCGGAGAGCCCTTCCGGCGCAGCGGACATGGCGGCA	202						
Qy	61	GCTCAGGCGCGCTGGGTGGCCCTTGGGGTGGCGCCCTGGGGCTGCTGTTTGTGCGC	120						
Db	203	GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTGGCGCCCTGGGGCTGCTGTTTGTGCGC	262						
Qy	121	TGCGGCTTTCATGATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180						
Db	263	TGCGGCTTGTTCATGATCCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	322						
Qy	181	TCCGCATAGACCCGAGCAGCTGTCTTTCGGGATGTGGAAGGAGATCCCGTCCCTTTCT	240						
Db	323	TCCGCATAGACCCGAGCAGCTGTCTTTCGGGATGTGGAAGGAGATCCCGTCCCTTTCT	382						
Qy	241	ACTTGTCTGTCTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCTAACGCCAGAAC	300						
Db	383	ACTTGTCTGTCTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCTAACGCCAGAAC	442						
Qy	301	CAGTAGTCCGGAGCGTGGACCCCTATGCTACAGGGAGTTCAGACAAAGGTCAACATCA	360						
Db	443	CAGTAGTCCGGAGCGTGGACCCCTATGCTACAGGGAGTTCAGACAAAGGTCAACATCA	502						
Qy	361	CTTTCATGACAAACGACACCGGTGCTCTTTCGGGAGAACCGCAGCTCCATTTCCAGCGTG	420						
Db	503	CTTTCATGACAAACGACACCGGTGCTCTTTCGGGAGAACCGCAGCTCCATTTCCAGCGTG	562						
Qy	421	ACAAGTCGCATGGCTCAGAGATGACTACATTTGATGTCCTTAACATCTTGGTCTGGGG	480						
Db	563	ACAAGTCGCATGGCTCAGAGATGACTACATTTGATGTCCTTAACATCTTGGTCTGGGG	622						
Qy	481	GCTCGATATTGATGGAGCAGCCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG	540						
Db	623	GCTCGATATTGATGGAGCAGCCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG	682						
Qy	541	TCACCATGGGCGCGGTCTTTTATGAACCGCAGTGTGGAGATCTGTGGGGCTATG	600						
Db	683	TCACCATGGGCGCGGTCTTTTATGAACCGCAGTGTGGAGATCTGTGGGGCTATG	742						
Qy	601	ACGATCCCTCTGTCATTTTCTCAACACGTACCTTCCAGACATGCTTCCCATAAAGGCA	660						
Db	743	ACGATCCCTCTGTCATTTTCTCAACACGTACCTTCCAGACATGCTTCCCATAAAGGCA	802						
Qy	661	AATTTGGCGCTGTTTGGGATGAACAACTCGAAATCTGGGGTCTTCACTGCTTCAAGG	720						
Db	803	AATTTGGCGCTGTTTGGGATGAACAACTCGAAATCTGGGGTCTTCACTGCTTCAAGG	862						
Qy	721	GCGTCCAGAAATTCAGCAGGATCCATCTGTGGACAAATGGAACGAGTCTCAGCAAGATCG	780						
Db	863	GCGTCCAGAAATTCAGCAGGATCCATCTGTGGACAAATGGAACGAGTCTCAGCAAGATCG	922						
Qy	781	ATTATTGGCATTTACAGCAGTGTAAACATGATCAATGGGACTTTCGGGCGAGATGTGGGCAC	840						

RESULT 6
BC004656
LOCUS
DEFINITION
MGC:5988 IMAGE:3498018, complete cds.
ACCESSION

BC004656 2512 bp mRNA linear ROD 09-JUL-2005
Mus musculus scavenger receptor class B, member 1, mRNA (cDNA clone
MGC:5988 IMAGE:3498018), complete cds.
BC004656

Db	923	ATTATTGGCATTCAGACAGTGTAAATCATGATCAATGGGACTTCCGGGCGAGATGTGGGCAC	982
Qy	841	CCTTCATGACACCCGAATCCTCGCTGGAATTTCTCAGCCCGGAGGATCAGGCTCCATGA	900
Db	983	CCTTCATGACACCCGAATCCTCGCTGGAATTTCTCAGCCCGGAGGATCAGGCTCCATGA	1042
Qy	901	AGCTGACCTTACACGAATCAAGGGTGTGTTGAAGGCATTTCCAGCTATCGCTTTCACGGCCC	960
Db	1043	AGCTGACCTTACACGAATCAAGGGTGTGTTGAAGGCATTTCCAGCTATCGCTTTCACGGCCC	1102
Qy	961	CGATATCTCTGTTTGGCAACGGGTCCGTCTACCCACCCAAAGGCTTCTGCCCATGCC	1020
Db	1103	CGATATCTCTGTTTGGCAACGGGTCCGTCTACCCACCCAAAGGCTTCTGCCCATGCC	1162
Qy	1021	GAGAGTCTGSCATTCAGAAATGTCAGACCTGACAGTGTGTCGCGCTCTGTTTCTCTCCC	1080
Db	1163	GAGAGTCTGSCATTCAGAAATGTCAGACCTGACAGTGTGTCGCGCTCTGTTTCTCTCCC	1222
Qy	1081	ACCCCACTTTTACAAACGGCGACCCCTGTGTGTGTCAGAAAGCTGTTTGTGTCTGAACCTTA	1140
Db	1223	ACCCCACTTTTACAAACGGCGACCCCTGTGTGTGTCAGAAAGCTGTTTGTGTCTGAACCTTA	1282
Qy	1141	ACCCAAAGGAGCATTCCTTGTTCCTTAGACATCCATCCGGTCACTGGGATCCCATGAAT	1200
Db	1283	ACCCAAAGGAGCATTCCTTGTTCCTTAGACATCCATCCGGTCACTGGGATCCCATGAAT	1342
Qy	1201	GTTCCTGTAAGATGTCAGCTGAGCCTCTACATCAAAATCTGTCAAGGCGATCGGCAACAG	1260
Db	1343	GTTCCTGTAAGATGTCAGCTGAGCCTCTACATCAAAATCTGTCAAGGCGATCGGCAACAG	1402
Qy	1261	GGAAGATCGAGCCAGTAGTTCCTGCGTGTGTCGAAACAGAGCGGAGCAATGGGTG	1320
Db	1403	GGAAGATCGAGCCAGTAGTTCCTGCGTGTGTCGAAACAGAGCGGAGCAATGGGTG	1462
Qy	1321	GCAAGCCCTTGAGACAGTTCCTACACAGCTGGTGTGATGTCGCCCAGGTTCTTCACTAGC	1380
Db	1463	GCAAGCCCTTGAGACAGTTCCTACACAGCTGGTGTGATGTCGCCCAGGTTCTTCACTAGC	1522
Qy	1381	CGCAGTATGTCGTGCGGGCTTGGAGGCTCTGTCGTGTCGTCATCATCTGCCAAC	1440
Db	1523	CGCAGTATGTCGTGCGGGCTTGGAGGCTCTGTCGTGTCGTCATCATCTGCCAAC	1582
Qy	1441	TGCGCAGCAGGAGAAATGCTTTTCTTGGAGTGTGTAGTAAAGGGCTCCAGGATA	1500
Db	1583	TGCGCAGCAGGAGAAATGCTTTTCTTGGAGTGTGTAGTAAAGGGCTCCAGGATA	1642
Qy	1501	AGGAGGCCATTCAGGCTTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGCGACGGTGC	1560
Db	1643	AGGAGGCCATTCAGGCTTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGCGACGGTGC	1702
Qy	1561	TGCAAGAGCCAGCTATAGGGTCTGGAAGACACTATAAGCCCCCAAACTCTGATAGCTT	1620
Db	1703	TGCAAGAGCCAGCTATAGGGTCTGGAAGACACTATAAGCCCCCAAACTCTGATAGCTT	1762
Qy	1621	GGTCAGACCCAGCCACCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC	1680
Db	1763	GGTCAGACCCAGCCACCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC	1822
Qy	1681	CCACCATGTCATGGCTGAGCCCCCAGATGTCAACCTGTTCGCGACGCAAGGCATAGG	1740
Db	1823	CCACCATGTCATGGCTGAGCCCCCAGATGTCAACCTGTTCGCGACGCAAGGCATAGG	1882
Qy	1741	ATGCCACCGCTGTGCAAAACAACTCAGGACCGGACAGGACAGACC	1785
Db	1883	ATGCCACCGCTGTGCAAAACAACTCAGGACCGGACAGGACAGACC	1927

QY 721 GCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAACGAGTCTCAGCAAGATCG 780
DB |||||
QY 863 GCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAACGAGTCTCAGCAAGATCG 922
DB |||||
QY 781 ATTATTGGCAATTCAGACAGTGTAAATGATCAATGGAGTCTCCGGGCAGATGTGGGCAC 840
DB |||||
QY 923 ATTATTGGCAATTCAGACAGTGTAAATGATCAATGGAGTCTCCGGGCAGATGTGGGCAC 982
DB |||||
QY 841 CTTTCATGACACCGGAATCTCGTGGAAATTTTCAGCCCGGAGGATGATGAGTTCATGTA 900
DB |||||
QY 983 CTTTCATGACACCGGAATCTCGTGGAAATTTTCAGCCCGGAGGATGATGAGTTCATGTA 1042
DB |||||
QY 901 AGCTGACCTTCAACGAATCAAGGCTGTTTGAAGCATTTCCACGATTCGCTTCCACGGCCC 960
DB |||||
QY 1043 AGCTGACCTTCAACGAATCAAGGCTGTTTGAAGCATTTCCACGATTCGCTTCCACGGCCC 1102
DB |||||
QY 961 CCGATACCTGTTTGGCAACGGGTCCGCTTACCCACCAACGAAGGCTTCTGGCCCATGCC 1020
DB |||||
QY 1103 CCGATACCTGTTTGGCAACGGGTCCGCTTACCCACCAACGAAGGCTTCTGGCCCATGCC 1162
DB |||||
QY 1021 GAGAGTCTGGCAATTCAGATGTCAGACCTGTCAGGTTTGTGGCCCTCTGTTTCTCTCCC 1080
DB |||||
QY 1163 GAGAGTCTGGCAATTCAGATGTCAGACCTGTCAGGTTTGTGGCCCTCTGTTTCTCTCCC 1222
DB |||||
QY 1081 ACCCCCACTTTTACACCGCGACCTCTGTTTGTTCAGAAAGTCTGTTTGTCTGAACCCCTA 1140
DB |||||
QY 1223 ACCCCCACTTTTACACCGCGACCTCTGTTTGTTCAGAAAGTCTGTTTGTCTGAACCCCTA 1282
DB |||||
QY 1141 ACCCAAGGAGCAATCTCTGTTTCTAGACATCCATCCGGTCACTGGGATCCCATGAACCT 1200
DB |||||
QY 1283 ACCCAAGGAGCAATCTCTGTTTCTAGACATCCATCCGGTCACTGGGATCCCATGAACCT 1342
DB |||||
QY 1201 GTTCTGTGAAGATGACATGAGCTCTGAGCTCTACATCAATCTGTCAAGGGATCGGGCAACAG 1260
DB |||||
QY 1343 GTTCTGTGAAGATGACATGAGCTCTGAGCTCTACATCAATCTGTCAAGGGATCGGGCAACAG 1402
DB |||||
QY 1261 GGAAGATCGAGCAGTAGTCTGCGCTGCTGTGTTTTCGAACAGAGCGGAGCAATGGGTG 1320
DB |||||
QY 1403 GGAAGATCGAGCAGTAGTCTGCGCTGCTGTGTTTTCGAACAGAGCGGAGCAATGGGTG 1462
DB |||||
QY 1321 GCAAGCCCTTGAGACGCTTCTACACGAGCTGTGTGCTGATGCCCGGCTTCTTCACTACG 1380
DB |||||
QY 1463 GCAAGCCCTTGAGACGCTTCTACACGAGCTGTGTGCTGATGCCCGGCTTCTTCACTACG 1522
DB |||||
QY 1381 GCGAGTATGTCTGCTGGGCTTGGAGGCTCTCTGTTGCTGTGTGCCCATCATCTGCCAAC 1440
DB |||||
QY 1523 GCGAGTATGTCTGCTGGGCTTGGAGGCTCTCTGTTGCTGTGTGCCCATCATCTGCCAAC 1582
DB |||||
QY 1441 TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTGTAAAGGGCTCCAGGATA 1500
DB |||||
QY 1583 TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTGTAAAGGGCTCCAGGATA 1642
DB |||||
QY 1501 AGGAGGCCATTCAGGCTTACTCTGAGTCCCTGATGTCAACAGCTGCCCAAGGGCAGCGTGC 1560
DB |||||
QY 1643 AGGAGGCCATTCAGGCTTACTCTGAGTCCCTGATGTCAACAGCTGCCCAAGGGCAGCGTGC 1702
DB |||||
QY 1561 TGCAGAGCCAGGCTATGAGGCTCTGAAGACACTATAAGCCGCCCAAACTGATAGCTT 1620
DB |||||
QY 1703 TGCAAGAGCCAGGCTATGAGGCTCTGAAGACACTATAAGCCGCCCAAACTGATAGCTT 1762
DB |||||
QY 1621 GGTTCAGACAGCCAGCCAGTCCCTPACACCCGCTTCTTTGAGGACTCTCTCAGCGGACAGC 1680
DB |||||
QY 1763 GGTTCAGACAGCCAGCCAGTCCCTPACACCCGCTTCTTTGAGGACTCTCTCAGCGGACAGC 1822
DB |||||
QY 1681 CCACAGTGCATGCGCTGAGCCGCCAGATGTCAACCTGTGCCGACGACGACATGAG 1740
DB |||||
QY 1823 CCACAGTGCATGCGCTGAGCCGCCAGATGTCAACCTGTGCCGACGACGACATGAG 1882
DB |||||
QY 1741 ATGCCACGATGTGCAAAAACAACTCAGGGACAGGGACAGACC 1785
DB |||||
QY 1883 ATGCCACGATGTGCAAAAACAACTCAGGGACAGGGACAGACC 1927
DB |||||

RESULT 7
AX419948
LOCUS AX419948 1607 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 285 from Patent WO0198537.
ACCESSION AX419948
VERSION AX419948.1 GI:21524315
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Lyamichev, V., Allawi, H., Dong, F., Neri, B. P. and Vener, I. T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 285 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
1..1607
/organism="Mus musculus"
/mol_type="unassigned RNA"
/db_xref="taxon:10090"
ORIGIN
Query Match 90.0%; Score 1607; DB 6; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 GCTCAAGAATGTCCGCATAGACCCGAGCAGCCTGCTCTTCGGGATGTGGAAGGAGATCCC 229
DB 1 GCTCAAGAATGTCCGCATAGACCCGAGCAGCCTGCTCTTCGGGATGTGGAAGGAGATCCC 60
QY 230 GGTCCCTTTCTACTTGTCTGTCTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCCTCAA 289
DB 61 GGTCCCTTTCTACTTGTCTGTCTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCCTCAA 120
QY 290 CGGCCAAGAACCCAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTCAGACAAA 349
DB 121 CGGCCAAGAACCCAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTCAGACAAA 180
QY 350 GGTCAACATCACCTTCAATGACAAACGACACCGTGTCTTCGTGGAGAACCGCAGCTCCA 409
DB 181 GGTCAACATCACCTTCAATGACAAACGACACCGTGTCTTCGTGGAGAACCGCAGCTCCA 240
QY 410 TTTTCCAGCTGTCAAGTCCGATGGCTCAGAGAGTGTACTTGTATGTACTGCTTAACATCTT 469
DB 241 TTTTCCAGCTGTCAAGTCCGATGGCTCAGAGAGTGTACTTGTATGTACTGCTTAACATCTT 300
QY 470 GGTCTCGGGGGCTCCATATGATGGAGCAAGCCCTGTGAGCTCAAGCTGATGATGAC 529
DB 301 GGTCTCGGGGGCTCCATATGATGGAGCAAGCCCTGTGAGCTCAAGCTGATGATGAC 360
QY 530 CTTGGCGCTGGTCAACATGGCGCAGCGTGTCTTTATGAACCGCACAGTTCGTGAGATCTT 589
DB 361 CTTGGCGCTGGTCAACATGGCGCAGCGTGTCTTTATGAACCGCACAGTTCGTGAGATCTT 420
QY 590 GTGGGCTATGAGCATTCCTTGTGCAATTTCTCAAACAGTACCTCCCGAGATGCTTCC 649
DB 421 GTGGGCTATGAGCATTCCTTGTGCAATTTCTCAAACAGTACCTCCCGAGATGCTTCC 480
QY 650 CATAAAGGGCAATTTGGGCTGTTTGTGGATGAACTCGAATTCCTGGGCTCTTCC 709
DB 481 CATAAAGGGCAATTTGGGCTGTTTGTGGATGAACTCGAATTCCTGGGCTCTTCC 540
QY 710 TGTCTTTCAGGGCGTCCAGAAATTTTCAGCAGGATTCATCTGGTGGACAAATGGAACGAGCT 769
DB 541 TGTCTTTCAGGGCGTCCAGAAATTTTCAGCAGGATTCATCTGGTGGACAAATGGAACGAGCT 600
QY 770 CAGCAAGATCGATTATTGGCAATTTTCAGCAGGATGTAACATGATGATGGGACTTCCGGGCA 829
DB 601 CAGCAAGATCGATTATTGGCAATTTTCAGCAGGATGTAACATGATGATGGGACTTCCGGGCA 660

ORIGIN

Query Match 85.7%; Score 1530; DB 9; Length 1530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 ATGGGCGGAGCTCCAGGGGCGCTGGGTGGCTTGGGGTGGGGCGCCCTGGGGCTGCTG 110
DB 1 ATGGGCGGAGCTCCAGGGGCGCTGGGTGGCTTGGGGTGGGGCGCCCTGGGGCTGCTG 60

QY 111 TTGTCTCGCTGGCGTGTGATGATCTCATGTGTGCTTCCCTCATCAAGAGAGAGTG 170
DB 61 TTGTCTCGCTGGCGTGTGATGATCTCATGTGTGCTTCCCTCATCAAGAGAGAGTG 120

QY 171 CTCAGGAATGTCCGATAGACCCGAGAGAGCTGTCTTCCGGATGTGGAGGAGATCCCC 230
DB 121 CTCAGGAATGTCCGATAGACCCGAGAGAGCTGTCTTCCGGATGTGGAGGAGATCCCC 180

QY 231 GTCCCTTTCTACTTGTCTACTTCTTCCGAAGTGTCAACCAACGAGGTCTCTCAAC 290
DB 181 GTCCCTTTCTACTTGTCTACTTCTTCCGAAGTGTCAACCAACGAGGTCTCTCAAC 240

QY 291 GGCAGAGCCAGTAGTCCGGAGCGTGAACCTATGTCTACAGGAGTTCAGACAAAG 350
DB 241 GGCAGAGCCAGTAGTCCGGAGCGTGAACCTATGTCTACAGGAGTTCAGACAAAG 300

QY 351 GTCAACATACCTTCAATGACACGACACGCTGTCTTCCGTGGAGAACCGAGCTCCAT 410
DB 301 GTCAACATACCTTCAATGACACGACACGCTGTCTTCCGTGGAGAACCGAGCTCCAT 360

QY 411 TTCAGAGCTGACAGTCCGAGTGTCTCAGAGAGTGAATCACTTGTCTTCCCTTAACATCTTG 470
DB 361 TTCAGAGCTGACAGTCCGAGTGTCTCAGAGAGTGAATCACTTGTCTTCCCTTAACATCTTG 420

QY 471 GTCTCGGGGGCTCGATATTGATGAGAGCAAGCTGTGAGCTGAACTGATGATGAC 530
DB 421 GTCTCGGGGGCTCGATATTGATGAGAGCAAGCTGTGAGCTGAACTGATGATGAC 480

QY 531 TTGGCGCTGTGTCACATGGGCGAGCGTCTTTATGAACCGCAGTTGGTGAGATCCCTG 590
DB 481 TTGGCGCTGTGTCACATGGGCGAGCGTCTTTATGAACCGCAGTTGGTGAGATCCCTG 540

QY 591 TGGGGCTATGACGATCCCTTCTGTCATTTCTCAACACGATGATCTCCAGACATGCTTCCC 650
DB 541 TGGGGCTATGACGATCCCTTCTGTCATTTCTCAACACGATGATCTCCAGACATGCTTCCC 600

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DB 601 ATAAAGGGGCAATTTGGCGCTTTGGTGGAGTGAACCACTCGAATTTCTGGGGTCTTCACT 660

QY 711 GTCTTACGGGGCTCCAGAAATTTACAGAGATCCATCTGTGGACAAATGGAACGGAATC 770
DB 661 GTCTTACGGGGCTCCAGAAATTTACAGAGATCCATCTGTGGACAAATGGAACGGAATC 720

QY 771 AGCAAGATCGAATATTGGCAATTCAGAGCAGTGTAACTGATCAATGGGAATTCGGGCGAG 830
DB 721 AGCAAGATCGAATATTGGCAATTCAGAGCAGTGTAACTGATCAATGGGAATTCGGGCGAG 780

QY 831 ATGTGGGCACTTCATGACACCGAATTCCTGGTGGAAATTTTCAGCCCGGAGGATGC 890
DB 781 ATGTGGGCACTTCATGACACCGAATTCCTGGTGGAAATTTTCAGCCCGGAGGATGC 840

QY 891 AGGTCCATGAGCTGACCTACAGATCAAGGTGTTTCAAGCAATTCACGATATCCG 950
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QY 951 TTCAGGCCCCCGATCTCTGTTTGGCAACGGGTCTCTACCCACCAACGAGGCTTC 1010
DB 901 TTCAGGCCCCCGATCTCTGTTTGGCAACGGGTCTCTACCCACCAACGAGGCTTC 960

QY 1011 TGCCCATGCGAGAGTCTGGCAATTCAGAAATGTGACACCTGAGGTTTGGTGGCGCTCTG 1070
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QY 1131 CTGAACCCCTAAACCCAAAGAGCAATTCCTTGTCTTAGACATCATCCCGTCACTGGGATC 1190
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QY 1251 GGGCAAAACAGGGAAGATCGAGCCAGTAGTCTTGCCTGTCTGTGGTTCGAAACAGAGCGGA 1310
DB 1201 GGGCAAAACAGGGAAGATCGAGCCAGTAGTCTTGCCTGTCTGTGGTTCGAAACAGAGCGGA 1260

QY 1311 GCATGGGTGGCAAGCCCTGAGCACCTTCTACACGACGTGTGTGTGATGCCCCAGGTT 1370
DB 1261 GCATGGGTGGCAAGCCCTGAGCACCTTCTACACGACGTGTGTGTGATGCCCCAGGTT 1320

QY 1371 CTTCACTAGCGCAGTATGTCTGTGGGCTTGGAGGCTCTGTGTGTGTCGCCATC 1430
DB 1321 CTTCACTAGCGCAGTATGTCTGTGGGCTTGGAGGCTCTGTGTGTGTCGCCATC 1380

QY 1431 ATCTGCAACTGCGCAGCGAGGAGAAATGCTTTTCTTGGAGTGTGTAGTAAAAAGGGC 1490
DB 1381 ATCTGCAACTGCGCAGCGAGGAGAAATGCTTTTCTTGGAGTGTGTAGTAAAAAGGGC 1440

QY 1491 TCCAGGATAAGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAG 1550
DB 1441 TCCAGGATAAGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAG 1500

QY 1551 GGCACGGTCTGCAAGAGCCCAAGCTATAG 1580
DB 1501 GGCACGGTCTGCAAGAGCCCAAGCTATAG 1530

RESULT 9
D89655 LOCUS
DEFINITION Rattus norvegicus mRNA for scavenger receptor class B, complete cds.
ACCESSION D89655
VERSION D89655.1 GI:1752796
KEYWORDS scavenger receptor Class B.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 Miyamoto, K., Mizutani, T. and Numata, Y.
AUTHORS cdNA cloning of rat scavenger receptor class B
TITLE Unpublished
JOURNAL 2 (bases 1 to 2392)
REFERENCE 2 Miyamoto, K.
AUTHORS Direct Submission
TITLE Submitted (03-DEC-1996) Kaoru Miyamoto, Institute for molecular and cellular regulation, Gunma Univ., Biosignal research center; Showa-machi, 3-39-15, Maebashi, Gunma, 371, Japan
JOURNAL [E-mail: kmiyamot@fmsr.sak.fukui-med.ac.jp, Tel: 81-272-20-8878, Fax: 81-272-20-8878]
FEATURES
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/strain="Wistar"
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Matches 1562; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY	61	GCTCCAGGCGCGCTGGGTGGCTTGGGGTTGGGCGCCCTGGGGCTCTGTTTGTCTGCGC	120
DB	131	GCTCCAGGCGCACGTGGGTGGCTTGGGGCTGGGCGTCTCTAGGGCTGCTGTGTCTGCGC	190
QY	121	TCGGCGTTGTCATGCTCTCATGGTGGCTCCCTCATCAAGCAGCAGGTCTCAAGATG	180
DB	191	TCGGCGTTATCATGATCTCATGGTGGCTCCCTCATCAAGCAGCAGGTCTCAAGATG	250
QY	181	TCGGCATAGACCCGAGCAGCTGTCTCTCGGGATGTGGAAGAGATCCCGCTCCCTTTCT	240
DB	251	TCGGCATAGACCCGAGCAGCTGTCTCTCGGGATGTGGAAGAGATCCCTGTCTCTCTCT	310
QY	241	ACTTGTCTGTACTTCTTCCAGAGTGTCTAAACCCAAACGAGTCTCTCAACGGCGAAGC	300
DB	311	ACTTGTCTGTACTTCTTCCAGAGTGTCTAAACCCCGAGGAGTCTTAAATGGCGCAGAAGC	370
QY	301	CAGTGTCCGGGAGCGTGGACCTTGTCTACAGGAGTTCAGACAAAGGTCAACATCA	360
DB	371	CAGTGTCCGGGAGCGGAGCCCTTGTCTACAGGAGTTCAGACAAAGGTCAACATCA	430
QY	361	CTTTCATAGCAACAGCACCGTGTCTCTCGTGAGAACCCGAGCTCTCAATTCAGCGCTG	420
DB	431	CTTTCATAGCAATGACACCGTGTCTCTACATAGAACCCGAGCTCTCGTTCAGGCCAG	490
QY	421	ACAAGTCGATGGCTCAGAGAGTGACTACATGTGCTGCTTAAACATCTTGGTCTGGGG	480
DB	491	ACAGGTCCCAGGGCTCAGAGAGTGACTACATGTGCTGCTTAAACATCTTGGTCTGGGAG	550
QY	481	GCTCGATATGATGGAGAGCAGCTGTGAGCTGTGAGCTGTGATGATGACCTTGGCGTGG	540
DB	551	GGGCGAGTATGATGGAGGACAAGCCCAAGCCTGTAAGCTGCTAAGTACCTTGGGGTTGG	610
QY	541	TCACCATGGGCGAGCGTCTTTTATGAACCGCACAGTTGTGTGAGATCCTGTGGGCTATG	600
DB	611	TCACCATGGGCGAGCGGCTTTTATGAACCGCACAGTTGTGTGAGATCCTGTGGGCTATG	670
QY	601	ACGATCCCTTCGTGCAATTTCTCAACAGTACCTTCCAGACATGCTTCCCAATAAGGGCA	660
DB	671	AAGATCCCTTGTGAATTTCTCTCAGCAAAATTTTCCAGACATGTTTCCCATCAAGGCA	730
QY	661	AATTTGGCTTGTGTGGATGAACAACTCGAATCTTGGGGTCTTCACTGTCTTCACGG	720
DB	731	AATTTGGCTTGTGTGGATGAACAACTCGAATCTTGGGGTCTTCACTGTCTTCACGG	790
QY	721	CGGTCCAGAAATTTTCAGCAGGATCCTCTGTGTGACAAATGCAACGAGTCTCAGCAAGATCG	780
DB	791	GTGTCCAGAAATTTTCAGCAGGATCCTCTGTGTGATAGTGAACGCGCTCAGCGAGTCA	850
QY	781	ATTATTGGCATTCAGAGCAGTGTAAACATGATCAATGAGGACTTCCGGGCGAGATGTGGGCA	840

RESULT 10

BC076504

LOCUS

DEFINITION

Rattus norvegicus

clone MGC:91637

INRAGE:7099863

complete cds.

ACCESSION

BC076504

VERSION

BC076504.1

GI:49904284

KEYWORDS

SOURCE

BC076504 2408 bp mRNA linear ROD 07-JUL-2004
Rattus norvegicus scavenger receptor class B, member 1, mRNA (cdna
clone MGC:91637 INRAGE:7099863), complete cds.

BC076504

BC076504.1

GI:49904284

KEYWORDS

SOURCE

Rattus norvegicus (Norway rat)

Db	851	ACTATTGGCATTCGGAACAGTGCACCATGATCAATGGTACTGCGGGCAGATGTGGCAC	910
QY	841	CTTTCTATGACACCCGGAATCTCTGCTGAAATTTCTTACGCGCGGAGGATGACAGGTCCATGA	900
Db	911	CATTATGACACCCGGAATCTCTGCTGAAATTTCTTACGCGCGGAGGATGACAGGTCCATGA	970
QY	901	AGTGTACCTAACACGAATCAAGGGTGTGTTGAAGGCAATCCACGATTCGCTTTCACGCGCC	960
Db	971	AGTGTACCTAACACGAATCAAGGGTGTGTTGAAGGCAATCCACGATTCGCTTTCACGCGCC	1030
QY	961	CGGATACTCTGTTTGCACAGGGTCTGCTTACCCACCCACGAAGGCTTCTGCGCATGCC	1020
Db	1031	CGGATACTCTGTTTGCACAGGGTCTGCTTACCCACCCACGAAGGCTTCTGCGCATGCC	1090
QY	1021	GAGAGTCTGGCATTGAGAATGTGACACCTGACAGCTTGGTGGCTCTGCTTCTCTCTCC	1080
Db	1091	GCGAGTCTGGCATTGAGAATGTGACACCTGACAGCTTGGTGGCTCTGCTTCTCTCTCC	1150
QY	1081	ACCCCACTTTTACAAACGCGGACCTCTGTGTGTGTCAGAAAGCTTTCTTGGTCTGAAACCTTA	1140
Db	1151	AGCCCACTTTTACAAATGCTGACCCCGTGTGTGTCAGAAAGCTTTCTTGGTCTGAAACCTTA	1210
QY	1141	ACCCCAAGGAGCATTCCTTGTCTTAGACATTCATCCGGTCACTGGGATCCCATGAACCT	1200
Db	1211	ACCCCAAGGAGCATTCCTTGTCTTAGACATTCATCCGGTCACTGGGATCCCATGAACCT	1270
QY	1201	GTTCGTGTGAAGTGCAGCTGAGCTCTACATCAAAATCTGTCAAGGGCATCGGCAACAG	1260
Db	1271	GTTCGTGTGAAGTGCAGCTGAGCTCTACATCAAAATCTGTCAAGGGCATCGGCAACAG	1330
QY	1261	GGAAGATCGAGCCAGTAGTCTTGGCGCTTGGAGGCTCTGCTGTGTTGCAACAGAGCGGAGT	1320
Db	1331	GGAAGATCGAGCCAGTAGTCTTGGCGCTTGGAGGCTCTGCTGTGTTGCAACAGAGCGGAGT	1390
QY	1321	GMAGCCCTTGAGCAGCTTCTACACGAGTGTGTGTGATGCCCCAGGTTCTTCACTACG	1380
Db	1391	GCAAGACCCCTGAAACAGCTTCTACACGAGTGTGTGTGATGCCCCAGGTTCTTCACTACG	1450
QY	1381	CGCAGTATGTGTCTGGGCTTGGAGGCTCTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1440
Db	1451	CGCAGTATGTGTCTGGGCTTGGAGGCTCTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTG	1510
QY	1441	TGCGAGCCAGGAGAAATGCTTTTCTTTTGGAGTGTGTGTTGTTGTTGTTGTTGTTGTTGTTG	1500
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QY	1501	AGAGGCCAATTCAGGCTTCTCTGAGTCTCTGATGTCAACAGTGTGCAAGGGCAAGGTGC	1560
Db	1571	AGAGGCCAATTCAGGCTTCTCTGAGTCTCTGATGTCAACAGTGTGCAAGGGCAAGGTGC	1630
QY	1561	TGCAAGAAGCCAGCTATAGGGTCTTGAAGACATATAGCCCCCCCCCAAACTGATAGCTT	1620
Db	1631	TGCAAGAAGCCAGCTATAGGGTCTTGAAGACATATAGCCCCCCCCCAAACTGATAGCTT	1690
QY	1621	GCTCAGACCCAGCCAGCTCTTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC	1680
Db	1691	GCTCAGACCCAGCCAGCTCTTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC	1750
QY	1681	CCACCAAGTCCATGGCTTGAAGCCCCCAGATGTCAACCTGTGCGCACGAC	1731
Db	1751	CCGCGAGTGCACAGTCTCTGAGCCCCCAGATGTCAACCTGTGCGCACGAC	1801

Db	722	ATTTGGCCTGTTCTGTTGGGATGAACGACTCGAGTTCTGGCGTCTTTCACCGTCTTTCACG	781
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Db	782	GTGTCCAGAAATTTTCAGCAAGATCCATCTGTGTGGATAGTGGAAACGGCTCAGCGAGGTCA	841
Qy	781	ATTTATGGCATTTCAGACAGTGTAAACATGATCAATGGACATTCGCGGACAGATGTGGGCAC	840
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Qy	841	CTTTCATGACACCCGGAATCTCTCGCTGGAAATTTCTTCAGCCCGGAGGACATGCAGGTCCATGA	900
Db	902	CATTTCATGACACCCGAATCTCTCACTGGAAATTTCTTCAGCCCAAGAGCCTGCGAGATCTATGA	961
Qy	901	AGCTGACCTTACAACGAATCAAGGGTGTTTGAAGGCATTTCCACAGTATCGCTTTCACGGCCCC	960
Db	962	AGCTCACCTTACAGGAATCAAGGGTGTTCGAAGGCATCCCCACATTATCGCTTTCACGGCCCC	1021
Qy	961	CCGATACTCTGTTTGGCCAAACGGGTCCGTCTACCCACCCAGCAAGGCTTCTGCCCCATGCC	1020
Db	1022	CCGATACTTGTGTTTGGCAACGGGTCCGTCTACCCACCTAATGAAGGCTTCTGCCCCGTGCC	1081
Qy	1021	GAGAGTCTGGCATTTCAGAAATGTCAAGCACTGACAGCTTGGTGCGCCCTCTGTTCTCTCCCC	1080
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Qy	1081	ACCCCCACTTTTACAACCGCCGACCTCTGTGTTGTCAGAAAGCTGTTTCTTGGTCTGAACCCCTA	1140
Db	1142	AGCCCCACTTCTACAATGCTGACCCCGTGCTGTACAGAAAGCTGTTCTTGGTCTGAACCCCTG	1201
Qy	1141	ACCCAAAGGAGCAATCTCTTGTGTTCTAGACATCCATCCGGTCACTGGGATGCCCATGAACT	1200
Db	1202	ACCCAAAGGAGCAATCTCTGTTCTTAGACATCCACCGGTCACTGGGATGCCCATGAACT	1261
Qy	1201	GTTCGTGGAAGATGCAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATCGGGCAACAG	1260
Db	1262	GTTCGTGGAAGATGCAGCTGAGTCTGTACATCAAAATCCGTCAAGGGGTCTGGGCAACAG	1321
Qy	1261	GGAAATTCGAGCCAGTAGTTCTGCCGTTGTGCTGTTTCGAAACAGAGCGGAGCAATGGGGTG	1320
Db	1322	GGAAATTCGAGCCAGTAGTCTGCCATTGCTGTGTTTCGAAACAGAGCGGAGTATGGGGTG	1381
Qy	1321	GCAAAGCCCTGAGCAGCTTCTACAGCAGCTGTGTGTGATGCCGCCAGGTTCTTCACTACG	1380
Db	1382	GCAAAGCCCTGAACACGCTTCTACAGCAGCTGTGTGTGATGCCGCCAGGTTCTTCACTACG	1441
Qy	1381	CGCAGTATGTCTGCTGGGGCTTCGGAGCCCTCCGTGCTGCTGGTCCCATCATCTGCCAAC	1440
Db	1442	CGCAGTATGTCTGCTGGGGCTTCGGAGCCCTCTGCTTCTGTGTGCCCATCATTTACCAAC	1501
Qy	1441	TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGGTAGTAAAGGGGCTCCCAGGATA	1500
Db	1502	TGCGCAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGGGGCTCCCAGGATA	1561
Qy	1501	AGAGGGCAATTCAGGCCCTACTCTGAGTCCCTGATGTCAACAGCTGTCCCAAGGGCAACGGTGC	1560
Db	1562	AGGAGGGCAATTCAGGCCCTACTCTGAGTCTCTGATGTCAACAGCTGTCCCAAGGGCAACGGTGC	1621
Qy	1561	TGCAAGAAGCAACGCTATAGGGTCTCGAAGACACTATAAGCCCCCCCCAACTGATAGCTT	1620
Db	1622	TGCNAGAACCAAGCTGTAGGGGCCAGAGACACCAAGCCCCCCCCAACTGATAGCTT	1681
Qy	1621	GGTCAGACCAAGCCACCCAGTCCCTACACCCCGCTTCTTGGAGGACTCTCTCAGCGGACAGC	1680
Db	1682	GGTCAGACCAAGCCAGTCCCTACACCCCGCTTCTCAGGAGTCTCTCTCAGCGGACAC	1741
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RESULT 11

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of the plasma membrane"
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ORIGIN

Query Match 81.4%; Score 1452.6; DB 9; Length 2401;
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58 CCGTCCCTTCAGGTCTCTGAGCCCGAGAGCTCTCGCGCGCGACGCGACATGGCGTCA 117
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118 GCTCCAGGCGACGCTGGGTGGCTTGGGGTTGGGGTTCTAGGGCTGCTGTTCTGGCG 177
121 TCGCGGTTGTCATGATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG 180
178 TCGCGGTTATCATGATCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG 237
181 TCCGCATAGACCCGAGCAGCTGCTCTTGGGGATGTGGAAGGAGATCCCGTCTCTTCT 240
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418 CTTTCAATGACACGACGACCTGCTCTTGGGGATGTGGAAGGAGATCCCGTCTCTTCT 477
421 ACAAGTCCGATGGCTCAGAGAGTGAATACATGTGCTGCTTAAACATCTTGTCTCTGGGG 480
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661 AATTGGCTGTTGTTGGGATGAACATCTCGAATTTCTGGGGTCTTCACTGTCTTCAAG 720

RESULT 13
RNU76205

LOCUS RNU76205 1674 bp mRNA linear ROD 21-JUL-2000
DEFINITION Rattus norvegicus scavenger receptor class B type I mRNA, complete cds.
ACCESSION U76205
VERSION U76205.1 GI:1679691
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1674)
AUTHORS Johnson, M.S., Svensson, P.A., Helou, K., Billig, H., Levan, G., Carlsson, L.M. and Carlsson, B.
TITLE Characterization and chromosomal localization of rat scavenger receptor class B type I, a high density lipoprotein receptor with a putative leucine zipper domain and peroxisomal targeting sequence
JOURNAL Endocrinology 139 (1), 72-80 (1998)
PUBMED 9421400
REFERENCE 2 (bases 1 to 1674)
AUTHORS Johnson, S.C.M., Svensson, P.A. and Carlsson, B.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1996) Research Center for Endocrinology & Metabolism (RCM), Endocrinology division, Inst. of Internal Medicine, Sahlgrenska University Hospital, Bruna Straaket 16, Goteborg 413 45, Sweden
FEATURES
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ORIGIN
Query Match 79.9%; Score 1426; DB 9; Length 1674;
Best Local Similarity 90.7%; Pred. No. 2.6e-301;
Matches 1519; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
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DB 1 GTCTCCTTCAGTTCCTGAGCCCGACGAGACTCTCGCGCGCGCAGCGGACATGGCGGT CAGC 60
QY 63 TCCAGGGCGCGCTGGGTGGCCCTTGGGGTTGGGGCCCTCGGGCTGTCTGTTGTCTGCGCTC 122
DB 61 TCCAGGGCAGCGCTGGGTGGCCCTTGGGGCTGGCGCTTCTAGGGCTGCTGTGCTGCGCTC 120
QY 123 GGCCTTTCATGATCCTCATGGTGCCTTCCCTCATCAAGCAGCAGGCTGCTCAAGAAATGTC 182
DB 121 GGCCTTTCATGATCCTCATGGTGCCTTCCCTCATCAAGCAGCAGGCTGCTCAAGAAATGTC 180

183 CGCATAGACCCGAGCAGCCTGCTCTTCGGGATGTGAAGGAGATCCCGCTCCCTTTCTAC 242
181 CGCATAGACCCGAGCAGCCTGCTCTTCGGGATGTGAAGGAGATCCCTGCTTCCTTTCTAC 240
243 TTGTCTGTCTACTTCTTCGAAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAAGCCA 302
241 TTGTCCGTCTACTTCTTCGAGGTGGTCAACCCCGAGCGAGGTCTCTAAATGGCCAGAAAGCCA 300
303 GTAGTCCGGAGCGGTGGAGCCCTATGTCTACAGGGAGTTCAGACAAAGAGGTCAACATCACC 362
301 GTAGTCCGGAGCGCGGAGCCCTATGTCTACAGGGAGTTCAGACAAAGAGGTAAACATCACC 360
363 TTCAATGACAAACACACACCCGTGCTCTTCGTGGAGAACCGCAGCCTCCATTTCCAGCCTGAC 422
361 TTCAATGACAAACACACCGGTGCTCTACATAGAGAACCGAAGCCTTCGTTCCAGCCAGAC 420
423 AAGTCCGATGGCTCAGAGAGTGAATCATGTACTGCTCCCTAAACATCTTGGTCTCTGGGGGGC 482
421 AGGTCCCGAGGCTCAGAGAGTGAATCATGTACTGCTCCCTAAACATCTTGGTCTCTGGAGGG 480
483 TCGATATTGATGAGAGCAAGCCTGTGAGCCTCAAGCTGATGATGACCTTGGCGCTGGTC 542
481 GCAGTGAATGATGAGAGCAAGCCTCAAGCCTGAAGCTGCTAATGACCTTTGGGGTTGGTC 540
543 ACCATGGGCGCAGCGTCTCTTTATGAACCCGACAGTTGGTGAATCCTGTGGGGCTATGAC 602
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601 GATCCCTTTGTGAATTTCTCTCAGCAAAATATTTCCAGACATGTTCCCCCATCAAGGCAAA 660
663 TTTGGCCTGTTTGGGATGACACTCGAATTTCTGGGGTCTTCACTGCTCTTCAGGGC 722
661 TTTGGCCTGTTGTTGGGATGAACGAGTTCTGGCGTCTTTCACCGCTTTCAGAGGT 720
723 GTCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGAAACGGAATCAGCAAGATCGAT 782
721 GTCAGAAATTCAGCAGGATCCATCTGGTGGATGAATGAGGAAACGCGCTCAGCGAGGTCAAC 780
783 TATTGGCATTCAGAGCAGTGTAAACATGATCAATGGGACTTTCGGGGCAGATGTGGGCAACC 842
781 TATTGGCATTCGGAACAGTGTCAACATGATCAATGGTACTTCCCGGCGAGATGTGGGCAACC 840
843 TTCATGACACCCGAATCTCGCTGGTGAATTTCTTCAGCCCGCGAGGCGATGCGATCCATGAAG 902
841 TTCATGACACCCGAATCTCGCTGGTGAATTTCTTCAGCCCGCGAGGCGATGCGATCCATGAAG 900
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Db 1550 CAGCCAGGAGAAATGCTTTTATTTTGGAGTGGTAGTAAAGGGCTCGCAGGATAAGGA 1609
Qy 1505 GGCCATTGAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCCCAGGGCACGGTGTGCA 1564
Db 1610 GGCCATTGAGGCTACTCTGAGTCTCTGATGTACACAGCTGCCAAGGGCACGGTGTGCA 1669
Qy 1565 AGAAGCCAAAGCTATAGGGTCTGGAAGACACTATAGCCCCCAACCTGATAGCTTGGTC 1624
Db 1670 AGAAGCCAAAGCTATAGGGTCTGGAAGACACTATAGCCCCCAACCTGATAGCTTGGTC 1729
Qy 1625 AGACCAGCCACCCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGCCAC 1684
Db 1730 AGACCAGCCATCCAGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCGC 1789
Qy 1685 CAGTGCCATGGCCTGAGCCCCCAGATGTCACACCTGT 1721
Db 1790 CAGTGCCATGGCCTGAG-CCCCAGATGTCACACCTGT 1825

Search completed: February 23, 2006, 22:46:13
Job time : 9000.94 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:34:57 ; Search time 1077.59 Seconds
(without alignments)
11039.845 Million cell updates/sec

Title: US-08-765-108-7
Perfect score: 1785
Sequence: 1 CCGTCTCTTCAGTCTCTGA.....TCAGGACGAGGACAGACC 1785

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	1785	2	AAX23404
2	1785	100.0	1785	2	AAX23404 Mouse sca
3	1785	100.0	1785	6	Az30616 Mouse sca
4	1785	100.0	1785	6	Abi99330 Mouse isc
5	1785	100.0	1785	12	Adj33917 Murine sc
6	1785	100.0	2496	13	Adj33336 Murine SR
7	1785	100.0	2496	13	Abd33431 Murine ca
8	1785	100.0	2496	13	Adr67032 Mouse can
9	1761	98.7	1785	14	Adz13454 Murine ca
10	1607	90.0	1607	6	Aeb03942 Murine SC
11	1582	88.6	1761	14	Abi46318 Mouse sca
12	1517	85.0	2382	14	Aeb03939 Murine SC
13	1459.4	81.8	2497	10	Adz13452-Murine ca
14	1459.4	81.8	2497	10	Adbs8616 Toxicity-
15	1459.4	81.8	2497	10	Adbs3264 Primary r
16	1459.4	81.8	2497	10	Abt42207 Toxicity
17	1396.2	78.2	1825	9	Adv41414 Rat cardi
18	1396.2	78.2	1825	12	Adc44926 Human cdn
19	1369.8	76.7	1788	2	Adj46120 Human var
					Aat10116 Hamster s

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

ALIGNMENTS

RESULT 1
AAX23404
ID AAX23404 standard; DNA; 1785 BP.
XX
AC AAX23404;
XX
DT 17-JUN-1999 (first entry)
XX
DE Mouse scavenger receptor class B-I DNA.
XX
KW Scavenger receptor class B type I; mouse; steroid production; HDL; cholesterol; cholesteryl ester transport; high-density lipoprotein; lipoprotein; liver; steroidogenic tissue; SR-BI; contraception; treatment; disorder; overproduction; underproduction; menopause; breast cancer; prostate cancer; endometriosis; fibroid tumour; ss.
XX
OS Mus sp.
XX
PN WO9911288-A1.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US018463.
XX
PR 05-SEP-1997; 97US-0057943P.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Krieger M;
XX
DR WPI; 1999-204984/17.
DR P-PSDB; AAW93575.
XX
PT Modification of steroid production in mammals - by administering modulator of SR-BI expression or activity.
XX
PS Disclosure; Page 80-81; 86pp; English.
XX
CC This invention describes a method for modifying steroid production in a mammal which comprises administering a compound that alters cholesterol or cholesteryl ester transport from high-density lipoprotein (HDL) or other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger

20 1369.8 76.7 1788 2 AAX23403
21 1369.8 76.7 1788 2 AAX30615
22 1369.8 76.7 1788 6 AAS33744
23 1369.8 76.7 1788 6 AAD33915
24 1369.8 76.7 1788 12 ADJ33334
25 1316.8 73.8 1788 14 AEB03941
26 1306.8 73.2 1546 14 AEA33429
27 1291 72.3 1531 13 ADS73684
28 1144.2 64.1 2637 14 ADZ13457
29 1144.2 64.1 3116 14 ADZ13463
30 1142.6 64.0 2558 4 ABA09256
31 1142.6 64.0 2630 9 ACD44925
32 1142.6 64.0 2630 12 ADJ46118
33 1141 63.9 2565 2 AAZ32194
34 1141 63.9 2566 3 AAA40750
35 1141 63.9 2566 9 AAL62623
36 1141 63.9 2566 12 ADJ61166
37 1133 63.5 2628 10 ADS40209
38 1133 63.5 2630 2 AAX24497
39 1133 63.5 2630 2 AAX24589
40 1127.8 63.2 3143 14 ADZ13465
41 1127.8 63.2 3144 13 ABD33433
42 1127.8 63.2 3144 13 ADR67035
43 1119 62.7 2604 10 ADR09617
44 1056.8 59.2 3185 14 ADZ13461
45 1048.4 58.7 1530 13 ADS73689

Aax23403 Hamster s
Aaz30615 Hamster S
Aas33744 CDNA enco
Aad33915 Hamster s
Adj33334 Hamster S
Aeb03941 Hamster S
Aea33429 SR-BI cdn
Ads73684 Rat SRB-I
Adz13457 Human can
Adz13463 Human can
Aba09256 Human SR-
Acd44925 Human cdn
Adj46118 Human cdn
Aaz32194 Human CLA
Aaa40750 Wild type
Aal62623 Human CD3
Adl61166 Human tyr
Ade40209 Human NOV
Aax24497 Human SR-
Aax24589 Human SR-
Abd33433 Human can
Adr67035 Human can
Ade09617 Novel DNA
Adz13461 Human can
Ads73689 Human SRB

CC receptor class B type I). This method is useful for female contraception,
CC for treating disorders characterised by overproduction of steroids, for
CC treating disorders characterised by underproduction of steroids,
CC especially menopause, for treating disorders that can be treated by
CC decreasing steroid production, especially breast cancer, prostate cancer,
CC endometriosis or fibroid tumours
XX

SQ Sequence 1785 BP; 386 A; 524 C; 475 G; 400 T; 0 U; 0 Other;

Query Match 100.0%; Score 1785; DB 2; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCTCCAGGGCGCGTGGGTGGCTTGGGGTTGGGGCCCTTGGGGCTGCTTTTGTGCGC 120
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DB 121 TCGGCGTGTGATGATCCTCATGTGCGCCCTCCATCAAGCAGCAGGTGCTCAAGATG 180
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QY 361 CTTTCAATGACAAACGACCGTGTCTTCTGGTGGAGAACCCGAGCTTCAATTCAGGCTG 420
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DB 421 ACAAGTCGATGGTTCAGAGAGTGATACATTTGATCTGCTTAAATCTTGGTCTGGGG 480
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DB 481 GCTCGATTTGATGGAGCAAGCCTGTGAGCCCTGAAAGCTGATGATGACCTTGGCGCTG 540
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DB 661 AATTGGCCCTGTTGTTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTTTCAAG 720
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DB 721 CGGTCCAGAAATTTTCAGCAGGATCATCTGGTGGACAAATGGAACGGACTCAGCAAGATCG 780
QY 781 ATTATTGGCAATTCAGACAGTGTAAATGATCAATGGGACTTCCGGGACATGTGGGCAC 840
DB 781 ATTATTGGCAATTCAGACAGTGTAAATGATCAATGGGACTTCCGGGACATGTGGGCAC 840
QY 841 CCTTCATGACACCCGAATCTCGCTGGAATTTCTTTCAGCCCGGGAGCATGAGGTCCATGA 900
DB 841 CCTTCATGACACCCGAATCTCGCTGGAATTTCTTTCAGCCCGGGAGCATGAGGTCCATGA 900

QY 901 AGCTGACCTTACAAACGAATCAAGGGTGTGTTGAAGGCATTCCTCAGTATCGCTTCAACGGCCC 960
DB 901 AGCTGACCTTACAAACGAATCAAGGGTGTGTTGAAGGCATTCCTCAGTATCGCTTCAACGGCCC 960
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DB 961 CCGATACTCTGTTTGGCAACGGGTCCGTCTACCCACCACGAAGGCTTCTGCGCATGCC 1020
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DB 1021 GAGAGTCTGGCATTCAGAATGTGACACCTGACAGGTTTGGTGGCCTCTGTTTCTCTCCC 1080
QY 1081 ACCCCCACTTTTACAAACGGCCCTGTTGTGTCAGAAGCTGTTTGTGTCGAACCCCTA 1140
DB 1081 ACCCCCACTTTTACAAACGGCCCTGTTGTGTCAGAAGCTGTTTGTGTCGAACCCCTA 1140
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DB 1141 ACCAAAGAGCATTCCTTGTTCCTAGACATCCATCCGCTCACTGGGATCCCCATGAAT 1200
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DB 1201 GTTCTGTGAAGATGACAGCTGAGCCTCTACATCAATCTGTCAAGGGCATCGGGCAACAG 1260
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DB 1261 GGAAGATCGAGCCAGTGTCTGCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
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DB 1321 GMAAGCCCTGAGCAGCTTCTACACGAGTGGTGTGATGCCCCAGGTTCTTCACTACG 1380
QY 1381 CGCAGTATGTGCTGCTGGGCTTGGAGGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTG 1440
DB 1381 CGCAGTATGTGCTGCTGGGCTTGGAGGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTG 1440
QY 1441 TGGCAGCCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
DB 1441 TGGCAGCCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
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DB 1561 TGCAGAAGCCAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1620
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DB 1621 GGTTCAGACCGACCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1680
QY 1681 CCACAGTGGCATGGCTGAGCCCCCAGATGTACACCTGTCCGACGACCGGCACATGG 1740
DB 1681 CCACAGTGGCATGGCTGAGCCCCCAGATGTACACCTGTCCGACGACCGGCACATGG 1740
QY 1741 ATGCCACGCACTGTCAAAAAAACAACCTCAGGACCCAGGACAGAC 1785
DB 1741 ATGCCACGCACTGTCAAAAAAACAACCTCAGGACCCAGGACAGAC 1785

RESULT 2

AAZ30616
ID AAZ30616 standard; cDNA; 1785 BP.

XX AAZ30616;

XX 18-JAN-2000 (first entry)

XX Mouse Scavenger receptor class BI gene.

XX Hamster; scavenger receptor; modulation; cholesterol transport; lipid;
KW lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;

Qy 61 GCTCAGGCGCGCTGGGTGACCTTGGGTTGGGCGCCCTGGGCTGCTGTTTCTGCGC 120
Db 61 GCTCAGGCGCGCTGGGTGACCTTGGGTTGGGCGCCCTGGGCTGCTGTTTCTGCGC 120
Qy 121 TCGGCGTTGTCATGATCCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG 180
Db 121 TCGGCGTTGTCATGATCCTCATGTGCGCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG 180
Qy 181 TCGCATAGACCCGAGCAGCCTGCTCTTGGGATGTGGAAGGAGATCCCGCTCCCTTTCT 240
Db 181 TCGCATAGACCCGAGCAGCCTGCTCTTGGGATGTGGAAGGAGATCCCGCTCCCTTTCT 240
Qy 241 ACTTGTCTGTACTTCTTCAAGTGGTCAACCCAAAGAGGTCTCTCAACGCGCAGAAAGC 300
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Qy 301 CAGTAGTCCGGGAGCGTGACCTATGCTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Db 301 CAGTAGTCCGGGAGCGTGACCTATGCTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Qy 361 CTTTCAATGACAAAGCAGCAGCCTGCTTGGGAGAACCGCAGCCTCCATTTCCAGCCTG 420
Db 361 CTTTCAATGACAAAGCAGCAGCCTGCTTGGGAGAACCGCAGCCTCCATTTCCAGCCTG 420
Qy 421 ACAAGTCGATGGTTCAGAGAGTGACTACATTTGACTGCTTAAACATCTTGGTCTGCGGG 480
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Db 541 TCACATGGGCGCAGCTGCTTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGCTATG 600
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Db 601 ACGATCCCTTGGTGCATTTTCTCAACAGTACCTCCAGACATGCTTCCCATAAAGGGCA 660
Qy 661 AATTGGCCTGTTTGGGATGAACAACTGCAATTCGGGGTCTTCACTGCTTCAAGG 720
Db 661 AATTGGCCTGTTTGGGATGAACAACTGCAATTCGGGGTCTTCACTGCTTCAAGG 720
Qy 721 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 780
Db 721 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 780
Qy 781 ATTAATGGCAATTCAGCAGGATGTAACATGATCAATGGGACCTTCGGGCGAGATGTGGGCAC 840
Db 781 ATTAATGGCAATTCAGCAGGATGTAACATGATCAATGGGACCTTCGGGCGAGATGTGGGCAC 840
Qy 841 CTTTCATGACACCGGAATCTCGTGGTGAATTTCTCAGCCCGGAGGCAATGAGGTCCATGA 900
Db 841 CTTTCATGACACCGGAATCTCGTGGTGAATTTCTCAGCCCGGAGGCAATGAGGTCCATGA 900
Qy 901 AGCTGACCTACAAGATCAAGGTTGTTGAAGGCAATTCACGATGCTTCAAGCGCC 960
Db 901 AGCTGACCTACAAGATCAAGGTTGTTGAAGGCAATTCACGATGCTTCAAGCGCC 960
Qy 961 CCGATACCTCTGTTGGCAACCGGCTCCGCTACCCACCAAGAGGCTTCTGCCCATGCCC 1020
Db 961 CCGATACCTCTGTTGGCAACCGGCTCCGCTACCCACCAAGAGGCTTCTGCCCATGCCC 1020
Qy 1021 GAGAGTCTGGCAATTCAGAAATCTCAGACCTGAGGTTGGTGGCGCTCTGTTTCTCTCCC 1080
Db 1021 GAGAGTCTGGCAATTCAGAAATCTCAGACCTGAGGTTGGTGGCGCTCTGTTTCTCTCCC 1080
Qy 1081 ACCCCCACTTTTACAAGCCGACCTGTTGTTGTCAGAGCTGTTTGGTCTGACCCCTA 1140
Db 1081 ACCCCCACTTTTACAAGCCGACCTGTTGTTGTCAGAGCTGTTTGGTCTGACCCCTA 1140

Qy 1141 ACCCAAGGAGCAATTCCTTCTCTAGACATCCATCCGCTCCTGCGATCCCATGAAC 1200
Db 1141 ACCCAAGGAGCAATTCCTTCTCTAGACATCCATCCGCTCCTGCGATCCCATGAAC 1200
Qy 1201 GTTCTGTGAAGATGACGCTGAGCTCTACATCAAACTGTCAAGGGCATCGGCAACAG 1260
Db 1201 GTTCTGTGAAGATGACGCTGAGCTCTACATCAAACTGTCAAGGGCATCGGCAACAG 1260
Qy 1261 GGAAGATCGAGCCAGTAGTTCTGCGCTTGTGGTTTCGAACAGAGCGAGCAATGGGTG 1320
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Qy 1321 GCAAGCCCTTGAGCAGCTTCTACACGAGCTGTGTCTGATGCCCCAGGTTCTTCACTACG 1380
Db 1321 GCAAGCCCTTGAGCAGCTTCTACACGAGCTGTGTCTGATGCCCCAGGTTCTTCACTACG 1380
Qy 1381 CGCAGTATGCTGCTGCGGCTTGGAGGCTCTCTGTTGCTGGTGCCCATCATCTGCCAAC 1440
Db 1381 CGCAGTATGCTGCTGCGGCTTGGAGGCTCTCTGTTGCTGGTGCCCATCATCTGCCAAC 1440
Qy 1441 TGGCGAGCCAGGAGAAATGCTTTTGTGGAGTGTGTAGTAAAGGGCTCCAGGATA 1500
Db 1441 TGGCGAGCCAGGAGAAATGCTTTTGTGGAGTGTGTAGTAAAGGGCTCCAGGATA 1500
Qy 1501 AGGAGCCATTCAGGCTACTCTGAGTCCCTGATGTCACAGTGCACAGGCGACGCTGC 1560
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Db 1621 GGTTCAGACAGCCAGCCAGTCCCTACACCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1680
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Qy 1741 ATGCCACGATGTCGAAAACAACTCAGGACCCAGGACAGGACC 1785
Db 1741 ATGCCACGATGTCGAAAACAACTCAGGACCCAGGACAGGACC 1785

RESULT 6

ABD33431

ID ABD33431 standard; cDNA; 2496 BP.

XX

AC ABD33431;

XX

DT 18-NOV-2004 (first entry)

XX

DE Murine cancer-associated (CA) cDNA MR07-081.

XX

KW Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
ss; cancer; cytostatic.

XX

OS Mus musculus.

XX

FN WO2004058146-A2.

XX

PD 15-JUL-2004.

XX

PF 15-DEC-2003; 2003WO-US040081.

XX

PR 17-DEC-2002; 2002US-00322281.

XX

PA (SAGR-) SAGRES DISCOVERY INC.

XX

PI Morris DW, Malandro MS;

XX

DR WPI; 2004-499109/47.

DR P-PSDB; ABO84950.
XX Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
PS Disclosure; SEQ ID NO 564; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents murine CA cDNA of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2496 BP; 517 A; 741 C; 660 G; 578 T; 0 U; 0 Other;
Query Match 100.0%; Score 1785; DB 13; Length 2496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGTCTCTTTCAGGTCTCTGAGCCCGGAGAGCCCTTCCGCGCACCGGACATGGGGGCA 60
DB 143 CCGTCTCTTTCAGGTCTCTGAGCCCGGAGAGCCCTTCCGCGCACCGGACATGGGGGCA 202
QY 61 GCTCCAGGGCGCGTGGGTGGCTTGGGGTTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 120
DB 203 GCTCCAGGGCGCGTGGGTGGCTTGGGGTTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 262
QY 121 TCGGCGTGTGCATGATCTCTATGTCGTCCTTCCCTCATAGCAGCAGTCTCAAGATG 180
DB 263 TCGGCGTGTGCATGATCTCTATGTCGTCCTTCCCTCATAGCAGCAGTCTCAAGATG 322
QY 181 TCGGCGTGTGCATGATCTCTATGTCGTCCTTCCCTCATAGCAGCAGTCTCAAGATG 240
DB 323 TCGGCGTGTGCATGATCTCTATGTCGTCCTTCCCTCATAGCAGCAGTCTCAAGATG 382
QY 241 ACTTGTCTGTCTACTTCTTCCAGAGTGTGTAACCCAAACGAGGTCTCAACGGCCAGAAC 300
DB 383 ACTTGTCTGTCTACTTCTTCCAGAGTGTGTAACCCAAACGAGGTCTCAACGGCCAGAAC 442
QY 301 CAGTAGTCCGGGAGCGTGGACCTTATGCTACAGGGAGTTCAGACAAAGGTCAACATCA 360
DB 443 CAGTAGTCCGGGAGCGTGGACCTTATGCTACAGGGAGTTCAGACAAAGGTCAACATCA 502
QY 361 CTTTCAATGACAAACGACCGTGTCTTCCGTGGAGAACCCGACGCTCCATTTCCAGCCTG 420
DB 503 CTTTCAATGACAAACGACCGTGTCTTCCGTGGAGAACCCGACGCTCCATTTCCAGCCTG 562
QY 421 ACAAGTCGCATGGCTCAGAGAGTGAATCAATGTATGCTTAACTTGGTCTCTGGGG 480
DB 563 ACAAGTCGCATGGCTCAGAGAGTGAATCAATGTATGCTTAACTTGGTCTCTGGGG 622
QY 481 GCTCGATATTGATGGAGAGCAACGCTGTGAGCCTGAGCTGATGACCTTGGCGCTGG 540
DB 623 GCTCGATATTGATGGAGAGCAACGCTGTGAGCCTGAGCTGATGACCTTGGCGCTGG 682
QY 541 TCACCATGGGCGACGCTGCTTTTATGAACCGCACAGTTGGTGGAGATCCTGTGGGGCTATG 600
DB 583 TCACCATGGGCGACGCTGCTTTTATGAACCGCACAGTTGGTGGAGATCCTGTGGGGCTATG 742
QY 601 ACGATCCCTTCTGTGCATTTTCTCAACACGTAACCTTCCAGACATGCTTCCCATAAAGGCA 660
DB 743 ACGATCCCTTCTGTGCATTTTCTCAACACGTAACCTTCCAGACATGCTTCCCATAAAGGCA 802

QY 661 AATTGGCCCTGTTTGTGGATGAACAACACTCGAATTTCTGGGTCTTCACTGTCTTCAACGG 720
DB 803 AATTGGCCCTGTTTGTGGATGAACAACACTCGAATTTCTGGGTCTTCACTGTCTTCAACGG 862
QY 721 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 780
DB 863 GCGTCCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGAATCAGCAAGATCG 922
QY 781 ATTATTGGCAATTCAGAGCAGTGTAAATGGAATTCCTGGGACTTCCGGGAGATGTGGGCAC 840
DB 923 ATTATTGGCAATTCAGAGCAGTGTAAATGGAATTCCTGGGACTTCCGGGAGATGTGGGCAC 982
QY 841 CTTTCAATGACACCCGAATCCTCGCTGGAATTTCTTACGCCCGGAGGATCAGGTCCATGA 900
DB 983 CTTTCAATGACACCCGAATCCTCGCTGGAATTTCTTACGCCCGGAGGATCAGGTCCATGA 1042
QY 901 AGCTGACCTTACCAACGAATCAAGGGTGTGTTGAAGGCAATTCCTCATGCTTTCACGGCCC 960
DB 1043 AGCTGACCTTACCAACGAATCAAGGGTGTGTTGAAGGCAATTCCTCATGCTTTCACGGCCC 1102
QY 961 CCGATATCTGTTTGGCAAGGGTCCGTCTACCCACCCCAAGAGGCTTTCGCCCATGCC 1020
DB 1103 CCGATATCTGTTTGGCAAGGGTCCGTCTACCCACCCCAAGAGGCTTTCGCCCATGCC 1162
QY 1021 GAGAGTCTGGCAATTCAGAAATGTCAACCTGCAAGTGTGGTGGCTCTGTCTTCTCTCCC 1080
DB 1163 GAGAGTCTGGCAATTCAGAAATGTCAACCTGCAAGTGTGGTGGCTCTGTCTTCTCTCCC 1222
QY 1081 ACCCCACATTTTACAAACGCCGACCTGTGTGTGAGAACTGTTTGTGCTGAAACCTTA 1140
DB 1223 ACCCCACATTTTACAAACGCCGACCTGTGTGTGAGAACTGTTTGTGCTGAAACCTTA 1282
QY 1141 ACCAAAGAGGATTCCTTGTTCCTAGACATCATCCGCTCACTGGGATCCCCATGAAT 1200
DB 1283 ACCAAAGAGGATTCCTTGTTCCTAGACATCATCCGCTCACTGGGATCCCCATGAAT 1342
QY 1201 GTTCTGTGAAGATGCAAGCTGAGCTCTACATCAATCTCTCAAGGGCATCGGCAACAG 1260
DB 1343 GTTCTGTGAAGATGCAAGCTGAGCTCTACATCAATCTCTCAAGGGCATCGGCAACAG 1402
QY 1261 GGAAGATCGAGCAGTGTCTGCGGTCTGCTGTGTTGCAACAGAGCGAGCAATCGGTG 1320
DB 1403 GGAAGATCGAGCAGTGTCTGCGGTCTGCTGTGTTGCAACAGAGCGAGCAATCGGTG 1462
QY 1321 GCNAGCCCTGAGCAGTGTCTACACGACGTGGTGTGATGCCAGGTTCTTCACTAG 1380
DB 1463 GCAAGCCCTGAGCAGTGTCTACACGACGTGGTGTGATGCCAGGTTCTTCACTAG 1522
QY 1381 CGCAGTATGTGTCTGCGGGCTTGGAGGCTCTCTGTGTGCTGGTGGCCATCATCTGCAAC 1440
DB 1523 CGCAGTATGTGTCTGCGGGCTTGGAGGCTCTCTGTGTGCTGGTGGCCATCATCTGCAAC 1582
QY 1441 TCGCAGCCAGGAGAAATGCTTTTGTGAGTGGTGTGTTGAGAGGCTCCAGGATA 1500
DB 1583 TCGCAGCCAGGAGAAATGCTTTTGTGAGTGGTGTGTTGAGAGGCTCCAGGATA 1642
QY 1501 AGAGGCCAATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGGCACGGTGC 1560
DB 1643 AGAGGCCAATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAAGGGCACGGTGC 1702
QY 1561 TGCAAGAAGCCAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1620
DB 1703 TGCAAGAAGCCAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1762
QY 1621 GGTTCAGACCCAGCCAGTCCCTACACCCCGCTTCTTGAAGACTCTTCAAGCGGACAGC 1680
DB 1763 GGTTCAGACCCAGCCAGTCCCTACACCCCGCTTCTTGAAGACTCTTCAAGCGGACAGC 1822
QY 1681 CCACAGTGCATGGCTGAGCCCCCAGATGTCAACCTGTCCGACCGCACCGCATGG 1740
DB 1823 CCACAGTGCATGGCTGAGCCCCCAGATGTCAACCTGTCCGACCGCACCGCATGG 1882

QY 1741 ATGCCAGCATGTGCAAAAACAACTCAGGACCGAGGACGACC 1785
Db 1883 ATGCCAGCATGTGCAAAAACAACTCAGGACCGAGGACGACC 1927

RESULT 7

ADR67032
ID ADR67032 standard; cDNA; 2496 BP.

XX AC
AC ADR67032;

XX 18-NOV-2004 (first entry)

DE Mouse cancer associated gene cDNA sequence SEQ ID NO:78.

XX cancer; cancer associated nucleic acid; cancer associated gene;
KW cancer associated protein; CAP; cytostatic; vaccine; gene therapy;
KW lymphoma; leukaemia; mouse; gene; ss.

XX Mus sp.

XX WO2004074321-A2.

XX 02-SEP-2004.

XX 17-FEB-2004; 2004WO-US005000.

XX 14-FEB-2003; 2003US-00367094.

XX 14-MAR-2003; 2003US-00388938.

XX 23-SEP-2003; 2003US-00669920.

XX 15-DEC-2003; 2003US-00737318.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Malandro MS;

XX WPI; 2004-652915/63.

XX P-PSDB; ADR67033.

XX New isolated cancer-associated polynucleotides and polypeptides useful

XX for diagnosing, preventing or treating cancers, especially lymphoma and

XX leukemia, or in screening for agents that modulate cancer.

XX Disclosure; SEQ ID NO 78; 166pp; English.

XX The present invention describes an isolated cancer associated (CA)

XX nucleic acid (1). Also described: (1) an expression vector comprising (1)

XX ; (2) a host cell comprising (1) or the expression vector; (3) a

XX microarray for detecting a CA nucleic acid; (4) an isolated cancer

XX associated protein (CAP) polypeptide, encoded within an open reading

XX frame of a CA sequence; (5) an isolated antibody, or its antigen binding

XX fragment, that binds to the above polypeptide; (6) a hybridoma that

XX produces the above monoclonal antibody; (7) a pharmaceutical composition

XX comprising the above antibody and a pharmaceutical excipient; (8) a kit

XX for detecting cancer cells, comprising the (monoclonal) antibody

XX described above; (9) methods for diagnosing cancer or for detecting the

XX presence or absence of cancer cells in an individual; (10) a method for

XX inhibiting growth of cancer cells in an individual; (11) a method for

XX delivering a therapeutic agent to cancer cells in an individual; (12) an

XX electronic library comprising the above polynucleotide or polypeptide, or

XX their fragments; (13) methods of screening for anticancer activity or for

XX a bioactive agent capable of modulating the activity of a CAP; (14)

XX methods for detecting cancer associated with expression of a polypeptide

XX in a test cell sample, or with the presence of an antibody in a test

XX serum sample; (15) a method for treating cancers; and (16) a method for

XX inhibiting the expression of CA gene in a cell. The CA sequences have

XX cytostatic activity, and can be used in vaccines, and in gene therapy.

XX The composition and methods are useful for detecting, diagnosing,

XX preventing and treating cancers, especially lymphoma and leukaemia. They

XX may also be used in screening for agents that modulate cancer. The

XX present sequence represents a cancer associated gene cDNA sequence, which

XX is used in the exemplification of the present invention.

XX

SQ Sequence 2496 BP; 517 A; 741 C; 660 G; 578 T; 0 U; 0 Other;
Query Match 100.0%; Score 1785; DB 13; Length 2496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCGTCTCTTTCAGTCTCTGAGCCCGAGAGCCCTTCCGCGCACGCGGACATGGGCGGCA	60
Db	143	CCGTCTCTTTCAGTCTCTGAGCCCGAGAGCCCTTCCGCGCACGCGGACATGGGCGGCA	202
QY	61	GCTCCAGGGCGCTGSGTGGGCTTGGGGTTGGGCGCTTGGGGTGGCTTGGCTTGGCTGCGC	120
Db	203	GCTCCAGGGCGCTGSGTGGGCTTGGGGTTGGGCGCTTGGGGTGGCTTGGCTTGGCTGCGC	262
QY	121	TCGGCGTTGTTCATGATCTCTCATGTCCTTCCCTCATCAAGCAGCAGGTCCTCAAGAATG	180
Db	263	TCGGCGTTGTTCATGATCTCTCATGTCCTTCCCTCATCAAGCAGCAGGTCCTCAAGAATG	322
QY	181	TCGGCATAGACCCGAGAGCCTGTCTTCGGGATGTGGAAGAGATCCCCGTCCTTTCT	240
Db	323	TCGGCATAGACCCGAGAGCCTGTCTTCGGGATGTGGAAGAGATCCCCGTCCTTTCT	382
QY	241	ACTTGTCTCTTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCCTCAAGCGGCGAGAGC	300
Db	383	ACTTGTCTCTTACTTCTTTCGAAGTGGTCAACCCAAACGAGGTCCTCAAGCGGCGAGAGC	442
QY	301	CAGTAGTCCGGGAGCGTGGACCTTATGTCTACAGGAGTTCAGACAAAGGTCACACATCA	360
Db	443	CAGTAGTCCGGGAGCGTGGACCTTATGTCTACAGGAGTTCAGACAAAGGTCACACATCA	502
QY	361	CTTCAATGACAAACGACACCGTGTCTTCTGTGGAGAACCGCAGCCTCCATTTCCAGCCTG	420
Db	503	CTTCAATGACAAACGACACCGTGTCTTCTGTGGAGAACCGCAGCCTCCATTTCCAGCCTG	562
QY	421	ACAAGTGCATGGCTCAGAGAGTGAATGATCTTCTAGTCTTCTTCTTCTTCTTCTTCTTCT	480
Db	563	ACAAGTGCATGGCTCAGAGAGTGAATGATCTTCTAGTCTTCTTCTTCTTCTTCTTCTTCT	622
QY	481	GCTCGATATTGATGGAGAGCAAGCCTGTGAGCTGAAGCTGATGATGACCTTGGCGCTGG	540
Db	623	GCTCGATATTGATGGAGAGCAAGCCTGTGAGCTGAAGCTGATGATGACCTTGGCGCTGG	682
QY	541	TCACCATGGGCGAGCGTGTCTTTATGAACCGCACAGTGGTGGAGATCCTGTGGGCTTATG	600
Db	683	TCACCATGGGCGAGCGTGTCTTTATGAACCGCACAGTGGTGGAGATCCTGTGGGCTTATG	742
QY	601	ACGATCCCTTCGTGCAATTTCTCAACAGTACCTCCAGACATGCTTCCATTAAGGGCA	660
Db	743	ACGATCCCTTCGTGCAATTTCTCAACAGTACCTCCAGACATGCTTCCATTAAGGGCA	802
QY	661	AATTTGGGCTGTGTGTGGATGAACAACTCGAATTTCTGGGGTCTTTCACCTGCTTACCGG	720
Db	803	AATTTGGGCTGTGTGTGGATGAACAACTCGAATTTCTGGGGTCTTTCACCTGCTTACCGG	862
QY	721	GGCTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAAACGAGCTCAGCAAGTCG	780
Db	863	GGCTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAAACGAGCTCAGCAAGTCG	922
QY	781	ATTATTTGGCATTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGCGAGATGTGGGCA	840
Db	923	ATTATTTGGCATTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGCGAGATGTGGGCA	982
QY	841	CCCTTCATGACACCGGAATCTCGCTGGAATTTCTTACGCGGAGGATGATGAGTCCATGA	900
Db	983	CCCTTCATGACACCGGAATCTCGCTGGAATTTCTTACGCGGAGGATGATGAGTCCATGA	1042
QY	901	AGCTGACCTACACGAATCAAGGGTGTGTAAGGCAATTCACGATATCGCTTTCACGGCCC	960
Db	1043	AGCTGACCTACACGAATCAAGGGTGTGTAAGGCAATTCACGATATCGCTTTCACGGCCC	1102
QY	961	CCGATATCTGTGTTGCAACAGGGTCTGCTTACCCACCCCAAGAGGCTTCTGCCCATGCC	1020
Db	1103	CCGATATCTGTGTTGCAACAGGGTCTGCTTACCCACCCCAAGAGGCTTCTGCCCATGCC	1162

Db 520 CCTCAATGACACGACACCGTGTCTTCTGTGGAGAACCGCAGCTCATATTTCCAGCGTG 579
Qy 421 ACAAGTCGCATGCTCAGAGAGTCACTACATTTGTAATGCTTAAACATCTTGTCTCTGGGG 480
Db 580 ACAAGTCGCATGCTCAGAGAGTCACTACATTTGTAATGCTTAAACATCTTGTCTCTGGGG 639
Qy 481 GCTCGATATTGATGAGAGCAGCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG 540
Db 640 GCTCGATATTGATGAGAGCAGCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG 699
Qy 541 TCACATGGGCGCAGCTGCTTTATGAACCGCACAGTTGGTGAGATCTCTGTGGGCTATG 600
Db 700 TCACATGGGCGCAGCTGCTTTATGAACCGCACAGTTGGTGAGATCTCTGTGGGCTATG 759
Qy 601 ACGATCCCTTGTGTCATTTCTCAACAGTACCTCCAGACATGCTTCCATAAAGGGCA 660
Db 760 ACGATCCCTTGTGTCATTTCTCAACAGTACCTCCAGACATGCTTCCATAAAGGGCA 819
Qy 561 AATTGGGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGCTTCACTGTCTTCAGG 720
Db 820 AATTGGGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGCTTCACTGTCTTCAGG 879
Qy 721 GCGTCCAGAAATTCAGCAGGATCATCTGTGGGACAAATGGAACGGAATCAGCAAGATCG 780
Db 880 GCGTCCAGAAATTCAGCAGGATCATCTGTGGGACAAATGGAACGGAATCAGCAAGATCG 939
Qy 781 ATTATGGCATTCAGACAGTGTAAATGATCAATGGGACTTCCGGGAGATGTGGGCAC 840
Db 940 ATTATGGCATTCAGACAGTGTAAATGATCAATGGGACTTCCGGGAGATGTGGGCAC 999
Qy 841 CTTTCATGACACCGGAATCTCGTGGAAATTTCTCAGCCGAGGAGATGAGGTCATGA 900
Db 1000 CTTTCATGACACCGGAATCTCGTGGAAATTTCTCAGCCGAGGAGATGAGGTCATGA 1059
Qy 901 AGCTGACCTCAACGAATCAAGGCTGTGAAGCATTTCCACGATGCTTTCACGGCC 960
Db 1060 AGCTGACCTCAACGAATCAAGGCTGTGAAGCATTTCCACGATGCTTTCACGGCC 1119
Qy 961 CCGATACCTGTGTTGCCAACGGGTCCTGTACCCACCAACGAAGCTTCTGCCCATGCC 1020
Db 1120 CCGATACCTGTGTTGCCAACGGGTCCTGTACCCACCAACGAAGCTTCTGCCCATGCC 1179
Qy 1021 GAGAGTCTGGCATTCAGAAATGACACCTGACAGTTTGTGGGCTCTGTCTCTCC 1080
Db 1180 GAGAGTCTGGCATTCAGAAATGACACCTGACAGTTTGTGGGCTCTGTCTCTCC 1239
Qy 1081 ACCCCCACTTTTACAACGCGACCTGTGTGTGTCAGAGCTGTTCTTGGTCTGAACCTTA 1140
Db 1240 ACCCCCACTTTTACAACGCGACCTGTGTGTGTCAGAGCTGTTCTTGGTCTGAACCTTA 1299
Qy 1141 ACCCAAGGAGCATTTCTTGTCTAGACATCCATCCGGTCACTGGGATCCCAATGAAT 1200
Db 1300 ACCCAAGGAGCATTTCTTGTCTAGACATCCATCCGGTCACTGGGATCCCAATGAAT 1359
Qy 1201 GTTCTGTGAAGATGACGTGACCTCTACATCAAAATCTGTCAAGGGCATCGGCAACAG 1260
Db 1360 GTTCTGTGAAGATGACGTGACCTCTACATCAAAATCTGTCAAGGGCATCGGCAACAG 1419
Qy 1261 GGAAGATCGAGCCAGTAGTGTGCGGCTGTGTGTGTCGACAGCGGAGCATGGGTG 1320
Db 1420 GGAAGATCGAGCCAGTAGTGTGCGGCTGTGTGTGTCGACAGCGGAGCATGGGTG 1479
Qy 1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGGTGTGTCGCGCCAGGTTCTTCACTACG 1380
Db 1480 GCAAGCCCTGAGCAGCTTCTACACGAGCTGGTGTGTCGCGCCAGGTTCTTCACTACG 1539
Qy 1381 CGCAGTATGTCTCTGGGCTTGGAGGCTCTGTGTGTCGTGTCGCCCATCATCTGCCAAC 1440
Db 1540 CGCAGTATGTCTCTGGGCTTGGAGGCTCTGTGTGTCGTGTCGCCCATCATCTGCCAAC 1599
Qy 1441 TGGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAAAGGGCTCCAGATA 1500
Db 1600 TGGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAAAGGGCTCCAGATA 1659

Qy 1501 AGGAGGCCATTAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGCAACGCTGC 1560
Db 1660 AGGAGGCCATTAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCAAGGCAACGCTGC 1719
Qy 1561 TGCAGAGCCAGCTACTAGGCTCCTGAGACACACTATAAGCCCCCAAACTGATAGCTT 1620
Db 1720 TGCAGAGCCAGCTACTAGGCTCCTGAGACACACTATAAGCCCCCAAACTGATAGCTT 1779
Qy 1621 GGTCCAGACAGCCACCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1680
Db 1780 GGTCCAGACAGCCACCCAGTCCCTACACCCCGCTTCTTGAAGACTCTCTCAGCGGACAGC 1839
Qy 1681 CCACCAAGTCCATGGCTGAGCCCCAGAGTGTCAACCTTCTCCGACGCGACATGG 1740
Db 1840 CCACCAAGTCCATGGCTGAGCCCCAGAGTGTCAACCTTCTCCGACGCGACATGG 1899
Qy 1741 ATGCCACGATGTGCANAACTCAGGGACCGGACAGACC 1785
Db 1900 ATGCCACGATGTGCANAACTCAGGGACCGGACAGACC 1944

RESULT 9

AEB03942
ID AEB03942 standard; cDNA; 1785 BP.

XX AEB03942;

XX AC AC

XX 25-AUG-2005 (first entry)

XX Murine Scavenger Receptor Class B-1 coding sequence, SEQ ID 3 #2.

XX Antilipemic; transgenic animal; Scavenger Receptor Class B-1;

XX high density lipoprotein receptor; cholesterol; lipid; gene; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 51..1580

XX FT /*tag= a

XX FT /product= "SR-BI"

XX XX

XX US2005136005-A1.

XX 23-JUN-2005.

XX 02-SEP-2004; 2004US-00933037.

XX 23-JUN-1994; 94US-00265428.

XX 19-JUN-1995; 95WO-US007721.

XX 15-NOV-1996; 96US-00749907.

XX 27-MAR-1997; 97US-00765108.

XX 30-AUG-1999; 99US-00385799.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Kozarsky K, Rigotti A, Krieger M;

XX WPI; 2005-457475/46.

XX P-PSDB; AEB03940.

XX New genetically engineered mouse or derivative cells with inactivated SR-

XX BI gene expression or activity, useful as a model for designing drugs

XX that can modulate cholesterol transport.

XX Disclosure; SEQ ID NO 3; 21pp; English.

XX The present invention relates to a novel genetically engineered mouse, or

XX cells derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene

XX expression or SR-BI activity has been inactivated. SR-BI is a high

XX density lipoprotein (HDL) receptor. It was found that estrogen

XX down-regulates SR-BI under conditions of upregulation of the low density

CC lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
CC adrenal membranes and other non-placental steroidogenic tissues from
CC animals treated with estrogen, but not in other non-placental non-
CC steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
CC tissue causes a decrease in blood cholesterol levels. The animal is
CC useful as a model for designing drugs that can modulate cholesterol
CC transport or that can stimulate or inhibit the binding to and lipid
CC movements mediated by SR-BI and redirect uptake and metabolism of lipids
CC and cholesterol by cells. The present sequence is a coding sequence for
CC SR-BI, which was used to illustrate the invention. Note: the SEQ ID 3
CC given in the sequence listing (the sequence shown in ABE03939) is stated
CC to be 1785 nucleotides in length. However, there appears to be a 1 to 3
CC nucleotide deletion at the end of each line of the sequence shown in the
CC sequence listing, resulting in a sequence that is 1761 nucleotides in
CC length. Therefore a corrected version of the sequence has been produced
CC with Ns added to replace the missing nucleotides (the sequence shown in
CC ABE03942). SEQ ID 3 is stated to encode SEQ ID 4 (given in ABE03940).
XX
SQ Sequence 1785 BP; 381 A; 520 C; 465 G; 395 T; 0 U; 24 Other;

Query Match 98.7%; Score 1761; DB 14; Length 1785;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1761; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 CCGTCTCCTTCAGGTCTCTGAGCCCGGAGAGCCCTTCGCGGCACGCGGACATGGGGGCA 60
Db 1 CCGTCTCCTTCAGGTCTCTGAGCCCGGAGAGCCCTTCGCGGCACGCGGACATGGGGGCA 60
Qy 61 GCTCCAGGGCGCGTGGGTGGCTTGGGTGGTGGCGCCCTTGGGGCTGCTTTTGTGCGC 120
Db 61 GCTCCAGGGCGCGTGGGTGGCTTGGGTGGTGGCGCCCTTGGGGCTGCTTTTGTGCGC 120
Qy 121 TCGCGTGTGTCATGCTCTATGGTGGCTCCCTCATCAGCAGCGAGTGTCTCAAGAATG 180
Db 121 TCGCGTGTGTCATGCTCTATGGTGGCTCCCTCATCAGCAGCGAGTGTCTCAAGAATG 180
Qy 181 TCGGCATAGACCCGAGCAGCTGTCTTCGCGGATGTGGAAGAGAGATCCCGCTCCCTTTCT 240
Db 181 TCGGCATAGACCCGAGCAGCTGTCTTCGCGGATGTGGAAGAGAGATCCCGCTCCCTTTCT 240
Qy 241 ACTTGTCTGTCTACTTCTCGAAGTGTCTCAACCCAAACGAGTGTCTCAACGGCCAGAAGC 300
Db 241 ACTTGTCTGTCTACTTCTCGAAGTGTCTCAACCCAAACGAGTGTCTCAACGGCCAGAAGC 300
Qy 301 CAGTAGTCCGGGACGCGTGTCTGTCTACAGGAGTTCACACAAAGGTCAACATCA 360
Db 301 CAGTAGTCCGGGACGCGTGTCTGTCTACAGGAGTTCACACAAAGGTCAACATCA 360
Qy 361 CCTTCAATGACACGACACCGTGTCTTCGCGAGAACCGCAGCTCCATTTCCAGCCTG 420
Db 361 CCTTCAATGACACGACACCGTGTCTTCGCGAGAACCGCAGCTCCATTTCCAGCCTG 420
Qy 421 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGCTGCTTAAACATCTTGGTCTCTGGGG 480
Db 421 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGCTGCTTAAACATCTTGGTCTCTGGGG 480
Qy 481 GCTCGATATTGTCAGCAGCAGCTGTGAGCTGTGAGCTGATGATGACCTTGGCGCTG 540
Db 481 GCTCGATATTGTCAGCAGCAGCTGTGAGCTGTGAGCTGATGATGACCTTGGCGCTG 540
Qy 541 TCACCATGGGCGCAGCGTGTCTTTATGAACCGCAGTGTGAGATCTCTGTGGGCTATG 600
Db 541 TCACCATGGGCGCAGCGTGTCTTTATGAACCGCAGTGTGAGATCTCTGTGGGCTATG 600
Qy 601 ACGATCCCTTGGTCAATTTTCTCAACACGTACTTCCAGACATGCTTCCATAAAGGGCA 660
Db 601 ACGATCCCTTGGTCAATTTTCTCAACACGTACTTCCAGACATGCTTCCATAAAGGGCA 660
Qy 661 AATTGGCCCTTTGTTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTACCG 720
Db 661 AATTGGCCCTTTGTTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTACCG 720
Qy 721 GCGTCCAGAAATTTTCAGCAGGATCCATCTGTGTGGACAAATGGAACGGACTCAGCAAGATCG 780

RESULT 10

721 GCGTCCAGAAATTTTCAGCAGGATCCATCTGGTGGACAAATGGAACGGACTCAGCAAGATCG 780
Qy 781 ATTATTGGCAATTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGACAGATGTGGGCAC 840
Db 781 ATTATTGGCAATTCAGAGCAGTGTAAATGATCAATGGGACTTCCGGGACAGATGTGGGCAC 840
Qy 841 CTTTCATGACACCGCAATCCTCGCTGGAATTTCTTACGCCGAGGAGCATGCAGGTCCATGA 900
Db 841 CTTTCATGACACCGCAATCCTCGCTGGAATTTCTTACGCCGAGGAGCATGCAGGTCCATGA 900
Qy 901 AGCTGACCTTACCAACCAATCAAGGGTGTGTTGAAGGCATTTCCACGTATCGCTTTCACGGCCC 960
Db 901 AGCTGACCTTACCAACCAATCAAGGGTGTGTTGAAGGCATTTCCACGTATCGCTTTCACGGCCC 960
Qy 961 CCGATACTCTGTTTGGCAACGGGTGCTGTACCCACCAACGAAGCTTCTGCGCCATGCC 1020
Db 961 CCGATACTCTGTTTGGCAACGGGTGCTGTACCCACCAACGAAGCTTCTGCGCCATGCC 1020
Qy 1021 GAGAGTCTGGCAATTCAGAAATGTCAGCAGCTGAGGTTTGGTGGCTCTGTTCTCTCC 1080
Db 1021 GAGAGTCTGGCAATTCAGAAATGTCAGCAGCTGAGGTTTGGTGGCTCTGTTCTCTCC 1080
Qy 1081 ACCCCACATTTTACCAACGCCGACCTGTGTTGTTCAGAAAGCTGTTTGTGCTGAACCCCTA 1140
Db 1081 ACCCCACATTTTACCAACGCCGACCTGTGTTGTTCAGAAAGCTGTTTGTGCTGAACCCCTA 1140
Qy 1141 ACCCAAGAGCAGATTCCTTGTTCCTAGACATCATCCGGTCACTGGGATCCCATGAAT 1200
Db 1141 ACCCAAGAGCAGATTCCTTGTTCCTAGACATCATCCGGTCACTGGGATCCCATGAAT 1200
Qy 1201 GTTCTGTGAAGATGCAAGTGAAGCTCTACATCAATCTGTCAAGGGCATCGGCAACAG 1260
Db 1201 GTTCTGTGAAGATGCAAGTGAAGCTCTACATCAATCTGTCAAGGGCATCGGCAACAG 1260
Qy 1261 GGAAGATCGAGCAGTGTGCTGCGTGTGTTGGAACAGAGCAGGAGCAATCGGTG 1320
Db 1261 GGAAGATCGAGCAGTGTGCTGCGTGTGTTGGAACAGAGCAGGAGCAATCGGTG 1320
Qy 1321 GCAGGCCCTGAGCAGCTGTCTACACGAGCTGGTGTGATGCCAGGTTCTTCACTAG 1380
Db 1321 GCAGGCCCTGAGCAGCTGTCTACACGAGCTGGTGTGATGCCAGGTTCTTCACTAG 1380
Qy 1381 CGCAGTATGCTGTCTGGGGCTTGGAGGCTCTCTGTGCTGTGGTCCCATCATCTGCAAC 1440
Db 1381 CGCAGTATGCTGTCTGGGGCTTGGAGGCTCTCTGTGCTGTGGTCCCATCATCTGCAAC 1440
Qy 1441 TGGCAGCCAGGAGAAATGCTTTTGTGAGTGGTAGTAAAGAGGGCTCCAGGATA 1500
Db 1441 TGGCAGCAGCAGGAGAAATGCTTTTGTGAGTGGTAGTAAAGAGGGCTCCAGGATA 1500
Qy 1501 AGAGGCCATTCAGGCTTACTGTAGTCCCTGATGTCAACAGCTGCCAAGGGCAGCGTGC 1560
Db 1501 AGAGGCCATTCAGGCTTACTGTAGTCCCTGATGTCAACAGCTGCCAAGGGCAGCGTGC 1560
Qy 1561 TGCAGAACCCAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1620
Db 1561 TGCAGAACCCAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCAAACTCTGATAGCTT 1620
Qy 1621 GGTTCAGACCCAGCCAGTCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGC 1680
Db 1621 GGTTCAGACCCAGCCAGTCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGC 1680
Qy 1681 CACAGTGCATGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGACGACATGG 1740
Db 1681 CACAGTGCATGGCTGAGCCCCCAGATGTCAACCTGTCCGACGACGACGACATGG 1740
Qy 1741 ATGCCCAACGATGTGCAAAACAACTCAGGGACCGAGGACAGACC 1785
Db 1741 ATGCCCAACGATGTGCAAAACAACTCAGGGACCNNGACAGACC 1785

841 CCTCATGACACCCGAATCTCGTGGATTTCTTACGCCGGAGGCATGAGGTCCATGA 900
901 AGCTGACCTACACGAATCAAGGGTGTGTTGAAGGCATTTCCACGATATCGCTTTCACGGCC 960
901 AGCTGACCTACACGAATCAAGGGTGTGTTGAAGGCATTTCCACGATATCGCTTTCACGGCC 960
961 CCGATATCTCTGTTTGGCCAAACGGGTCCGTCTACCCACCAAGAGGCTTCTGCCCATGCC 1020
961 CCGATATCTCTGTTTGGCCAAACGGGTCCGTCTACCCACCAAGAGGCTTCTGCCCATGCC 1019
1021 GAGAGTCTGGCATTGAGAAATGTCAGCACTGTCAGGTTTGGTGGCCCTCTGTTCTCTCCC 1080
1020 GAGAGTCTGGCATTGAGAAATGTCAGCACTGTCAGGTTTGGTGGCCCTCTGTTCTCTCCC 1078
1081 ACCCCCACTTTTACACGCCGACCTCTGTTGTCAGAAAGTGTCTTGGTCTGAACCTTA 1140
1079 ACCCCCACTTTTACACGCCGACCTCTGTTTTCAGAAAGTGTCTTGGTCTGAACCTTA 1137
1141 ACCCAAGGAGCATCTCTGTTTCTAGACATCCATCGGTCACTGGGATCCCATGAAC 1200
1138 ACCCAAGGAGCATCTCTT-TTCTAGACATCCATCGGTCACTGGGATCCCATGAAC 1196
1201 GTTCTGTGAAGATGACGTGAGCTCTACATCAATCTGTCAAGGCGATCGGCGAAGAC 1260
1197 GTTCTGT-AGATGACGTGAGCTCTACATCAATCTGTCAAGGCGATCGGCGAAGAC 1254
1261 GGAAGATCGAGCAGTAGTGTCTGCGTGTGTTGTCGAACAGCGAGCAATGGGTG 1320
1255 GGAAGATCGAGCAGTAGTGTCTGCGTGTGTTGTCGAACAGCGAGCAATGGGTG 1313
1321 GCAAGCCCTGAGCAGCTTCTACACGAGTGTGTGTCGTCAGGTTCTTCACTAAG 1380
1314 GCAAGCCCTGAGCAGCTTCTACACGAGTGTGTGTCGTCAGGTTCTTCACTAAG 1372
1381 CGAGTATGTCTGCTGGGCTTGGAGCCTCTGTTGCTGTGCTCCATCATCTGCCAAC 1440
1373 CGAGTATGTCTGCT-GGGCTTGGAGCCTCTGTTGCTGTGCTCCATCATCTGCCAAC 1431
1441 TGGCAGCAGGAGAAATGCTTTTGTGAGTGTGTGAGTGTGTAAAGGGCTCCAGGATA 1500
1432 TGGCAG-CAAGAGAAATGCTTTTGTGAGTGTGTGAGTGTGTAAAGGGCTCCCA-GATA 1489
1501 AGGAGGCATTCAGGCTTCTGAGTGTCTGATGTCCAGAGTGTCCAAAGGCGACGTGC 1560
1490 AGGAGGCATTCAGGCTTCTGAGTGTCTGATGTCCAGAGTGTCCAAAGGCGACGTGC 1548
1561 TGCAGAGCCAGCTATAGGCTTCTGAGACACTATAAGCCCCCCTGATGATCTT 1620
1549 TGCAGAGCCAGCTATAGGCTTCTGAGACACTATAAGCCCCCCTGATGATCTT 1605
1621 GGTTCAGACAGCCAGCTCCCTACACCCCGCTTCTTGGAGTGTCTCTCAGCGGACAGC 1680
1606 GGTTCAGACAGCCAGCTCCCTACACCCCGCTTCTTGGAGTGTCTCTCAGCGGACAGC 1662
1681 CCACAGTGTGATGCTGAGCCCTCCAGATGTACACTGTTCGACAGCGACGACATGG 1740
1663 CCACAGTGTGATGCTGAGCCCTCCAGATGTACACTGTTCGACAGCGACGACATGG 1719
1741 ATGCCAGCATGTGCAAAACACTCAGGAC 1774
1720 ATGCCAGCATGTGCAAAACACTCAGGAC 1753

RESULT 12

ID ADZ13452 standard; cDNA; 2382 BP.

AC AC

ADZ13452;

16-JUN-2005 (first entry)

XX Murine cancer-associated cDNA #108.

XX

KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX cytostatic; gene; ss.
OS Mus sp.
XX WO2005031001-A2.
XX 07-APR-2005.
XX 23-SEP-2004; 2004WO-US031617.
XX 23-SEP-2003; 2003US-00669920.
XX (CHIR) CHIRON CORP.
XX Morris DW, Malandro MS;
XX WPI; 2005-273395/28.
XX P-PSDB; ADZ13453.

Nucleic acid array useful for detecting cancer associated nucleic acid,
comprises two or more nucleic acid probes.

Disclosure; SEQ ID NO 972; 198pp; English.

The invention relates to a nucleic acid array for detecting a cancer
associated (CA) nucleic acid, comprising two or more nucleic acid probes.
The invention also relates to a peptide array comprising two or more
isolated polypeptides encoded by a CA nucleic acid sequence, a compound
that binds to a polypeptide, an isolated antibody or its fragment which
binds to a polypeptide, which is prepared by immunizing a host animal
with a composition comprising the polypeptide or its antigen binding
fragment and collecting cells from the host expressing antibodies against
the antigen or its antigen binding fragment, a composition comprising the
antibody and a carrier, a method of screening for anticancer activity, a
method of detecting a CA nucleic acid, a method of diagnosing cancer, a
method of treating cancer and a method of inhibiting expression of a CA
nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
nucleic acids. The antibody is useful for detecting the presence or
absence of cancer cells in an individual which involves contacting cells
from the individual with the antibody and detecting a complex of a CA
protein from the cancer cells and the antibody, where the detection of
the complex correlates with the presence of cancer cells in the
individual. The composition is useful for inhibiting growth of cancer
cells in an individual or for delivering a therapeutic agent to cancer
cells in an individual. The invention is also useful for diagnosing
cancer, for treating cancer and for inhibiting expression of a CA gene in
a cell. This sequence represents murine cancer-associated cDNA of the
invention.

XX SQ Sequence 2382 BP; 486 A; 720 C; 626 G; 550 T; 0 U; 0 Other;

Query Match 85.0%; Score 1517; DB 14; Length 2382;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 0; Indels 129; Gaps 1;

QY 1 CCCTCTCTCTTCCAGTCTCTGAGCCCGAGAGCCCTTCCGCGCACGGGACATGGGGGCA 60

Db 160 CCGTCTCTCTTCCAGTCTCTGAGCCCGAGAGCCCTTCCGCGCACGGGACATGGGGGCA 219

QY 61 GCTCCAGGGCGCGCTGGGTGGCTTGGGGTGGGGCGCCCTTGGGGCTGCTGTTTCTGTCGC 120

Db 220 GCTCCAGGGCGCGCTGGGTGGCTTGGGGTGGGGCGCCCTTGGGGCTGCTGTTTCTGTCGC 279

QY 121 TCGGCGTGTTCATGATCTCTCATGTCGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGATG 180

Db 280 TCGGCGTGTTCATGATCTCTCATGTCGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGATG 339

QY 181 TCCGCATAGACCCGAGCAGCTCTCTCGGATGTGGAGGAGATCCCGTCCCTTCTTCT 240

Db 340 TCCGCATAGACCCGAGCAGCTCTCTCGGATGTGGAGGAGATCCCGTCCCTTCTTCT 399

QY 241 ACTTGTCTGTCTACTTCTTTCGAAGTGTGTCAACCAACAGAGGTCTCTCAACGCGCAGAAGC 300

Db 400 ACTTGTCTGTCTACTTCTTGAAGTGGTCAACCAAGAGGTCTCTCAACGGCCAGAGC 459
Qy 301 CAGTAGTCCGGAGCGTGGACCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
Db 460 CAGTAGTCCGGAGCGTGGACCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 519
Qy 361 CTTTCAATGACAACGACACCGTGTCTTGTGGAGAACCGCAGCCTCCATTTCCAGCCTG 420
Db 520 CTTTCAATGACAACGACACCGTGTCTTGTGGAGAACCGCAGCCTCCATTTCCAGCCTG 579
Qy 421 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGTACTGCCCTAAACATCTTGGTCTCTGGGG 480
Db 580 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGTACTGCCCTAAACATCTTGGTCTCTGGGG 639
Qy 481 GCTCGATATTGATGGAGAGCAGCCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG 540
Db 640 GCTCGATATTGATGGAGAGCAGCCTGTGAGCCTGAAGCTGATGATGACCTTGGCGCTGG 699
Qy 541 TCACCATGGGCGAGCGTGTCTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGGCTATG 600
Db 700 TCACCATGGGCGAGCGTGTCTTTATGAACCGCACAGTTGGTGAGATCCTGTGGGGCTATG 759
Qy 601 ACAGTCCCTTCTGTGCAATTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 660
Db 760 ACAGTCCCTTCTGTGCAATTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 819
Qy 661 AATTGGCCCTGTTTGGGATGAACAACTCGAATTCCTGGGGTCTTCACTGTCTTCAACGG 720
Db 820 AATTGGCCCTGTTTGGGATGAACAACTCGAATTCCTGGGGTCTTCACTGTCTTCAACGG 879
Qy 721 GCGTCCAGAAATTTCCAGCAGATCCATCTGTGGACAAATGGAACGGACTCAGCAAGATCG 780
Db 880 GCGTCCAGAAATTTCCAGCAGATCCATCTGTGGACAAATGGAACGGACTCAGCAAGATCG 939
Qy 781 ATTATTGGCAATTCAGACAGTGAACATGATCAATGGGACTTCGGGCGAGATGTGGGCAC 840
Db 940 ATTATTGGCAATTCAGACAGTGAACATGATCAATGGGACTTCGGGCGAGATGTGGGCAC 999
Qy 841 CTTTCATGACACCGAATCTCGTGAATTTCTCAGCCCGGAGGATGAGGTCATGA 900
Db 1000 CTTTCATGACACCGAATCTCGTGAATTTCTCAGCCCGGAGGATGAGGTCATGA 1059
Qy 901 AGCTGACTCAACGAATCAAGGGTGTGAAGGCAATTCACGATCGCTTCAACGGCCC 960
Db 1060 AGCTGACTCAACGAATCAAGGGTGTGAAGGCAATTCACGATCGCTTCAACGGCCC 1119
Qy 961 CCGATACTCTGTTTGCCAAACGGGTCCGCTCTACCCACCAACGAAGGCTTCTGCCCATGCC 1020
Db 1120 CCGATACTCTGTTTGCCAAACGGGTCCGCTCTACCCACCAACGAAGGCTTCTGCCCATGCC 1179
Qy 1021 GAGAGTCTGGCATTCAGAAATGTGAGACCTGTGAGGTTTGGTGCGCTCTGTCTCTCCC 1080
Db 1180 GAGAGTCTGGCATTCAGAAATGTGAGACCTGTGAGGTTTGGTGCGCTCTGTCTCTCCC 1239
Qy 1081 ACCCCCACTTTTACAACGCGACCTGTGTGTGTCAGAGCTGTCTTGGTCTGAACCCCTA 1140
Db 1240 ACCCCCACTTTTACAACGCGACCTGTGTGTGTCAGAGCTGTCTTGGTCTGAACCCCTA 1299
Qy 1141 ACCCAAGGAGCATTCCTTGTCTTAGACATCCATCCGCTCACTGGGATCCCATGAACT 1200
Db 1300 ACCCAAGGAGCATTCCTTGTCTTAGACATCCATCCGCTCACTGGGATCCCATGAACT 1359
Qy 1201 GTTCTGTGAGATGACGTAGCTCTTACATCAATCTGTCAAGGGCATCGGGCAACAG 1260
Db 1360 GTTCTGTGAGATGACGTAGCTCTTACATCAATCTGTCAAGGGCATCGGGCAACAG 1419
Qy 1261 GGAAGATCGACCATGATGTTCTGCGGTGTGTCGATCGAGCGGAGCATGGGTG 1320
Db 1420 GGAAGATCGACCATGATGTTCTGCGGTGTGTCGATCGAGCGGAGCATGGGTG 1479
Qy 1321 GCAAGCCCTGTGAGCAGCTTCTACACGAGCTGGTGTGATGCCCGGCTTCTTCACTACG 1380

Db 1480 GCAAGCCCTGAGCAGCTTCTTACACGACGCTGGTCTGATGCCCGCAGGTTCTTCACTACG 1539
Qy 1381 CCGAGTATGTCTGTGGGGCTTGGAGGCTCTCTGTGGTGGTCCCATCATCTGCCAAC 1440
Db 1540 CCGAGTATGTCTGTGGGGCTTGGAGGCTCTCTGTGGTGGTCCCATCATCTGCCAAC 1599
Qy 1441 TGGCAGCAGCAGGAGAAATGCTTTTGTGGAGTGGTAGTAAAGGGCTCCAGGATA 1500
Db 1600 TGGCAGACC----- 1608
Qy 1501 AGGAGCCATTCAAGCCTACTCTGAGTCCCTGATGTCAACAGTGCACAGGGCACGGTGC 1560
Db 1609 ----- 1608
Qy 1561 TGCAGAGCCAAAGCTATAGGTCCTGAAGACACTATAGAGCCCCCAAACTGATAGCTT 1620
Db 1609 -----AGGGTCTCTGAAGACACTATAGAGCCCCCAAACTGATAGCTT 1650
Qy 1621 GGTACAGCAGCAGCAGCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1680
Db 1651 GGTACAGCAGCAGCAGCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1710
Qy 1681 CCACAGTCCCATGGCTGAGCCCCCAGATGTACACCTGTCCGACGCAACGGCAGATGG 1740
Db 1711 CCACAGTCCCATGGCTGAGCCCCCAGATGTACACCTGTCCGACGCAACGGCAGATGG 1770
Qy 1741 ATGCCCCAGCTGTGCAGAAACAACTCAGGGACCGGACAGACC 1785
Db 1771 ATGCCCCAGCTGTGCAGAAACAACTCAGGGACCGGACAGACC 1815

RESULT 13
ADB58616
ID ADB58616 standard; DNA; 2497 BP.
XX
AC ADB58616;
XX AC
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 3642.
XX
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
XX drug screening; toxicity assay; ds.
XX Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PP 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgins B, Castle A, Elashoff M;
XX WPI; 2003-689530/65.
XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
PT markers in liver tissues or cells for drug screening and toxicity assays,
PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.
XX
PS Claim 1; SEQ ID NO 3642; 1156pp; English.
CC
CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the

CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect
CC of a compound, identifying an agent that modulates the onset or
CC progression of a toxic response, predicting the cellular pathways that a
CC compound modulates in a cell, and identifying an agent that modulates at
CC least one activity of a protein. The method and compositions of the
CC present invention using a database of genes having liver toxin-induced
CC differential expression, are useful in identifying toxicity markers in
CC liver tissues or cells for drug screening and toxicity assays. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;

Query Match 81.8%; Score 1459.4; DB 10; Length 2497;

Best Local Similarity 90.6%; Pred. No. 0; Mismatches 161; Indels 0; Gaps 0;

Matches 1556; Conservative 0;

Qy	1	CCGCTCTCCCTCAGGTCTCTGAGCCCGGAGGACCCCTTCGCGCAGCGCGACATGGCGCGCA	60
Db	153	CCGTCCTCTCAGGTCTCTGAGCCCGGAGGACCCCTTCGCGCAGCGCGACATGGCGCGTCA	212
Qy	61	GCTCCAGGCGCGTGGGTGCGCTTGGGGTTGGGCGCCCTGGGCTGCTGTTCCTGCGC	120
Db	213	GCTCCAGGCGCGTGGGTGCGCTTGGGGTTGGGCGCCCTGGGCTGCTGTTCCTGCGC	272
Qy	121	TGGGCTGTTCATGTCCTCATGTGCGCTCCCTCATCAGCAGGCTCTCAAGATG	180
Db	273	TGGGCTGTTCATGTCCTCATGTGCGCTCCCTCATCAGCAGGCTCTCAAGATG	332
Qy	181	TCCGCATAGACCCGAGCAGCGCTGCTTCTGGGATGTGGAAGGATCCCGCTCTTCT	240
Db	333	TCCGCATAGACCCGAGCAGCGCTGCTTCTGGGATGTGGAAGGATCCCGCTCTTCT	392
Qy	241	ACTTGTCTGTCTACTTCTTGAAGTGTGTCCTCAACCAAGAGGTCTCAAGCGCAGAAC	300
Db	393	ACTTGTCTGTCTACTTCTTGAAGTGTGTCCTCAACCAAGAGGTCTCAAGCGCAGAAC	452
Qy	301	CAGTAGTCCGGAGCGTGGACCTTATGCTCAGGAGTTCAGACCAAGGTCAACATCA	360
Db	453	CAGTAGTCCGGAGCGTGGACCTTATGCTCAGGAGTTCAGACCAAGGTCAACATCA	512
Qy	361	CTTTCATGACCAACACACCGTGTCTTCTGAGGAGACCGCAGCGCTCCATTTCCAGCTG	420
Db	513	CTTTCATGACCAACACACCGTGTCTTCTGAGGAGACCGCAGCGCTCCATTTCCAGCTG	572
Qy	421	ACAAAGTCGATGGCTCAGAGAGTGACTACATTTGACTGCTTAAACATCTTGGTCTCGGGG	480
Db	573	ACAAAGTCGATGGCTCAGAGAGTGACTACATTTGACTGCTTAAACATCTTGGTCTCGGGG	632
Qy	481	GCTCGATTTGATGAGAGGAGCGCTGTGAGCCTGAGAGCTGATGATGACCTTGGCGCTGG	540
Db	633	GCTCGATTTGATGAGAGGAGCGCTGTGAGCCTGAGAGCTGATGATGACCTTGGCGCTGG	692
Qy	541	TCACATGGGCGCGGTGCTTTTATGACCCGACAGTGTGGTGTGATCTGTGGGCTATG	600
Db	693	TCACATGGGCGCGGTGCTTTTATGACCCGACAGTGTGGTGTGATCTGTGGGCTATG	752
Qy	601	ACGATCCCTTCTGTCATTTCTCAACACGTACCTCCAGACATGCTTCCCATAAAGGCGCA	660
Db	753	ACGATCCCTTCTGTCATTTCTCAACACGTACCTCCAGACATGCTTCCCATAAAGGCGCA	812
Qy	661	AATTTGGCTGTTGTTGGGATGAACAACTGAAATTTCTGGGGTCTTCACTGCTTCACGG	720
Db	813	AATTTGGCTGTTGTTGGGATGAACAACTGAAATTTCTGGGGTCTTCACTGCTTCACAG	872
Qy	721	CGGTCCAGAAATTCAGCAGGATCATCTGTGGGAGCAATGAACGAGCTCAGCAGATCG	780
Db	873	GTGTCCAGAAATTCAGCAGGATCATCTGTGGGAGCAATGAACGAGCTCAGCAGATCG	932

Qy	781	ATTATTGGCATTCAGAGCAGTGTAAATGATGATCAATGGGACTTCGGGCGACATGTGGCGAC	840
Db	933	ACTATTGGCATTCGGACAGTGTCAACATGATCAATGGTACTGCGGGCGACATGTGGCGAC	992
Qy	841	CTTTCATGACACCGCAATCTCGCTGGAAATCTTTCAGCCCGGAGGATGAGGTTCCATGA	900
Db	993	CATTTCATGACACCGCAATCTCTCTGGAATCTTTCAGCCCGGAGGATGAGGTTCCATGA	1052
Qy	901	AGCTGACCTTCAACAGCAATCAAGGGTGTTCAGAGCATTTCCACGATTCGCTTTCACGCCCC	960
Db	1053	AGCTGACCTTCAACAGCAATCAAGGGTGTTCAGAGCATTTCCACGATTCGCTTTCACGCCCC	1112
Qy	961	CCGATACCTTGTTCGCAACGGGTCTGACCCACCAAGAGGTTCTGCGCCATGCC	1020
Db	1113	CCGATACCTTGTTCGCAACGGGTCTGACCCACCAAGAGGTTCTGCGCCATGCC	1172
Qy	1021	GAGAGTCTGGCATTCAGAAATGTCAGACCTTCAGGTTTGTGGCGCTCTGTTCTCTCCCC	1080
Db	1173	GCGAGTCCGGCATTCAGAAATGTCAGACCTTCAGGTTTGTGGCGCTCTGTTCTCTCCCC	1232
Qy	1081	ACCCCACTTTTACACCGCGACCTGTGTGTTCAGAAAGCTGTTCTTGGTCTGAAACCTTA	1140
Db	1233	AGCCCACTTTTACACCGCGACCTGTGTGTTCAGAAAGCTGTTCTTGGTCTGAAACCTTA	1292
Qy	1141	ACCCAAAGAGCATTTCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCGCATGAAC	1200
Db	1293	ACCCAAAGAGCATTTCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCGCATGAAC	1352
Qy	1201	GTTCGTGGAAGTGCAGCTGAGGCTCTACATCAATCTGTCAAGGGCATCGGGCAACAG	1260
Db	1353	GTTCGTGGAAGTGCAGCTGAGGCTCTACATCAATCTGTCAAGGGCATCGGGCAACAG	1412
Qy	1261	GGAAGTTCGAGCGCAGTAGTTCTGCGCTTGTCTGTTTCGAACAGAGCGGAGTATGGGTG	1320
Db	1413	GGAAGTTCGAGCGCAGTAGTTCTGCGCTTGTCTGTTTCGAACAGAGCGGAGTATGGGTG	1472
Qy	1321	GCAAGCCCCCTGAGGACGTTCTTACAGCAGCTGGTGTGATGCCCGAGGTTCTTCACTACG	1380
Db	1473	GCAAGCCCCCTGAGGACGTTCTTACAGCAGCTGGTGTGATGCCCGAGGTTCTTCACTACG	1532
Qy	1381	CGCAGTATGCTGCTGGGGCTTCGGGCTTCCTGCTTCTGTTGCTGCTCCATCTGCTCAAC	1440
Db	1533	CGCAGTATGCTGCTGGGGCTTCGGGCTTCCTGCTTCTGTTGCTGCTCCATCTGCTCAAC	1592
Qy	1441	TGGCGCAGCAGGAGAAATGCTTTTGTTCGAGTGTGTAGTAAAGAGGCTCCCGAGGATA	1500
Db	1593	TGGCGCAGCAGGAGAAATGCTTTTATTTTGGAGTGTGTAGTAAAGAGGCTCCCGAGGATA	1652
Qy	1501	AGGAGGCAATTCAGGCTTACTCTGAGTCTCTGATGTCCAGCTGCAAGGGCAAGTGC	1560
Db	1653	AGGAGGCAATTCAGGCTTACTCTGAGTCTCTGATGTCCAGCTGCAAGGGCAAGTGC	1712
Qy	1561	TGCAAGNAGCAAGCTATAGGCTCTGAAACACTATAAGCCCCCCCCAACTGATAGCTT	1620
Db	1713	TGCAAGNAGCAAGCTATAGGCTCTGAAACACTATAAGCCCCCCCCAACTGATAGCTT	1772
Qy	1621	GCTCAGACCAAGCAGCCAGTCCCTTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAGC	1680
Db	1773	GCTCAGACCAAGCAGCCAGTCCCTTACACCCGCTTCTTGAAGGACTCTCTCAGCGGACAGC	1832
Qy	1681	CCACCAAGTCCAGTGGCTGAGCCCCCAGATGTTCACAC	1717
Db	1833	CCGCGAGTCCAGTCTCTGAGCCCCCAGATGTTCACAC	1869

RESULT 14

ADB53264

ID ADB53264 standard; DNA; 2497 BP.

XX

AC ADB53264;

XX 04-DEC-2003 (first entry)

DT

XX

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3806.
XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX

OS Rattus norvegicus.

XX WO2003065993-A2.

PN 14-AUG-2003.

PD 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.

XX 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373601P.

PR 19-APR-2002; 2002US-0373602P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-MAY-2002; 2002US-0378655P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elashoff M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.

XX Claim 44; SEQ ID NO 3806; 874pp; English.

XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

XX Sequence 2497 BP; 549 A; 731 C; 662 G; 555 T; 0 U; 0 Other;

XX Query Match 81.8%; Score 1459.4; DB 10; Length 2497;

XX Best Local Similarity 90.6%; Pred. No. 0;

XX Matches 1556; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

Qy 1 CCGTCTCTTCAGTCTGAGCCCGAGGCCCTTCGCGCGCAGCGGACATGGCGGCA 60

Db 153 CCGTCTCTTCAGTCTGAGCCCGAGGACTCTCGCGCGCAGCGGACATGGCGGCA 212

Qy 61 GCTCCAGGCGCGTGGGCTTGGGCTTGGGCGCCCTGCTGTTGCTGCGC 120

Db 213 GCTCCAGGCGCGTGGGCTTGGGCTTGGGCTGCTGTTGCTGCGC 272

Qy 121 TGGCGTTCATGATCCATGTTGCTCCCTCATCAAGCAGCAGGCTCAAGAATG 180

Db 273 TGGCGTTCATGATCCATGTTGCTCCCTCATCAAGCAGCAGGCTCAAGAATG 332

Qy 181 TCCGATAGACCCGAGCAGCTGCTCCGATGTGGAGAGAGATCCCGTCCCTTTCT 240

Db 333 TCCGATAGACCCGAGCAGCTGCTCCGATGTGGAGAGAGATCCCTGTTCTCTTCT 392

Qy 241 ACTTGTCTCTACTTCTTGAAGTGTCAACCCAAACGAGGTCTCAACGCGCAGAAC 300

Db 393 ACTTGTCCGTCTACTTCTTGAAGTGTCAACCCAGCGAGGTCTCAACGCGCAGAAC 452

Qy 301 CAGTAGTCCGGGAGCGTGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCA 360

Db 453 CAGTAGTCCGGGAGCGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCA 512

Qy 361 CCTTCAATGACAAACGACACCGGTCTCTCGTGAGAACCGCAGCCTCCATTTCCAGCCTG 420

Db 513 CCTTCAATGACAAATGACACCGGTCTCTCAATAGAGAACCGAGCCTTCGTTCCAGCCTG 572

Qy 421 ACAAGTCCGATGGCTCAGAGAGTACTACATTGTACTGCTTAACATCTTGGTCTCTGGGG 480

Db 573 ACAGTCCCAGGGCTCAGAGAGTACTACATTGTACTGCTTAACATCTTGGTCTCTGGGG 632

Qy 481 GCTCGATATGATGGAGACGAGCCTGTGAGCTGAAGCTGATGATGACCTTGGCGCTGG 540

Db 633 GGGCAGTGTATGATGGAGGCAAGCCCAAGCCTCGAAGCTGCTTAATGACCTTGGGGTTGG 692

Qy 541 TCACCATGGGCCAGCGTCTTTTATGAACCGCACAGTGTGTGAGATCCTGTGGGGCTATG 600

Db 693 TCACCATGGGCCAGCGGCTTTATGAACCGCACAGTGTGTGAGATCCTGTGGGGCTATG 752

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Db 813 AATTGGCTCTGTTGTTGGATGAACACTCGAATTTCTGGGTCTTCACTGTCTTACCG 872

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Db 873 GTGTCCAGAAATTTACAGCAAGTCCATCTGTGTGATGAAGTGAACGAGCTCAGCAAGATCG 932

Qy 781 ATATTGGCATTACAGCAGTGTAAACATGATCAATGGGACTTCCGGGAGATGTGGGCAC 840

Db 933 ACTATTGGCATTCCGGAACAGTGTCAACATGATCAATGGTACTGCGCGGAGATGTGGGCAC 992

Qy 841 CCTTCATGACACCGGAATCTCGCTGGAATTTCTTCAGCCGGAGGATGAGGCTCCATGA 900

Db 993 CATTCATGACACCGGAATCTCTCACTGGAATTTCTTCAGCCAGAGGCTGAGATCTATGA 1052

Qy 901 AGCTGACCTACACAGAAATCAAGGGTGTGTAAGGCAATTCACGATCGCTTCAACGCGCC 960

Db 1053 AGCTGACCTACACAGAAATCAAGGGTGTGTAAGGCAATTCACGATCGCTTCAACGCGCC 1112

Qy 961 CCGATATCTGTTTGGCAACGGGTCCGCTTACCCACCAACGAGGCTTCTGCGCCATGCC 1020

Db 1113 CCGATATCTGTTTGGCAACGGGTCCGCTTACCCACCTAATGAAGGCTTCTGCGCGTGC 1172

Qy 1021 GAGAGTCTGGCATTGAGATGTGAGACCTGAGGTTTGGTGGCCTCTGTTTCTCTCCC 1080

Db 1173 GCGAGTCCGCGCATTCAGAAATGTGAGACCTGAGGTTTGGTGGCCTCTGTTTCTCTCCC 1232

Qy 1081 ACCCCCACTTTTACACGCGACCTGTGTGTGTAAGAGCTGTTCTTGGTCTGAACCCCTA 1140

Db 1233 AGCCCCACTTCTACAAATGTGACCCCGTGTGTGTAAGAGCTGTTCTTGGTCTGAACCCCTG 1292

Qy 1141 ACCCAAGAGGAGCATCTCTGTTCTTCTAGACATCCATCCGCTCACTGGGATCCCATGAAT 1200

[illegible]

Qy	421	ACAAAGTCGCATGGCTCAGAGAGTGA	CTACATGTATCTGCCTAAACATCTTGGTCTCTGGGG	480
				481
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Qy	481	GCTCGATATTGATGGAGAGCAAGCCT	GTGAGCTGTAGCTGATGATGACCTTGGCGCTGG	540
Db	633	GGGCAGTGTATGAGAGGACAAGCCCA	CAAGCCTGAAGCTGCTAAATGACCTTGGGGTTGG	692
Qy	541	TCACATGGGCGACGCTGCTTTTATGAA	CCGCACAGTTGCTGAGATCCTCTGGGGGCTATG	600
Db	693	TCACCATGGGCGACGGGCGCTTTATGAA	CCGCACGGTTGCTGAGATCCTCTGGGGGCTACG	752
Qy	601	ACGATCCCTTCTGTGCAATTTTCTCAAC	ACGCTACCTCCAGACATGCTTCCATAAAGGGCA	660
Db	753	AAGATCCCTTGTGAAATTTCTCAGCAAA	TATTTCTCCAGACATGTTCTCCCATCAAAAGCA	812
Qy	661	AAATTTGGCCTGTTTGTGGGATGAA	CAAACTCGAATTTCTGGGGTCTTCACTGTCTTACCG	720
Db	813	AAATTTGGCCTGTTTGTGGGATGAA	CACTCGAATTTCTGGCGTCTTCAACGTTTCAACAG	872
Qy	721	CGCTCCAGAAATTTCAGCAGGATCCAT	CTGCTGGACAAATGGAACGGACTCAGCAAGATCG	780
Db	873	GTGTCCAGAAATTTCAGCAAGATCCAT	CTGCTGGATAGTGGACGCGCTCAGCGAGGTCA	932
Qy	781	ATTATTTGGCAATTCAGACAGTGTAA	CAATGGAATTTCCGGGCAGATGTGGGCAC	840
Db	933	ACTATTTGGCAATTCGGAACAGTGC	AAACATGATCAATGGTACTGCGCGGCAGATGTGGGCAC	992
Qy	841	CTTTCATGACACCCGAATCCTCGT	CGAAATTTCTCAGCCCGGAGGCATCAGATCCCATGA	900
Db	993	CATTTCATGACACCCGAATCTCTCA	CTGGAATTTCTTCAGCCCCAGAAAGCTCGAGATCTATGA	1052
Qy	901	AGCTGACCTTACAACGAATCAAGGG	TGTTGAAAGGCATTTCCAGATATCGCTTTCACGGCGCC	960
Db	1053	AGCTCACTTACCAGGAATCAAGGGT	GTTCGAAGGCATCCCCACTTATCGCTTTCACGGCGCC	1112
Qy	961	CCGATACTCTGTTTGGCCAAAGGGT	CCGTCTACCCACCAAGAGGCTTCTGGCCCATGCC	1020
Db	1113	CCGATACTCTGTTTGGCCAAAGGGT	CCGTCTACCCACCAATGAAGGCTTCTGGCCCGTGCC	1172
Qy	1021	GAGAGTCTGGCAATTCAGAAATGT	CAGCACTGTGAGCTTGTGGCGCTCTGTTTCTCTCCC	1080
Db	1173	GCGAGTCTGGCAATTCAGAAATGT	CAGCACTGTGAGCTTGTGGCGCTCTGTTTCTCTCCC	1232
Qy	1081	ACCCCCACTTTTACAACCCCGAC	CCCTGTGTGTGCAGAAAGCTGTTCTTGGTCTGAACCCCTA	1140
Db	1233	AGCCCCACTTCTACAATGCTGAC	CCCCGTGTGTGCAGAAAGCTGTTCTTGGTCTGAACCCCTG	1292
Qy	1141	ACCCAAAGGAGCAATCTTGTTCCT	AGACATCCATCCGGTCACTGGGATCCCATGAACT	1200
Db	1293	ACCCAAAGGAGCAATCTTGTTCCT	AGACATCCACCCGGTCACTGGGATCCCATGAACT	1352
Qy	1201	GTTCTGTGAAGATCAGCTGAGCTCT	CTACATCAAAATCTGTCAAGGGGCATCGGGCAACAACAG	1260
Db	1353	GTTCCGTGAAGATCAGCTGAGCT	CTGTACATCAAAATCCGTCAAGGGGCGTGGGGCAACAACAG	1412
Qy	1261	GGAAAGTCGAGCCAGTAGTTCG	CCGTTCTGCTGGTTTCGAACGAGCGGAGCAATGGGGTG	1320
Db	1413	GGAAAGTCGAGCCAGTAGTTCG	CCGTTCTGCTGGTTTCGAACGAGCGGAGTATGGGGTG	1472
Qy	1321	GCAAGCCCTGAGCAGGTTCTPAC	ACGAGCTGGTGTGATGCCCCAGGTTCTTTCACCTACG	1380
Db	1473	GCAAGACCCCTGAACACGTTCTPAC	ACGAGCTGGTGTGATGCCCCAGGTTCTTTCACCTACG	1532
Qy	1381	CGCAGTATGTCTGCTGGGGCTT	CGAGCCCTCTGCTCTTGGTGCCCATCATTTTACCAAC	1440
Db	1533	CGCAGTATGTCTGCTGGGGCTT	CGAGCCCTCTGCTCTTGGTGCCCATCATTTTACCAAC	1592
Qy	1441	TGCGAGCCAGGAGAAATGCTTTT	TTGTTTGGAGTGTGTAGTAAAAAAGGCTCCACAGATA	1500
Db	1593	TGCGCAGCCAGGAGAAATGCTTTT	TTTATTTTGGAGTGTGTAGTAAAAAAGGCTCGCAGATA	1652

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 17:45:57 ; Search time 7281.38 Seconds
 (without alignments)
 11469.657 Million cell updates/sec

Title: US-08-765-108-7
 Perfect score: 1785
 Sequence: 1 CCGTCTCTTCAGGTCTTGA.....TCAGGACACGGACAGACC 1785

Scoring table: IDENTITY NUC
 Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_hic.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_est7.*
- 9: gb_ges1.*
- 10: gb_ges2.*
- 11: gb_ges3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	2441	4	AK033114 Mus muscu
2	1785	100.0	2497	4	AK028191 Mus muscu
3	1513.8	84.8	2310	4	AK010622 Mus muscu
4	1364	76.4	1364	10	AY412682 Mus muscu
5	959	53.7	2751	4	BC022087 Homo sapi
6	957.4	53.6	2515	4	CR607701 full-leng
7	941.6	52.8	1364	10	AY412680 Homo sapi
8	852.4	47.8	902	5	BUS17714 AGENCOURT
9	821.4	46.0	879	3	BI651436 603298176
10	802.2	44.9	979	5	BQ917716 AGENCOURT
11	802.2	44.9	1364	10	AY412681 Pan trogl
12	790.8	44.3	907	2	BI218548 602938062
13	763.2	42.8	838	2	BG970988 602920227
14	758.2	42.5	987	3	BI410841 602963757
15	734.4	41.1	883	3	BI854754 603381709
16	732.8	41.1	814	2	BI249128 602992465
17	728.4	40.8	766	3	BI330909 602983203
18	719.8	40.3	802	2	BI159464 602919988
19	716.6	40.1	765	7	CK031774 AGENCOURT
20	708	39.7	792	7	CK128415 AGENCOURT
21	700.2	39.2	837	3	BI872207 603396535
22	693.6	38.9	824	2	BG921302 602824148

ALIGNMENTS

23	689.2	38.6	794	3	BI327672	BI327672 602979182
24	683.2	38.3	704	7	CO432282	CO432282 UI-M-HX0-
25	681	38.2	918	5	BQ947347	BQ947347 AGENCOURT
26	670.8	37.6	1088	3	BM553238	BM553238 AGENCOURT
27	656	36.8	842	3	BI663520	BI663520 603287994
28	652.4	36.5	835	2	BF235778	BF235778 602026938
29	651.4	36.5	740	2	BI079037	BI079037 602873305
30	644.8	36.1	830	2	BG519503	BG519503 602577778
31	640.4	35.9	643	1	AI323064	AI323064 mj57c02.Y
32	638	35.7	771	1	AI037085	AI037085 uel9b11.Y
33	635.6	35.6	909	2	BF533326	BF533326 602073786
34	634.2	35.5	753	2	BI145538	BI145538 602910547
35	630.4	35.3	655	8	CK220978	CK220978 MNS36731
36	627.8	35.2	819	7	CK023231	CK023231 AGENCOURT
37	625.8	35.1	723	2	BG965924	BG965924 602829714
38	623.2	34.9	968	5	BQ877329	BQ877329 AGENCOURT
39	620.4	34.8	728	7	CO425633	CO425633 UI-M-HU0-
40	616.4	34.5	618	7	CF900992	CF900992 A0322E06-
41	616.4	34.5	618	7	CF901018	CF901018 A0322H01-
42	612.4	34.3	636	3	BI328695	BI328695 602984633
43	606.8	34.0	719	3	BI332830	BI332830 602985640
44	604.8	33.9	913	5	BO670423	BO670423 AGENCOURT
45	601.2	33.7	661	2	BF151308	BF151308 uz14f08.Y

AK033114	2441 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	Mus musculus 15 days embryo male testis cDNA, RIKEN full-length			
DEFINITION	enriched library, clone:8030433C21 product:scavenger receptor class B1, full insert sequence.			
ACCESSION	AK033114	GI:26328836		
VERSION	AK033114.1	GI:26328836		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
PUBMED	10349636			
REFERENCE	1			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Suni, N., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Konno, H., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ogawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
PUBMED	11076861			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research			

TITLE	Group Phase I & II Team.			
	Analysis of the mouse transcriptome based on functional annotation			
JOURNAL	of 60,770 full-length cDNAs			
	Nature 420, 563-573 (2002)			
REFERENCE	6 (Bases 1 to 2441)			
	Adachi, J., Aizawa, K., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.			
JOURNAL	Direct Submission			
	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-ree@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)			
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.			
	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. .2441			
FEATURES	source			
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	polyA_site			
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	Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1785; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
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61	GCTCCAGGGCGCGCTGGGTGGCCCTTGGGGTGGGGCCCTTGGGGCTGCTGTTTGTCTGGC	120
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1108	GAGAGTCTGGCATTCAGAAATGTCAGACCTGACAGGTTTGGTGGCCCTCTCTGTTCTCTCCC	1167
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Db 628 TCACATGGGCGACGCTGCTTTTATGAACCGCACAGTTTGTGTGAGATCCTGTGGGCTATG 687
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Qy 841 CCTTCATGACACCCGAATCTCGTGGTGAATTTCTTACGCCGGAGGATGACAGTTCATGA 900
Db 928 CCTTCATGACACCCGAATCTCGTGGTGAATTTCTTACGCCGGAGGATGACAGTTCATGA 987
Qy 901 AGCTGACTACAAGCAATCAAGGGTGTGTGAAGGCATTTCCACATGCTCGTTCACGGGCC 960
Db 988 AGCTGACTACAAGCAATCAAGGGTGTGTGAAGGCATTTCCACATGCTCGTTCACGGGCC 1047
Qy 961 CCGATACTCTGTTTGCACCAAGGGTCCGTTACTACCCACCAAGAGGCTTCTGCCCATGCC 1020
Db 1048 CCGATACTCTGTTTGCACCAAGGGTCCGTTACTACCCACCAAGAGGCTTCTGCCCATGCC 1107
Qy 1021 GAGAGTCTGGCATTCAGAAATGTACGACCTGTGACAGTTTGTGGCCCTCTGTGTTCTCTCCC 1080
Db 1108 GAGAGTCTGGCATTCAGAAATGTACGACCTGTGACAGTTTGTGGCCCTCTGTGTTCTCTCCC 1167
Qy 1081 ACCCCCACTTTTACACGCGACCTGTGTTGTGTCAGAGCTGTGTTGTGTCGACCCCTA 1140
Db 1168 ACCCCCACTTTTACACGCGACCTGTGTTGTGTCAGAGCTGTGTTGTGTCGACCCCTA 1227
Qy 1141 ACCCAAGGAGCATTCCTTGTCTTAGACATCCATCCGTCACCTGGGATCCCATGAAC 1200
Db 1228 ACCCAAGGAGCATTCCTTGTCTTAGACATCCATCCGTCACCTGGGATCCCATGAAC 1287
Qy 1201 GTTCTGTGAAGATGACGTAGCTCTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1260
Db 1288 GTTCTGTGAAGATGACGTAGCTCTACATCAAAATTTGTCAAGGGCATCGGGCAACAG 1347
Qy 1261 GGAAGATCGAGCCAGTAGTTCTGCGCTGTGTCGTTTGTGACAGCGGAGCAATGGGTG 1320
Db 1348 GGAAGATCGAGCCAGTAGTTCTGCGCTGTGTCGTTTGTGACAGCGGAGCAATGGGTG 1407
Qy 1321 GCAAGCCCTTGAGCAGCTTTTACACGAGCTGTGTCGATGCCCGCAGGCTTCTCACTACG 1380
Db 1408 GCAAGCCCTTGAGCAGCTTTTACACGAGCTGTGTCGATGCCCGCAGGCTTCTCACTACG 1467
Qy 1381 CGCAGTATGTCGTCGCGGCTTGAGGCTCTCTGTTGTCGTCGTCGTCGTCGTCGTCGTCG 1440
Db 1468 CGCAGTATGTCGTCGCGGCTTGAGGCTCTCTGTTGTCGTCGTCGTCGTCGTCGTCGTCG 1527
Qy 1441 TGCCAGCCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
Db 1528 TGCCAGCC----- 1536
Qy 1501 AGGAGGCCATTTCAGGCCCTACTCTTGATGTCCTGATGTCAACAGCTGCAAGGGCAGCGTGC 1560
Db 1537 ----- 1536
Qy 1561 TGCAGAGGCCAAGCTATAGGGTCTGTGAAGACACTATTAAGCCCCCCCCAAACCTGTAGCTT 1620
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Qy 1621 GGTGACACGAGCACCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1680
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Qy 1681 CCACCAAGTCCATGGCTGAGCCCCCAGATGTACACCTGTTCGACACGACGCACATGG 1740
Db 1639 CCACCAAGTCCATGGCTGAGCCCCCAGATGTACACCTGTTCGACACGACGCACATGG 1698
Qy 1741 ATGCCACGATGTGCAGAAACAACTCAGGACCAGGACAGACC 1785
Db 1699 ATGCCACGATGTGCAGAAACAACTCAGGACCAGGACAGACC 1743

RESULT 4
AY412682 1364 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus SCAR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY412682
VERSION AY412682.1 GI:39768647
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1364)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1364)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1364
/genes="SCAR1"
/locus_tag="HCM4638"

gene
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Query Match 76.4%; Score 1364; DB 10; Length 1364;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 ATGTGGAAGGAGATCCCGTCCCTTTCTACTTGTCTGTCTACTTCTTCTGCTGTCTTCTTCTG 272
Db 1 ATGTGGAAGGAGATCCCGTCCCTTTCTACTTGTCTGTCTACTTCTTCTGCTGTCTTCTTCTG 60
Qy 273 CCAAAAGAGTCTCAACGGCCAGAACCCAGTAGTCGGGAGCGTGACCCCTATGCTAC 332
Db 61 CCAAAAGAGTCTCAACGGCCAGAACCCAGTAGTCGGGAGCGTGACCCCTATGCTAC 120
Qy 333 AGGGAGTTGACAGAAAGGTCAACATCCTTCAATGACAAACACCCGTCCTTCGTCG 392
Db 121 AGGGAGTTGACAGAAAGGTCAACATCCTTCAATGACAAACACCCGTCCTTCGTCG 180
Qy 393 GAGAACCGCAGCCTCCATTTTCCAGCCTGACAGTCGATGGCTCAGAGAGTACTACATT 452
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[illegible]

Db	1261	AGTGGTAGTAAAGGGCTCCAGGATTAAGAGGCGCAATTCAGGCGTACTCTGAGTCCCTG	1322
QY	1533	ATGTACACAGCTGCCAAGGGCACGGTGCTGCAAGAGCCAAAGCT	1576
Db	1321	ATGTACACAGCTGCCAAGGGCACGGTGCTGCAAGAGCCAAAGCT	1364
RESULT 5	BC022087	2751 bp mRNA linear	HTC 01-APR-2004
LOCUS	HTC	Homo sapiens scavenger receptor class B, member 1, mRNA (CDNA clone IMAGE:3010672), with apparent retained intron.	
DEFINITION	BC022087	HTC.	
ACCESSION	BC022087.1	GI:18314599	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBLISHED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
FEATURES			
source			

ORIGIN		/plasmid="pCMVSPORT_6"
Query Match		53.6%; Score 957.4; DB 4; Length 2515;
Best Local Similarity		79.1%; Pred. No. 1.6e-242;
Matches 1138; Conservative		0; Mismatches 301; Indels 0; Gaps 0;
Qy	14	GTCTGAGCCCGAGAGCCCTTCCGCGACGCGGACATGCGGCGGACGCTCAAGGGGCGG 73
Db	161	GCCCTGCGAGCGCGGGTGGGCGCCCGAGCGCGGACACATGCGCTGCTCCGCGCAAGCGG 220
Qy	74	CTGGGTGCGCTTGGGGTGGGGCCCTCGGGGCTGCTTTTCTGCGCTCGGGTGTGAT 133
Db	221	CTGGGCTGCCGGGGGCGCTGGGGGCTGCGGGGGTACTGTGCGCTGTGCTGGGCGCTGTCAT 280
Qy	134	GATCTCTATGTGTCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTCGCGATAGACCC 193
Db	281	GATCGTATGTGCGCTCGCTCATCAAGCAGCAGGTCTTAAAGAACGTGCGCATGACGCC 340
Qy	194	GAGCAGCCTGTCTTTCGGGATGTGGAAGGAGATCCCGTCCCTTTCTACTTGTCTGTCTA 253
Db	341	CAGTAGCCTGTCTTCAACATGTGGAAGGAGATCCCTATCCCTTCTATCTCTCGCTCTA 400
Qy	254	CTTCTTCAAGTGTTCACCCCAAGCAGGTCTTCAAGGAGTCAACATCACCTTCAATGACAA 313
Db	401	CTTCTTCAAGTGTTCACCCCAAGCAGGTCTTCAAGGAGTCAACATCACCTTCAATGACAA 460
Qy	314	CGGTGACCTGTCTACAGGAGTTCAGACAAAGGTCAACATCACCTTCAATGACAA 373
Db	461	CGCGGGCCCTACGTGTACAGGAGTTCAGGACAAAGGACATCACCTTCAACAAACA 520
Qy	374	CGACACCGTGTCTTTCGTGGAGAACCGCAGCGCTCCATTTCCAGCGCTGACAAAGTCGCGATG 433
Db	521	CGACACCGTGTCTTTCGTGGAGAACCGCAGCGCTCCATTTCCAGCGCTGACAAAGTCGCGATG 580
Qy	434	CTCAGAGTGAATCATATGTAATGCTACGCTTCAACATCTTGTGCTCTGGGGGCTCGATTTGAT 493
Db	581	CTCGAGAGCGACTACATCGTCTATGCCCAACATCTCTGCTTGGGTGCGGGGCTGATGAT 640
Qy	494	GGAGAGCAAGCTGTGAGCGCTTGAAGCTGATGACCTTGGCGCTGGTCCACCATGGGCA 553
Db	641	GGAGATAGCCCATGACCTTGAAGCTGATGACCTTGGCGCTGGTCCACCATGGGCA 700
Qy	554	CGGTCTTTTATGAACCGCACAGTGTGTGAGATCCTGTGGGGCTATGACGATCCCTTCTGT 613
Db	701	ACGTGCTTTCATGAACCGCACAGTGTGTGAGATCCTGTGGGGCTATGACGATCCCTTCTGT 760
Qy	614	GCATTTCTCAACAGTACCTCCGAGCATGCTTCCCATAAAGGGCAATTTGGCGCTGTT 673
Db	761	GAATCTCATCAACAGTACTTTCCAGGCATGTTCCCTTTCAAGGACAAAGTTCCGATATT 820
Qy	674	TGTTGGGATGAACACTCGAATCTTGGGGTCTTCACTGCTTTCAGGGCGTCCAGAAATT 733
Db	821	TGCTGAGTCAACAACTCCGACTTGGGGCTTTCACGGTGTTCAGGGGGTCCAGAACT 880
Qy	734	CAGCAGGATCCATCTGTGTGACAAATGGAACGGACTCAGCAAGATTCGATTTATGCGATTC 793
Db	881	CAGCAGGATCCATCTGTGTGACAAATGGAACGGGCTGAGCAAGTGTGATCTTGGCATTC 940
Qy	794	AGAGCAGTGTAAATGATCAATGGGACTTTCGGGCGAGATGTTGGGACCTCTTCATGACACC 853
Db	941	CGATCAGTGCACATGATCAATGGAATCTTCTGGGCAAAATGTGGCGCCCTTCATGACTCC 1000
Qy	854	CGAATCTCTGCTGGAAATCTTTCAGCCCGGAGCATGCAAGTCCATGAAGCTGACCTACAA 913
Db	1001	TGAGTCTCTGCTGGAGTCTTACAGCCCGGAGGCTTCCGATCTCCATGAAGCTAAATGACAA 1060
Qy	914	CGAATCAAGGGTGTGTTGAAGGATTCACCAAGTATCGCTTTCAGGGCCCGGCTACTCTGTT 973
Db	1061	GGAGTCAGGGTGTGTTGAAGGATTCACCAAGTATCGCTTCTGCTTCCGCTCCCAAAACCTGTT 1120
Qy	974	TGCCAACGGGTCTGTTTACCAACCAAGAGGCTTCTGCCCATGTCGCGAGAGTCTGGCAT 1033

Db	1121	TGCCAACGGGTCCATCTATACCCACCAACGAAAGGCTTCTGCGCGTGTGGAGTCTGGAAT 1180
Qy	1034	TCAGAATGTGAGCACCTGCGAGTTGTGGCGCTCTCTTTCTCTCCACCCCACTTTTA 1093
Db	1181	TCAGAAGTGTGAGCACCTGCGAGTTGTGGCGCTCTCTTTCTCTCCCACTCTCACTTCT 1240
Qy	1094	CAACGCCGACCTGTGTGTGTCAGAACTGTTCTTGGTGTGAACCTTAACCAAGAGGACA 1153
Db	1241	CAACGCTGACCCGGTCTTGGCAGAAAGCGTGACTGGCGTGCACCTTAACAGAGGAGACA 1300
Qy	1154	TTCTCTGCTTCTAGACATCCATCCGCTCAGTGGGATCCCATGAATCTGTTCTGTGAAGAT 1213
Db	1301	CTCTCTGCTTCTAGACATCCATCCGCTCAGTGGGATCCCATGAATCTGTTCTGTGAAGAT 1360
Qy	1214	GCAGTGAAGCTCTATACATCAAACTGTCAAGGGCATCGGCAACAGAGAGATCGAGCC 1273
Db	1361	GCAGTGAAGCTCTATACATCAAACTGTCAAGGGCATCGGCAACAGAGATCGAGCC 1420
Qy	1274	AGTAGTCTGCGGTGTGTGTTGAAACAGAGCGGAGCAATGGTGGCAAGCCCTGAG 1333
Db	1421	TGTGCTCTGCGGTGTGTGTTGAAACAGAGCGGAGCAATGGTGGCAAGCCCTGAG 1480
Qy	1334	CAGCTTCTACAGCAGCTGTGTGATGCCCGAGTCTTCTACCTACGCGCAGTATGTCT 1393
Db	1481	CACATTTACACTCAGCTGTGTGATGCCCGAGTCTTCTACCTACGCGCAGTATGTCT 1540
Qy	1394	GCTGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCCATCATCTGCCAACTGCGCAGCAGG 1452
Db	1541	CCTGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCCATCATCTGCCAACTGCGCAGCAGG 1599

RESULT 7	AV412680	1364 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AV412680				
DEFINITION	Homo sapiens SCARBI gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AV412680				
VERSION	AV412680.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Fanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2. (bases 1 to 1364)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Fanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
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Query Match 52.8%; Score 941.6; DB 10; Length 1364;
Best Local Similarity 80.6%; Pred. No. 2.2e-238;
Matches 1100; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy	213	ATGTGGAAGGAGATCCCGTCCCTTTCTACTTGTCTGTCTACTTCTTTCGGAAGTGGTCAAC	272
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Qy	273	CCAAACGAGGTCCTCAACGGCCAGAAGCAGTAGTCCGGGAGCGTGACCCCTATGTCTAC	332
Db	61	CCCAGCAGATCTCTGAAGGGGAGAAGCCGAGGTGGGGAGCGCGGCCCTACGTGTAC	120
Qy	333	AGGAGGTTTCAGACAAAGAGTCAACATCACCTTTCAATGACACACGACCGGTCTTCGTG	392
Db	121	AGGAGTTTCAGGCACAAAGCAACATCACCTTTCAACACAAACGACACCGTGTCTTCTC	180
Qy	393	GAGAACCGCAGCCTCCATTTCCAGCCTGACAAAGTCGCAATGGCTCAGAGAGTACTACAT	452
Db	181	GAGTACCGCACCTTCCAGTTCCAGCCCTCCAAAGTCCCAAGCTCCGAGAGCGACTACATC	240
Qy	453	GTACTGTCTACATCTTGGTCTCTGGGGGCTCGATATTGATGGAGACCAAGCTGTGAGC	512
Db	241	GTATGCCCAACATCTCTGGTCTTGGGTGGCGGTGATGATGGAGATAAGCCCATGACC	300
Qy	513	CTGAAGCTGATGATGACCTTGGCGCTGGTCAACATGGGCCAGCGTGTCTTTATGAACCGC	572
Db	301	CTGAAGCTCATCATGACCTTGGCATTCACACCCCTCGCGGAAGTGTCTTCATGAACCGC	360
Qy	573	ACAGTTGTGATGATCTGTGGGGCTATGACGATCCCTCTGTGCAATTTTCTCAACACGTAC	632
Db	361	ACTGTGGTGTGATCATGTGGGGGTACAAAGGACCCCTTGTGAATCTCATCAACAAGTAC	420
Qy	633	CTCCACAGATGCTTCCCATAAAGGGCAAAATTTGGCTGTGGTGGATGAACAACTCG	692
Db	421	TTTCCAGCATGTTCCCTCTCAAGBACAAGTTCGGATTTTGTGAGCTCAACACTCC	480
Qy	693	AAATCTGGGGTCTTCACTGTCTTCAACGGGGTCCAGAAATTTTTCAGCAGATCCATCTGGT	752
Db	481	GACTCTGGGCTCTTCAAGGTGTTCACGGGGTCCAGAACATCAGCAGGATCCACCTCGT	540
Qy	753	GACAAATGAACGGAATCAGCAAGATGATTAATTTGGCAATTCAGAGCATGTAAATGATC	812
Db	541	GACAAGTGAACGCGGCTGAGCAAGGTTGACTTCTGGCATTCGGATCAGTGAACATGATC	600
Qy	813	AATGGGATCTCCGGGAGATGTGGGACCTTTCATGACACCCGAATCTCGCTGGAATTC	872
Db	601	AATGGAATCTTGGGCAAAATGTGGCCCTTCAAGTACTCTGAGTCTCTGCTGGAGTTC	660
Qy	873	TTACGCCGGAGGATGAGGTCCATGAAGCTGACCTACACGAATCAAGGGTGTGAA	932
Db	661	TACAGCCGGAGGCTGCGGATCCATGAGCTAATGTACAAGGATCAGGGGTGTTGAA	720
Qy	933	GGCATTTCCAGATATGCTTCAACGGCCCCGATATCTCTGTTTGGCAACGGGTCCGTCTAC	992
Db	721	GGCATCCCCACATATCTGCTGTGGCTCCCAAAACCTGTTTGGCAACGGGTCCATCTAC	780
Qy	993	CCACCCACGAAGGCTTCTGCCATCGCAGAGTCTGCAATTCAGATGTCAAGCACTTCG	1052
Db	781	CCACCCACGAAGGCTTCTGCCGCTGCTGGAGTCTGGAATTCAGAACGTCAGCACCTTCG	840
Qy	1053	AGGTTTGTGTGGCTCTGTTTCTCTCCACCCCACTTTTCAACGCGGACCTGTGTG	1112
Db	841	AGGTTTCACTGCCCCCTGTTTCTCTCCCATCTCTCACTCTCTCAACGCGGACCGGTTCTG	900
Qy	1113	TCAGAGCTGTTTCTGTTCTGAACCTTCAACCAAGGAGCATCTCTGTTTCTCTAGACATC	1172
Db	901	GCAGAAGCGGTGACTGGGCTTCACCTTAAACAGGAGGACACTCTCTGTTCTCTGAGATC	960
Qy	1173	CATCGGTCATCTGGATCCCATGAATCTGTTCTGTGAAGTCAAGCTGAGCTCTACATC	1232
Db	961	CACCGGTTCAGGGNAATCCCATGAATCTCTGTGAATCTGAGCTGAGCTCTACATG	1020
Qy	1233	AAATCTGTCAAGGGCATCGGGCAAAACAGGGAAGATCGAGCCAGTAGTTCTGCGCGTGTG	1292

Db	1021	AAATCTGTGCGAGCATTTGGACAAATCGGCAAGATTGAGCCTGTGTCTCTGCGCTGCTC	1080
Qy	1293	TGCTTTCGAACAGAGCGGAGCAATGGGTGGCAAGCCCTGAGCAGCTTCTACAGCAGCTG	1352
Db	1081	TGCTTTCGAAGAGAGCGGGCCCATGGAGGGGAGACTCTTTCACACATTTCTACATCAGCTG	1140
Qy	1353	GTCTCATGCCCCAGAGTCTTTCACACTACGGCGAGTATGTGTCTGCGGCTTGGAGGCGCTC	1412
Db	1141	GTGTTGATGCCAAGGTGATGCACTATGCCAGTAGCTCTCTGCGCTGGGCTGGGCTC	1200
Qy	1413	CTGTTCTGTGTCCTCATCTGCCCCATCTGCCAACTGCGCAGCAGGAGAAATGCTTTTGTG	1472
Db	1201	CTGCTGTGCTGCTCTGCTATCTGCTCCAAATCCGAGGCCAAGAGAAATGCTATTATTG	1260
Qy	1473	AGTGTGATGATAAAGGGTCCAGAGTAAGGAGGCCATTCAGGCGCTACTCTGAGTCCCTG	1532
Db	1261	AGTAGTAGTAAAGGGCTCAAGAGTAAGGAGGCCATTCAGGCGCTATTCTGAATCCCTG	1320
Qy	1533	ATGTCACAGCTGCCAAGGGCACGGTGTGCTGCAAGAGCCAAAGCT	1576
Db	1321	ATGACATCAGCTCCCAAGGGCTCTGTGCTGCGAGGAAGCAAACT	1364

RESULT 8
BU517714
LOCUS
DEFINITION
AGENCOURT_10165932 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6515330 5', mRNA sequence.

ACCESSION
BU517714
VERSION
BU517714.1 GI:22825240
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 902)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL4092 Row: b column: 03
High quality sequence stop: 700.

FEATURES
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Location/Qualifiers
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/strain="FVB/N-3"
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/clone="IMAGE:6515330"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
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/clone_lib="NCI_CGAP Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 47.8%; Score 852.4; DB 5; Length 902;
Best Local Similarity 99.7%; Pred. No. 9.5e-215;
Matches 864; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy 480 GGCTCGATATTGATGGAGCAAGCTCTGAGCCTTGAAGCTGATGATCACTTGGCGCTG 539
Db 61 GGCTCGATATTGATGGAGCAAGCTCTGAGCCTTGAAGCTGATGATGATGATGATGATG 120
Qy 540 GTCACCATGGCCAGCGTCTTTATGAAACCGACAGTTGGTGAGATCTTGGGGCTAT 599
Db 121 GTCACCATGGCCAGCGTCTTTATGAAACCGACAGTTGGTGAGATCTTGGGGCTAT 180
Qy 600 GAAGATCCCTTCTGTCATTTCTCAACAGTACCTCCAGACATGCTTCCATAAGGGC 659
Db 181 GAAGATCCCTTCTGTCATTTCTCAACAGTACCTCCAGACATGCTTCCATAAGGGC 240
Qy 660 AAATTTGGCCCTGTTGTTGGGATGAACAACCTCGAATCTGGGCTTCCACGTCTTCAAG 719
Db 241 AAATTTGGCCCTGTTGTTGGGATGAACAACCTCGAATCTGGGCTTCCACGTCTTCAAG 300
Qy 720 GCGTCCAGAAATTTAGCAGGATCCATCTGGTGGCAAAATGGAACGGACTCAGCAAGATC 779
Db 301 GCGTCCAGAAATTTAGCAGGATCCATCTGGTGGCAAAATGGAACGGACTCAGCAAGATC 360
Qy 780 GATTATTGGCAATTCAGACGAGTGAACATGATGAGACTTCGGGCGAGATGGGCA 839
Db 361 GATTATTGGCAATTCAGACGAGTGAACATGATGAGACTTCGGGCGAGATGGGCA 420
Qy 840 CCCTTCATGACACCGAATCTCGTGAATTTCTTCCGCGGAGGATGAGTCCATG 899
Db 421 CCCTTCATGACACCGAATCTCGTGAATTTCTTCCGCGGAGGATGAGTCCATG 480
Qy 900 AAGCTGACCTCAACGAATCAAGGGTGTGTTGAAGGCAATTCACAGTATCGCTTCAAGGCC 959
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Db 541 CCCGATCTCTGTTGCGCAACGGTCCGCTTACCCACCAAGAGGCTTTCGCCATG 600
Qy 1020 CGAGATCTGCGCATTCAGATGTCAGACCTGCGAGTTGTTGGTGGCCTCTGTTCTCC 1079
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Qy 1080 CACCCCACTTTTACACCGCCAGCCCTGTGTTGTCAGAAAGCTGTTCTGGTCTGAACCT 1139
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Qy 1140 AACCCAAAGAGCATCTCTGTTCTAGACATCCATCCGGTCACTGGGATCCCATGAAC 1199
Db 721 AACCCAAAGAGCATCTCTGTTCTAGACATCCATCCGGTCACTGGGATCCCATGAAC 780
Qy 1200 TGTCTGTGAGATGACAGTCTGAGCTCTACATCAAAATCTGTCAAGGGCATC- GGGCAAC 1258
Db 781 TGTCTGTGAGATGACAGTCTGAGCTCTACATCAAAATCTGTCAAGGGCATC- GGGGCAAC 840
Qy 1259 AGGGAAGATCGAGCCAGTGTCTGCCC 1285
Db 841 AGGGAAGATCGAGCCAGTGTCTGCCC 867

RESULT 9
BI651436
LOCUS
DEFINITION 603298176F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5338795 '5',
mRNA sequence.
ACCESSION BI651436
VERSION BI651436.1 GI:15565672
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 879)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1860 row: 9 column: 20
High quality sequence stop: 819.

FEATURES
source

Location/Qualifiers
1..879
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:5338795"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

ORIGIN

Query Match 46.0%; Score 821.4; DB 3; Length 879;
Best Local Similarity 98.8%; Pred. No. 1.6e-206;
Matches 870; Conservative 0; Mismatches 6; Indels 5; Gaps 4;
Qy 772 GCAAGATCGATTATTGGCATTTCAGAGCAGTGTACATGATCAATGGGACTTCCGGGAGA 831
Db 1 GCAAGATCGATTATTGGCATTTCAGAGCAGTGTACATGATCAATGGGACTTCCGGGAGA 60
Qy 832 TGTGGGCACTCTTCATGACACCCGAATCTCGCTGGAAATCTTCAGCCCGGAGGCGATGCA 891
Db 61 TGTGGGCACTCTTCATGACACCCGAATCTCGCTGGAAATCTTCAGCCCGGAGGCGATGCA 120
Qy 892 GGTCCATGAAGTGAACCTACAAAGATCAAGGGTGTGTTGAAGGCAATTCACACGTATCGCT 951
Db 121 GGTCCATGAAGTGAACCTACAAAGATCAAGGGTGTGTTGAAGGCAATTCACACGTATCGCT 180
Qy 952 TCAGGGCCCGGATACCTCTGTTGCCAAGCGGTCCGTCTACCCACCCCAAGGCTTCT 1011
Db 181 TCAGGGCCCGGATACCTCTGTTGCCAAGCGGTCCGTCTACCCACCCCAAGGCTTCT 240
Qy 1012 GCCCATGCCAGAGTCTGGCAATTCAGAAATGTCAGACCTGTCAGGTTTGGTGGCGCTCTGT 1071
Db 241 GCCCATGCCAGAGTCTGGCAATTCAGAAATGTCAGACCTGTCAGGTTTGGTGGCGCTCTGT 300
Qy 1072 TTCTCTCCCAACCCCACTTTTACAAAGCCCAAGCCCTGTGTTGTTCAGAAAGCTGTTCCTGGTC 1131
Db 301 TTCTCTCCCAACCCCACTTTTACAAAGCCCAAGCCCTGTGTTGTTCAGAAAGCTGTTCCTGGTC 360
Qy 1132 TGAACCTTACCCAAAGAGCATTTCTGTTGCTTACATCATCCATCCCGTCACTGGGATCC 1191
Db 361 TGAACCTTACCCAAAGAGCATTTCTGTTGCTTACATCATCCATCCCGTCACTGGGATCC 420
Qy 1192 CCATGAAGTGTCTGTGAAGATGAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATCG 1251
Db 421 CCATGAAGTGTCTGTGAAGATGAGCTGAGCCTCTACATCAAAATCTGTCAAGGGCATCG 480
Qy 1252 GGCAACAGGGGAAGATCGAGCCAGTAGTCTCGCGTGTGCTGTGTGTCGAACAGAGCGGAG 1311
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1 (bases 1 to 1364)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1364)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
1..1364
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1364
/gene="SCARB1".
/locus_tag="HCM4638"

gene

ORIGIN

Query Match 44.9%; Score 802.2; DB 10; Length 1364;
Best Local Similarity 69.5%; Pred. No. 2.3e-201;
Matches 948; Conservative 0; Mismatches 416; Indels 0; Gaps 0

QY 213 ATGTGAAGAGATCCCCCTTCTACTTGTCTGTCTACTTCTTCTGAGAGTGGTCAAC 277
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QY 273 CCAAACGAGTCTCTCAACGGCCAGAGCCAGTAGTCCGGGACGCTGGACCTTGTCTAC 333
DB 61 CCACGCGAGTCTGAAGGGCGGAAAGCCGAGGTCCGGACGCGGGCCCTTCTGTAC 120

QY 333 AGGAGTTTCAGACAAAGGTCAACATCACCTTCAATGACAAACGACACCGCTGTCTGTG 397
DB 121 AGGGAGTTTCAGGCACAAAGCAACATCACCTTCAACAAATGACACCGTGTCTTCTC 180

QY 393 GAGAACGGAGCTCTCAATTCAGCTTCAGATCGCATCGCTCAGAGATGACTACATT 457
DB 181 GAGTACCGCACCTTCAGTTCCAGCTCCAGCTCCCAAGTCCCAAGGTCGAGAGGACTAC 243

QY 453 GTACTGCTTAAACATCTTGGTCTCTGGGGGCTCGATATTGATGGAGCAAGCTGTGAGC 511
DB 241 GTCATGCCCAACATCTGTCTTGGGTGGGGGTGATGATGAGAAATAGCCCATGACC 300

QY 513 CTGAAGCTGATGATGACCTTGGCGCTGGTCCACCATGGGCGACGCTGCTTTTATGAACCG 577
DB 301 CTGAAGCTCATCATGACCTTGGCATTCACACCTTCGGGCAAGCTGCTTTCATGAACCGC 360

QY 573 ACAGTTGGTGAGATCTGTGGGGCTATGACGATCCCTTCGTGCATTTTCTCAACACGTAC 633
DB 361 ACTGTGGGTGAGATCATGTGTGGGGCTACAAGGACCCCTTGTGAACCTCATCAACAAGT 421

QY 633 CTCCTCAGACATGCTCCCATAAAGGCAATTTGGCCTGTTTGGTGGATGACCAACTCG 697
DB 421 TTTTCCAGGCATGTCTCCCTTCAAGGACAAGTTCGGATATTTCGTGAGCTCAACACTCC 480

QY 693 AATTCTGGGCTCTTCACTGTCTTCAGGGCGTCCAGAAATTTTCAGCAGGATCCATCTCGTG 753
DB 481 GACNNNGGCTCTTCAAGTGTTCAGGGGGTCCAGAACATCAGCAGGATCCACCTCGTG 543

QY 753 GACAAATGGAACGGACTTCAGCAAGATCGAATTATGGCAATTCAGACGAGTGAACATGATC 813

[illegible]

Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1243 row: 1 column: 15
High quality sequence stop: 798.
Location/Qualifiers

1. 907
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_L49"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 44.3%; Score 790.8; DB 2; Length 907;
Best Local Similarity 94.8%; Pred. No. 2.2e-198;
Matches 861; Conservative 0; Mismatches 42; Indels 5; Gaps 4;

Qy 699 GGGGTCTTCACTGCTTTACGGGGCTCCAGAAATTCAGCAGATCCATCTGGTGACAAA 758
Db 1 GGGGTCTTCACTGCTTTACGGGGCTCCAGAAATTCAGCAGATCCATCTGGTGACAAA 60

Qy 759 TGGACCGACTCAGCAGATCGATTATTTGGCAATTCAGACGAGTGAATCAATGATCAATGGG 818
Db 61 TGGACCGACTCAGCAGATCGATTATTTGGCAATTCAGACGAGTGAATCAATGATCAATGGG 120

Qy 819 ACTTCCGGGAGATGTGGGACCTTTCATGACACCGCAATCTCTCGTGGAAATCTTCAGC 878
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Qy 879 CCGAGGCATCAGGTCCATGAAGCTGACCTTACCAAGCAATCAAGGGTGTGTAAGGCATT 938
Db 181 CCGAGGCATCAGGTCCATGAAGCTGACCTTACCAAGCAATCAAGGGTGTGTAAGGCATT 240

Qy 939 CCGAGTATCGCTTACGGCCCCCGATCTCTGTTGGCAAGGGTGGTCTACCCACC 998
Db 241 CCGAGTATCGCTTACGGCCCCCGATCTCTGTTGGCAAGGGTGGTCTACCCACC 300

Qy 999 AACGAAGGCTTCTGCCATCGCGAGAGTCTGGCAATTCAGATGTCAGCACCCTGAGGTTT 1058
Db 301 AACGAAGGCTTCTGCCATCGCGAGAGTCTGGCAATTCAGATGTCAGCACCCTGAGGTTT 360

Qy 1059 GGTGGCCTCTGTTTCTCTCCACCCCACTTTTACACGCGGACCTGTGTTCAGAA 1118
Db 361 GGTGGCCTCTGTTTCTCTCCACCCCACTTTTACACGCGGACCTGTGTTCAGAA 420

Qy 1119 GCTGTTCTGTGTGAACCCCTAACCCAAAGAGCAATTCCTTGTTCCTAGACATCCATCG 1178
Db 421 GCTGTTCTGTGTGAACCCCTAACCCAAAGAGCAATTCCTTGTTCCTAGACATCCATCG 480

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Qy 1239 GTCAAGGGCATCGGCAAAAGGGAAGATCGAGCAGTAGTTCCTGCCGTGCTGTGGTTC 1298
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Qy 1299 GAAACAGCGGAGCAATGGGTGGCAGCCCTTGAGCAGCTTCTACACGAGCTGGTGTG 1358
Db 601 GAAACAGCGGAGCAATGGGTGGCAGCCCTTGAGCAGCTTCTACACGAGCTGGTGTG 660

Qy 1359 ATG-CCCCAGGTTCTTCACTACCGCAGTATGTGCTGGGGCTTGGAGCCTCCTGTT 1417
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Qy 1418 GCTGGTGCCCATCATCTGCCAACTGCGCAGCCAGGAGAAATGCTTTTGTGGAGTGG 1477
Db 721 TGCTGGTGCCCATCATCTG-CAACTGGCGCAGCCAGGAGAAATGCTTTTGTGGAGTGG 779

Qy 1478 TA--GTAAAGAGGCTCCAGAGTAAAGAGGCGCATTCAGGCTACTCTGAGTCCCTGATG 1535
Db 780 TACGTGAAAAGGGCTCCAGGATAGCGAGCCATTCAGGCTACTCTGAGTCCCTGATG 839

Qy 1536 TCACCAAGCTCCCAAGGCGACGGTCTGCAAGAGCAAGCTATAGGCTCTCTGAAGACACT 1595
Db 840 TCCCAAGTTGCCAAGGGCGCGGTGGTCCCAAGAGCCAGGTATAGGG-CTTGAAGACACT 898

Qy 1596 ATAAGCCC 1603
Db 899 TTAGCCCC 906

RESULT 13
BG870988
LOCUS
DEFINITION
602792027F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923247 5', mRNA sequence.
ACCESSION
BG870988
VERSION
BG870988.1 GI:14221528
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
1 (bases 1 to 838)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10844 row: e column: 08
High quality sequence stop: 829.
Location/Qualifiers

1. 838
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_SG2"
/notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 42.8%; Score 763.2; DB 2; Length 838;
Best Local Similarity 97.2%; Pred. No. 4.6e-191;
Matches 819; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

Qy 614 GCATTTTCTCAACACGCTACCTCCAGACATGCTTCCCATAAAGGCAAAATTTGGCCTGTT 673
Db 1 GCATTTTCTCAACACGCTACCTCCAGACATGCTTCCCATAAAGGCAAAATTT--GGCCTGT 58

Qy 674 TGTGGATGAACAACACTCGAAATTTCTGGGGTCTTCACTGTCTTCAACGGGCGTCCAGAAATTT 733


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Db 481 GTCACTGGGATCCCATGAACCTGGTCTTGTGAAGATGCAGCTGAGCCCTACATCAAAATC 540
Qy TGTCAAGGGATCGGCAAAACAGAGGATGACGAGTGTCTGCGGTGCTGCTGTT 1297
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Db 601 CGAACAGAGCGGAGCAATGGGTGGCAAGCCCTGAGCACGTTCTACACGAGCTGGTGCT 660
Qy 1358 GATG-CGCCAGTTCCTACACGCGGATGATGCTGCTGGGCTTGGAGGCTCTCTGT 1416
Db 661 GATGCCCCAGTTCCTACACGCGGATGATGCTGCTGGGCTTGGAGGCTCTCTGT 720
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Db 721 TGCTGGTGGCCATCATCTGCCAAACTGCGAGCCAGGAGAAATGCTTTGCGAGTGGT 780
Qy 1476 GGTAGTAAAAAGGGCTCCAGGATAAGAGGCCAATTCAGGCGCTA---CTCTGAGTCCCTG 1532
Db 781 AGTA--AAAGGGTTCAGGATAAGAGGCCAATTCAGGCGCTACTTCTGAGTCCCTGTA 838
Qy 1533 ATGTCACAGCTGCAAGGGGCAACGGTGTGCAAGAACCAAGTATAGGCTCTTGAAGAC 1592
Db 839 TGTCCACAGCTGCAAGGGGCAACGGTGTGCAAGAACCAAGTATAGGCTCTTGAAGA 898
Qy 1593 ACTATAGCCCCCAACCTGATAGCTTGTGTCAGACGAGCCAGCTCCCTACACCCCG 1652
Db 899 AACCTATAGGCCCAAACTGATAGCTTGTGTCAGACGAGCCAGCTCCCTACACCCCG 958
Qy 1653 CTTCTTGA 1660
Db 959 CTTGAGGA 966
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RESULT 15
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LOCUS 603381709P1 NCI_CGAP_Mam6 Mus musculus cdna clone IMAGE:5387427 5',
DEFINITION 883 bp mRNA linear EST 10-OCT-2001
mRNA sequence.
ACCESSION BI854754
VERSION BI854754.1 GI:15995501
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11987
High quality sequence stop: 775.
Location/Qualifiers
1. 883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:538742"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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FEATURES

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source
1. 883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:538742"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/clone_lib="NCI_CGAP_Mam6"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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ORIGIN
Query: Match 41.1%; Score 734.4; DB 3; Length 883;
Best Local Similarity 96.1%; Pred. No. 2.1e-183;
Matches 786; Conservative 0; Mismatches 26; Indels 6; Gaps 3;
Qy 1 CCGTCTCTCTTCAGGTCTGAGCCCGAGAGCCCTTCCGCGCACGCGGACATGGCGGCA 60
Db 65 CCGTCTCTCTTCAGGTCTGAGCCCGAGAGCCCTTCCGCGCACGCGGACATGGCGGCA 124
Qy 61 GCTTCAGAGGGCGCTGGGTGGCCCTTGGGGTTGGGGCCCTTGGGGCTGCTGTTTGTGCGC 120
Db 125 GCTTCAGAGGGCGCTGGGTGGCCCTTGGGGTTGGGGCCCTTGGGGCTGCTGTTTGTGCGC 184
Qy 121 TCGGCGTTGTCATGATCCCTCATGTCCTCCCTCATCAAGCAGCAGGTCTCAAGAATG 180
Db 185 TCGGCGTTGTCATGATCCCTCATGTCCTCCCTCATCAAGCAGCAGGTCTCAAGAATG 244
Qy 181 TCGGCGATAGACCCGAGCAGCCTGCTCTTCCGGGATGTGGAGAGATCCCGTCCCTTTCT 240
Db 245 TCGGCGATAGACCCGAGCAGCCTGCTCTTCCGGGATGTGGAGAGATCCCGTCCCTTTCT 304
Qy 241 ACTTGTCTGTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCAACGCGCAGAAC 300
Db 305 ACTTGTCTGTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCAACGCGCAGAAC 364
Qy 301 CAGTAGTCCGGGAGCGTGGACCCCTATGCTACAGGGAGTTTCAGACAAAGGTCAACATCA 360
Db 365 CAGTAGTCCGGGAGCGTGGACCCCTATGCTACAGGGAGTTTCAGACAAAGGTCAACATCA 424
Qy 361 CTTTCAATGACAAACGACACACCGTGTCTTTCGTGGAGAACCCGAGCTCCATTTCCAGCGT 420
Db 425 CTTTCAATGACAAACGACACACCGTGTCTTTCGTGGAGAACCCGAGCTCCATTTCCAGCGT 484
Qy 421 ACAAGTCCGATGCTCAGAGAGTGATACATTTGATGTCCTTAAACATCTTGGTCTTGGGG 480
Db 485 ACAAGTCCGATGCTCAGAGAGTGATACATTTGATGTCCTTAAACATCTTGGTCTTGGGG 544
Qy 481 GCTCGATATTGATGGAGAGCAAGCCCTGTGAGCCTGAGCTGATGATGACCTTGGCGCTGG 540
Db 545 GCTCGATATTGATGGAGAGCAAGCCCTGTGAGCCTGAGCTGATGATGACCTTGGCGCTGG 604
Qy 541 TCACCATGGGCCAGCGTGTCTTTTATGAACCG-CACAGTTGGTGAGATCTCTGTGGGGCTAT 599
Db 605 TCACCATGGGCCAGCGTGTCTTTTATGAACCGCACACAGTTGGTGAGATCTCTGTGGGGCTAT 664
Qy 600 GAGCATCCCTTCGTGCAATTTTCTCAACACATGCTCTCCAGACATGCTTCCATTAAGGGC 659
Db 665 GAGCATCCCTTCGTGCAATTTTCTCAACACATGCTCTCCAGACATGCTTCCATTAAGGGC 724
Qy 660 AAATTTGGCCTGTTTGTGGGATGAACTCGAATTTCTGGGGTCTTCACTGCTCTT---C 716
Db 725 AAATTTGGCCTGTTTGTGGGATGAACTCGAATTTCTGGGGTCTTCACTGCTCTTCACT 784
Qy 717 ACGGGCGTCCAGAAATTTTCAGCAGGATCCATCTGTTGGAGCAAAATGGAAACGGAC--TCAGCA 774
Db 785 CGGGCGTCCCAAAATTTTCAGCAGGACCATCTGTTGGGCCCAAAATGGAGCGGCTCCGCA 844
Qy 775 AGATCGAATATTGGCATTCAGAGCAGGTGTAACATGATC 812
Db 845 AAATCGAATATTGGCTTCCAGAGCAGGTGTAACATGATC 882
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 18:01:48 ; Search time 308.241 Seconds
(without alignments)
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Perfect score: 1785
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

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- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCRUS_COMB.seq.*
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- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1785	100.0	1785	2	US-08-749-907-3
3	1785	100.0	1785	3	US-09-241-581B-7
4	1785	100.0	1785	3	US-09-385-799-3
5	1785	100.0	1785	6	PCT-US95-07721-7
6	1396.2	78.2	1825	2	US-08-890-980-3
7	1396.2	78.2	1825	3	US-08-890-979-3
8	1396.2	78.2	1825	3	US-09-032-894-3
9	1396.2	78.2	1825	3	US-09-031-626-3
10	1389.8	76.7	1788	2	US-08-559-505-1
11	1389.8	76.7	1788	2	US-08-749-907-1
12	1369.8	76.7	1788	3	US-09-241-581B-3
13	1369.8	76.7	1788	3	US-08-265-428-3
14	1369.8	76.7	1788	3	US-09-385-799-1
15	1369.8	76.7	1788	6	PCT-US95-07721-3
16	1142.6	64.0	2630	2	US-08-890-980-1
17	1142.6	64.0	2630	3	US-08-890-979-1
18	1142.6	64.0	2630	3	US-09-032-894-1
19	1142.6	64.0	2630	3	US-09-031-626-1
20	1141	63.9	2566	3	US-09-270-542-124
21	1141	63.9	2566	3	US-09-054-272-58
22	1141	63.9	2566	3	US-10-024-396-3
23	956.6	53.6	2595	3	US-09-949-016-2296
24	263.6	14.8	719	3	US-10-024-396-11

25 185.8 10.4 485 3 US-10-024-396-12 Sequence 12, Appl
26 162.2 9.1 4465 3 US-09-949-016-2027 Sequence 2027, Ap
27 139.6 7.8 41322 3 US-10-024-396-13 Sequence 13, Appl
28 139.6 7.8 90472 3 US-09-949-016-14038 Sequence 14038, A
29 138 7.7 481 2 US-08-890-980-11 Sequence 11, Appl
30 138 7.7 481 3 US-08-890-979-11 Sequence 11, Appl
31 138 7.7 481 3 US-09-032-894-11 Sequence 11, Appl
32 138 7.7 481 3 US-09-031-626-11 Sequence 11, Appl
33 127.8 7.2 397 3 US-09-513-999C-2451 Sequence 2451, Ap
34 111 6.2 526 2 US-08-890-980-8 Sequence 8, Appli
35 111 6.2 526 3 US-08-890-979-8 Sequence 8, Appli
36 111 6.2 526 3 US-09-032-894-8 Sequence 8, Appli
37 111 6.2 526 3 US-09-031-626-8 Sequence 8, Appli
38 106.8 6.0 450 2 US-08-890-980-16 Sequence 16, Appl
39 106.8 6.0 450 3 US-08-890-979-16 Sequence 16, Appl
40 106.8 6.0 450 3 US-09-032-894-16 Sequence 16, Appl
41 106.8 6.0 450 3 US-09-031-626-16 Sequence 16, Appl
42 106.6 6.0 495 2 US-08-890-980-7 Sequence 7, Appli
43 106.6 6.0 495 3 US-08-890-979-7 Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-08-559-505-3
; Sequence 3, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
; OTHER INFORMATION: encode the amino acid sequence for the murine Scavenger Recept

US-08-559-505-3

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Query Match      100.0%; Score 1785; DB 2; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CCGTCTCCTTCAGGTCTCAGAGCCCGAGAGCCCTTCCGCGCACCGGAGCATGGGGGCA 60
QY 61 GCTCCAGGCGCGCTGGGTGGCTTGGGGTTGGGCGCCCTTGGGGCTGCTGTTTGTGCGC 120
DB 61 GCTCCAGGCGCGCTGGGTGGCTTGGGGTTGGGCGCCCTTGGGGCTGCTGTTTGTGCGC 120
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DB 121 TCGGCGTGTGATGATCCTCATGGTGGCTTCCCTCATCAAGCAGCAGGTGCTCAAGATG 180
QY 181 TCGGCATAGACCCGAGCAGCTGTCTTCCGGGATGTGGAAGGAGATCCCGCTCCCTTTCT 240
DB 181 TCGGCATAGACCCGAGCAGCTGTCTTCCGGGATGTGGAAGGAGATCCCGCTCCCTTTCT 240
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DB 361 CTTTCAATGACAAACGACACCGTGTCTTCCGTGAGAACCCGAGCTCCATTTCCAGCCTG 420
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DB 421 ACAAGTCGCATGGCTCAGAGAGTGAATCAATGTGCTTAAACATCTTGGTCTTGGGG 480
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DB 661 AATTGGCCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCAAG 720
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DB 721 GCGTCCAGAAATTTCCAGCAGGATCATCTGTGGGAAATGGAACGAGTCTCAGCAAGATCG 780
QY 781 ATTAATTGGCATTCAGAGCAGTGAATGATGATCAATGGGACTTCCGGGAGATGTTGGGCAC 840
DB 781 ATTAATTGGCATTCAGAGCAGTGAATGATGATCAATGGGACTTCCGGGAGATGTTGGGCAC 840
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DB 841 CTTTCATGACACCCGAATCTCGCTGGAATTTTCAGCCCGGAGGATGAGGTCCATGA 900
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DB 901 AGCTGACCTCAACGAATCAAGGGTGTGGAAGGCAATTCACCATGATGCTTCAAGCCCC 960
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DB 961 CCGATACTCTGTTTCCAAAGGGTCCGCTTCAACCCAAAGAGGCTTCTGCCCATGCC 1020
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QY 1021 GAGAGTCTGGCATTCAGAATGTGACACCTGACAGTTTGTGTCGCTCTGTTTCTCTCCC 1080
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QY 1081 ACCCCACATTTTACAAACGCGCACCTTGTGTTGTGAGAACTGTGTTGTGTAACCCCTA 1140
DB 1081 ACCCCACATTTTACAAACGCGCACCTTGTGTTGTGAGAACTGTGTTGTGTAACCCCTA 1140
QY 1141 ACCAAAGAGCATTCCTTGTTCCTAGACATCATCCGCTCACTGGGATCCCATGAAT 1200
DB 1141 ACCAAAGAGCATTCCTTGTTCCTAGACATCATCCGCTCACTGGGATCCCATGAAT 1200
QY 1201 GTTCTGTGAAGATGACAGCTGAGCTCTACATCAAAATCTGTCAAGGSCATCGGSCAAACAG 1260
DB 1201 GTTCTGTGAAGATGACAGCTGAGCTCTACATCAAAATCTGTCAAGGSCATCGGSCAAACAG 1260
QY 1261 GGAAGATCGAGCAGTAGTCTTGTGCTGTGGTTCGAAACAGAGCGGAGCAATGGGTG 1320
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DB 1321 GCAAGCCCTGAGCAGCTTCTACACGAGCTGTGTGATGATGCCCCAGGTTCTTCACTACG 1380
QY 1381 CGCAGTATGTGCTGTGGGCTTGGAGGCTCTCTGTGCTGTGGTCCCATCATCTGCCAAC 1440
DB 1381 CGCAGTATGTGCTGTGGGCTTGGAGGCTCTCTGTGCTGTGGTCCCATCATCTGCCAAC 1440
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DB 1441 TGGCAGCAGGAGAAATGCTTTTGTGTTGGAGTGTGTAGTAAAGAGGCTCCAGGATA 1500
QY 1501 AGAGGCCATTCAGGCTACTCTGAGTCTGTGATGTCACAGCTGCAAGGGGACCGGTG 1560
DB 1501 AGAGGCCATTCAGGCTACTCTGAGTCTGTGATGTCACAGCTGCAAGGGGACCGGTG 1560
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DB 1561 TGCAGAAAGCCAGCTATAGGCTCTGAGAGACACTATAAGCCCCCAACCTGATAGCTT 1620
QY 1621 GGTTCAGACAGCAGCAGTCCCTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGC 1680
DB 1621 GGTTCAGACAGCAGCAGTCCCTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGC 1680
QY 1681 CACAGTGCATGCGCTGAGCCCCCAGATGTACACCTGTCCGACGACGACGACATGG 1740
DB 1681 CACAGTGCATGCGCTGAGCCCCCAGATGTACACCTGTCCGACGACGACGACATGG 1740
QY 1741 ATGCCACAGCATGTGCAAAACAACTCAGGGACCGGGACAGACC 1785
DB 1741 ATGCCACAGCATGTGCAAAACAACTCAGGGACCGGGACAGACC 1785
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RESULT 2

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US-08-749-907-3
; Sequence 3, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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Db 1681 CCACAGTGCATGGCTGAGCCCGCCAGATGTACACCTTCGCGACGACGACATGG 1740
QY 1741 ATGCCACGATGTGCAAAACAACTCAGGACCGGACGACGACC 1785
Db 1741 ATGCCACGATGTGCAAAACAACTCAGGACCGGACGACGACC 1785
RESULT 3
US-09-241-581B-7
; Sequence 7, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241.581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through
; 1577 encode the amino acid sequence
; for the murine Scavenger Receptor
; Class BI."
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-241-581B-7
Query Match 100.0%; Score 1785; DB 3; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 301 CAGTAGTCCGGAGCGGTGAGACCTTATGTCTACAGGAGTTCAGACAAAGGTCAACATCA 360
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Db 421 ACAAGTCGCATGGCTCAGAGAGTGACTACATTTGTACTGCTTAACATCTTGGTCTCTGGGG 480
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QY 541 TCACCATGGGCCAGCGTCTTTTATGAACCGCACAGTTCGTGAGATCCTGTGGGGCTATG 600
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Db 601 AGCATCCCTTCGTGCAATTTCTCAACACGTACTCTCCAGACATGCTTCCCATAAAGGGCA 660
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QY 1081 ACCCCCACTTTTCAACGCGGACCTGTGTTGTGAGAGCTGTTCTTGGTCTCAACCCCTA 1140
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QY 1141 ACCCAAAGGAGCATTCCTTGTCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1200
Db 1141 ACCCAAAGGAGCATTCCTTGTCTAGACATCCATCCGGTCACTGGGATCCCCATGAAC 1200
QY 1201 GTTCTGTGAAGATGACGTGAGCTCTTACATCAAAATCTGTCAAGGGGATCGGGAAACAG 1260
Db 1201 GTTCTGTGAAGATGACGTGAGCTCTTACATCAAAATCTGTCAAGGGGATCGGGAAACAG 1260
QY 1261 GGAAGATCGAGCAGATGTTCTGCGTGTGCTGTGTTGCAACAGAGCGGAGCAATGGTG 1320
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Db 1381 GCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGGTGGCCATCATCTGCCAAC 1440
QY 1441 TGGCAGCAGGAGAAATGCTTTTGTGTTGGAGTGTGTAAAGGGCTCCAGGATA 1500
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Db 1501 AGGAGGCCATTGAGGCTTCTGAGTCCCTGATGTCCACAGCTGCCAAGGGCAGCGTGC 1560
QY 1561 TGCAGAGCAGCAGCTATAGGGTCTGAAGACATATAAGCCGCCCCAAACCTGATAGCTT 1620
Db 1561 TGCAGAGCAGCAGCTATAGGGTCTGAAGACATATAAGCCGCCCCAAACCTGATAGCTT 1620
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QY 1741 ATGCCCAAGCATGTGCAAAAACAACTCAGGGAACAGGGAAGAGC 1785
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RESULT 5

PCT-US95-07721-7

; Sequence 7, Application PC/TUS9507721

; GENERAL INFORMATION:

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; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through
; OTHER INFORMATION: 1577 encode the amino acid sequence
; OTHER INFORMATION: for the murine Scavenger Receptor
; OTHER INFORMATION: Class BI."
PCT-US95-07721-7
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Query Match 100.0%; Score 1785; DB 6; Length 1785;
Best Local Similarity 100.0%; Fred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 TCGGCATAGACCCGAGAGCGCTGCTTTCGGGATGTGGAGGAGATCCCGTCCCTTTCT 240
Db 181 TCGGCATAGACCCGAGAGCGCTGCTTTCGGGATGTGGAGGAGATCCCGTCCCTTTCT 240
QY 241 ACTTGTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCCTCAACGCGGACAGAGC 300
Db 241 ACTTGTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCCTCAACGCGGACAGAGC 300
QY 301 CAGTAGTCCGGGAGCGTGGACCCCTATGTCTACAGGGAGTTTCAGACAAAGGTTCAACATCA 360
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TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 156..1682
US-08-890-979-3

Query Match 78.2%; Score 1396.2; DB 3; Length 1825;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

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QY	65	CAGGCGCGCTGGGTGGCTTGGGGTGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	124
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QY	125	CGTTGTCATGATCCTCATGTGTCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTCG	184
DB	230	TGTGTTATGATCCTCGTGTGCTCCCTCGCTCATCAACAGCAGGTACTGAAGAAATGTCG	289
QY	185	CATAGACCCGAGCAGCTGCTCTCGGGATGTGAAGAGATGCCCTGCTCCCTTCTACTT	244
DB	290	CATAGACCCGAGCAGCTGCTCTTGAATGTGAAGAGATGCCCTGCTCCCTTCTACTT	349
QY	245	GTCTGCTACTTCTTCAAGTGGTCAACCAAGAGTCTCAACGCGCAGAGCCAGT	304
DB	350	GTCCGCTACTTCTTCAAGTGGTCAATCCAGCGAGATCCCTGAAGGGTGAAGCCAGT	409
QY	305	AGTCCGGGAGCGTGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCACCTT	364
DB	410	AGTCCGGGAGCGTGGACCTATGCTACAGGAGTTCAGACAAAGGTCAACATCACCTT	469
QY	365	CAATGACAAACGACCGTCTCTTGTGGAGAACCGGAGCTCCATTTCCAGCTGACAA	424
DB	470	CAATGACAAATGACTGTCTTGTGGAGAACCGGAGCTCCATTTCCAGCGGACAG	529
QY	425	GTGCGATGGCTCAGAGAGTACATGCTGCTTAACTTGTGCTCTGCGGGGCTC	484
DB	530	GTCCGAGCGCTCTGAGAGTACATGCTTAACTTGTGCTCTGCGGGGCGC	589
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DB	590	AGTAATGATGGAGCAAGCTGTGAGCGCTGAGCTGATGATGCTTGGGCTGGCCAC	649
QY	545	CATGGGCGAGCTGCTTTATGAACCGACAGTTGGTGGAGATCCTGCGGGCTATGACGA	604
DB	650	CTTGGGCGAGCTGCTTTATGAACCGACAGTTGGTGGAGATCCTGCGGGCTATGACGA	709
QY	605	TCCCTTCGTGATTTCTCAACAGTACTCCCGACATGCTTCCCAATAAGGGCAATT	664
DB	710	TCCCTTCGTGATTTCTCAACAGTACTCCCGACATGCTTCCCAATAAGGGCAATT	769
QY	665	TGGCTGTTGTTGGGATGAACAACTCGAATTTGGGGTCTTCACTGCTTTCAGGGCGT	724
DB	770	CGGCTGTTGTTGGGATGAACAACTCAGACTCTGGGCTCTTCACTGTTTCAGGGCGT	829
QY	725	CCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGAACGAGTCTCAGCAAGATCGATTA	784
DB	830	CCAGAAATTCAGCAGGATCCATCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCACTA	889
QY	785	TTGGCATTTCAGAGCAGTGTAACTGATCAATGGGACTTCCGGGAGATGTGGGACCCCTT	844
DB	890	CTGGCATTTCAGAGCAGTGTAACTGATCAATGGGACTTCCGGGAGATGTGGGACCCATT	949

QY	845	CATGACACCCGAATCTCTGCTGGAATTTTTCAGCCCGGAGGATGCAAGTCTCATGAAGCT	904
DB	950	CATGACACCCCGAGTCTCTGCTGGAATTTTTCAGTCCGGAAGCTGCAAGTCTATGAAGCT	1009
QY	905	GACCTACACGAATCAAGGGTGTTCAGGCAATTCACAGATATGCTTTCAGGCGCCCGA	964
DB	1010	CACCTACCATGATTCAGGGGTGTTCAGGCAATTCACAGATATGCTTTCAGGCGCCCGA	1069
QY	965	TACTCTGTTTGGCAAGGGTCCGTCTACCCACCAACGAAGGCTTCTGCCCCTGCGGAGA	1024
DB	1070	AACCTGTTTGGCAATGGGTCTGTTTACCCACCAATGAAGTTCCTGCCCCTGCGTGA	1129
QY	1025	GTCTGCAATTCAGATGTTCAGCACTGCAAGTTTGGTGGCTCTGTTTCTTCCCAACC	1084
DB	1130	ATCCGCAATTCAGAAATGTTCAGCACTGCAAGTTTGGTGGCTCTGTTTCTTCCCAACC	1189
QY	1085	CCACTTTTCAACGCGCCCTGTTGTTCAGAACTGTTTCTGCTGCTGCTGCTGCTGCTG	1144
DB	1190	TCATTTTCAATGCAAGCCCTGTTGTTCAGAACTGTTTCTGCTGCTGCTGCTGCTGCTG	1249
QY	1145	AAAGGAGCATTCCTTGTTCCTAGACATCCATCCGCTCAGTGGATCCCATGAATCTGTC	1204
DB	1250	AAAGGAGCATTCCTTGTTCCTAGACATCCATCCGCTCAGTGGATCCCATGAATCTGTC	1309
QY	1205	TGTGAAGATGCACTGAGCCTCTACATCAATCTGTCAAGGGCATCGGGCAACAGGGAA	1264
DB	1310	TGTGAAGATGCACTGAGCCTCTACATCAATCTGTCAAGGGCATCGGGCAACAGGGAA	1369
QY	1265	GATCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1324
DB	1370	GATCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1429
QY	1325	GCCCTTCAGCAGCTTCTACACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1384
DB	1430	GCCCTTCAGCAGCTTCTACACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1489
QY	1385	GTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1444
DB	1490	GTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1549
QY	1445	CAGCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1504
DB	1550	CAGCAGGAGAAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1609
QY	1505	GGCATTTCAGGCTTCTCTGAGTCCCTGATGTCACAGCTGTCACAGGCGGCTGCTG	1564
DB	1610	GGCATTTCAGGCTTCTCTGAGTCCCTGATGTCACAGCTGTCACAGGCGGCTGCTG	1669
QY	1565	AGAAGCCAAAGCTATAGGGTCTTGAAGACACTATAAGCCCGCCCAACCTGATAGTTC	1624
DB	1670	AGAAGCCAAAGCTATAGGGTCTTGAAGACACTATAAGCCCGCCCAACCTGATAGTTC	1729
QY	1625	AGAAGCCAAAGCTATAGGGTCTTGAAGACACTATAAGCCCGCCCAACCTGATAGTTC	1684
DB	1730	AGAAGCCAAAGCTATAGGGTCTTGAAGACACTATAAGCCCGCCCAACCTGATAGTTC	1789
QY	1685	CAGTGCATGGCTGAGCCCGGAGTGTACACCTGT	1721
DB	1790	CAGTGCATGGCTGAG-CCCCAGATGTACACCTGT	1825

RESULT 8
US-09-032-894-3
; Sequence 3, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980

RESULT 9
US-09-031-626-3
; Sequence 3, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031.626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890.979

EARLIER FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1825
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (156)..(1682)
US-09-031-626-3

Query Match 78.2%; Score 1396.2; DB 3; Length 1825;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

QY 5 CTCCTTCAGGTCCTGAGCCCGAGAGCCCTTCGCGCAGCGAGATGGCGGAGCTC 64
DB 110 CCCCTTCAGTCCCTGAGCCCGAGCCCGGCGCGAGATGGCGGAGCTC 169
QY 65 CAGGCGCGCTGGGTGGCTTGGGGTTGGGGCGCCCTGGGGCTGCTGTTGCTGGCTCGG 124
DB 170 CAGGCGCGCTGGGTGGCTTGGGGTTGGGGCGCCCTGGGGCTGCTGTTGCTGGCTCGG 229
QY 125 CGTTGTCATGATCCTCATGTGTCCTCCCTCATCAAGCAGCAGGTGCTCAAGATGTCG 184
DB 230 TGTGTTTATGATCCTCATGTGTCCTCCCTCATCAAGCAGCAGGTGCTCAAGATGTCG 289
QY 185 CATAGACCCGAGCAGCTGCTTCGCGATGCTGAAGAGATCCCGTCCCTTCTACTT 244
DB 290 CATAGACCCGAGCAGCTGCTTCGCGATGCTGAAGAGATCCCGTCCCTTCTACTT 349
QY 245 GTCTGCTACTTCTTCGAAGTGGTCAACCCAAAGAGGTCTCAACGGCCAGAGCCAGT 304
DB 350 GTCCGTCTACTTCTTCGAAGTGGTCAACCCAGGATCTTAAGGGTGGAGCCAGT 409
QY 305 AGTCGGGAGGTGGACCTATGCTACAGGAGTTGAGCAAAAGGTCAACATCACCTT 364
DB 410 AGTCGGGAGGTGGACCTATGCTACAGGAGTTGAGCAAAAGGTCAACATCACCTT 469
QY 365 CAATGACACGACACCTGCTTCGTTGGAGACCGCAGCTCCATTTCCAGCTGACAA 424
DB 470 CAATGACACGACACCTGCTTCGTTGGAGACCGCAGCTCCATTTCCAGCTGACAA 529
QY 425 GTCCATGCTCAGAGAGTACTACTGCTTACTGCTTAAATCTGCTGCTGGGGGCTC 484
DB 530 GTCCATGCTCAGAGAGTACTACTGCTTAAATCTGCTGCTGGGGGCTC 589
QY 485 GATATGATGAGAGCAAGCTGTGAGCTGAGCTGAGCTGATGATGATGATGATGATG 544
DB 590 AGTAATGATGAGAGCAAGCTGTGAGCTGAGCTGAGCTGATGATGATGATGATGATG 649
QY 545 CATGGGCGAGGCTGCTTTATGACCGCAGTTGGTGGATCCTGTTGGGGCTATGACGA 604
DB 650 CTTGGGCGAGGCTGCTTTATGACCGCAGTTGGTGGATCCTGTTGGGGCTATGACGA 709
QY 605 TCCCTTCGTGATTTCTTCAACAGTACTTCCAGACATGCTTCCCATAAAGGCAAT 664
DB 710 TCCCTTCGTGATTTCTTCAACAGTACTTCCAGACATGCTTCCCATAAAGGCAAT 769
QY 665 TGGCCTGTTTGTGGGATGAACAACTCGAAATCTGGGGTCTTCACTGCTTTCAGGGCGT 724
DB 770 CGGCTGTTTGTGGGATGAACAACTCGAAATCTGGGGTCTTCACTGCTTTCAGGGCGT 829
QY 725 CCAGAAATTCAGAGGATCCATCTGGTGGACAAATGGAACGGATCAGAGATCGATTA 784
DB 830 CCAGAAATTCAGAGGATCCATCTGGTGGACAAATGGAACGGATCAGAGATCGATTA 889
QY 785 TTGCAATTCAGAGGATGAACATGATCAATGGGACTTCCGGGAGATGTTGGGACCTT 844
DB 890 CTTGCAATTCAGAGGATGAACATGATCAATGGGACTTCCGGGAGATGTTGGGACCTT 949
QY 845 CATGACACCGGAATCTCTCGCTGGAAATTTCTTCAGCCCGAGGAGCATGAGGTCCATGAAGCT 904

DB 950 CATGACACCGGAGTCTCTCGCTGGAAATTTCTTCACTCCGGAAGCTGCGAGTCTATGAAGCT 1009
QY 905 GACCTACACGAATCAAGGGTGTTCGAAGGCAATTCACACGATATCGTTTACGGCCCCCGA 964
DB 1010 CACTTACCATGATTCAAGGGTGTTCGAAGGCAATTCACACGATATCGTTTACAGCCCCATA 1069
QY 965 TACTCTGTTTGGCAACGGGTTCCTTACCCACCAAGAGGCTTCTGCCCATTGCGGAGA 1024
DB 1070 AACTTGTGTTGCAATGGGTCTGTTTACCCCAATGAAGTTCCTGCGCGTCTGGA 1129
QY 1025 GTCTGGCATTCAGAAATGTCAGACCTGCAAGTTCGTTGGTGGCTCTGTTCTTCTCCACCC 1084
DB 1130 ATCCGGCATTCAGAAATGTCAGACCTGCAAGTTCGTTGGTGGCTCTGTTCTGTCACACCC 1189
QY 1085 CCACTTTTACACCGCCGACCTGCTGTTGTCAGAAAGCTGTTCTTGGTCTGAACCTTAACCC 1144
DB 1190 TCACTTACATGACAGCCCTGCTGTCATCAGAAAGCTGTTCTGGTCTGAACCTTAACCC 1249
QY 1145 AAGGAGCATTCCTGTTCTAGACATCCATCCGTCATCTGGGATCCCATGAATGTTTC 1204
DB 1250 AAGGAGCATTCCTGTTCTAGACATCCATCCGTCATCTGGGATCCCATGAATGTTTC 1309
QY 1205 TGTGAAGTGCAGTGCAGCTCTACATCAAAATCTGTCAGGGCATCGGGCAACAGGAA 1264
DB 1310 TGTGAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1369
QY 1265 GATCGAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
DB 1370 GATCGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1429
QY 1325 GCCCTTGAGCAGCTTCTACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
DB 1430 GCCCTTGAGCAGCTTCTACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1489
QY 1385 GTATGCTGCTGGGCTTGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1444
DB 1490 GTATGCTGCTGGGCTTGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
QY 1445 CAGCAGGAGAAATGCTTTTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGT 1504
DB 1550 CAGCAGGAGAAATGCTTTTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGT 1609
QY 1505 GGCCATTCAGGCTTCTGAGTCCCTGATGTCAACAGCTGCCAAGGGCAAGGCTGCTGCTGCA 1564
DB 1610 GGCCATTCAGGCTTCTGAGTCTCTGATGTCAACAGCTGCCAAGGGCAAGGCTGCTGCTGCA 1669
QY 1565 AGAAGCCAGCTATAGGCTCTGAGACATATAAGCCCCCAAACTGATAGCTTGGTC 1624
DB 1670 AGAAGCCAGCTATAGGCTCTGAGGCTCCCAAGACACACAGCCCCCAAACTGATAGCTTGGTC 1729
QY 1625 AGAAGCCAGCTATAGGCTCTGAGGCTCCCAAGACACACAGCCCCCAAACTGATAGCTTGGTC 1684
DB 1730 AGAAGCCAGCTATAGGCTCTGAGGCTCCCAAGACACACAGCCCCCAAACTGATAGCTTGGTC 1789
QY 1685 CAGTGCATGCTGAGCCCCCAGATGTACACCTGT 1721
DB 1790 CAGTGCATGCTGAG-CCCCAGATGTACACCTGT 1825

RESULT 10
US-08-559-505-1
; Sequence 1, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/559,505
APPLICATION NUMBER: US/08/559,505
FILING DATE: 29-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 156..1683
OTHER INFORMATION: /function= "Nucleotides 156 through 1683
OTHER INFORMATION: encode the amino acid sequence for the Hamster Scavenger Receptor
US-08-559-505-1

Query Match 76.7%; Score 1369.8; DB 2; Length 1788;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 5 CTCCTTCAGTCTGAGCCCGAGAGCCCTTCGCGGCACCGGACATGGCGCGGAGCTC 64
DB 110 CCCCTTCAGTCTGAGCCCGAGAGCCCGGCGGCACACGCGGACATGGCGCGGAGCGC 169
QY 65 CAGGCGCGCTGGTGGCTTGGGTTGGGCGCCCTGGGCTGCTTTGCTGGCTCGG 124
DB 170 CAGGCGCGCTGGTGGCGTGGGCTGGGCGTGGGCGTGGGCTGGGCTGGGCTGGG 229
QY 125 CGTTGTATGATCTCATGTGCGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATGTCCG 184
DB 230 TGTGTTATGATCTCTGTATGCGCTCGCTCATCAACAGCAGGTACTGAAGATGTCCG 289
QY 185 CATAGACCCGAGCAGCTGTCTTTCGGGATGTGGAAGGAGATCCCGTCCCTTTCTACTT 244
DB 290 CATAGACCCGAGCAGCTGTCTTTCGCAATGTGGAAGGAGATCCCTGTACCTTCTACTT 349
QY 245 GTCTGTCTACTCTTTCGAAGTGTCAACCAAGCAGGTCTCAACGCGCAGGACGAGT 304
DB 350 GTCCGTCTACTCTTTCGAGGTGTCAATCCAGCGAGATCCTAAGGGTGAAGACGAGT 409
QY 305 AGTCCGGGAGCTGGACCTCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCACCTT 364
DB 410 AGTCCGGGAGCTGGACCTCTATGTCTACAGGAAATTCAGACATGAAGCCAAACATCCTT 469
QY 365 CAATGACAAACAGACCGCTGTCTTTCGGGAGAACCGCAGCTCCTCAATTCAGCCTGACAA 424
DB 470 CAATGACAAATGATCTGTCTTTCGGGAGCACCGCAGCTCCTCAATTCAGCCTGACAG 529
QY 425 GTCCGATGGCTCAGAGAGTACTACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 484
DB 530 GTCCGATGGCTCAGAGAGTACTACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 589
QY 485 GATATTGATGGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGATGATGATGATGATGATG 544

DB 590 AGTAATGATGGAGAGCAAGTCTGAGGCTGAAGCTGATGATGATGATGATGATGATGATGAT 649
QY 545 CATGGCCAGCGCTGCTTTTATGAACCGCAGCTTGGTGAATCCTGTGGGGCTATGACGA 604
DB 650 CTTGGCCAGCGTGCCTTTATGAACCGAAACAGTTGGTGAATCCTGTGGGGCTATGAGGA 709
QY 605 TCCTCTTCGTGATCTTCTCAACACAGTACCTCCAGACATGCTTCCCATAAAGGGCAAT 664
DB 710 TCCTCTTCGTGAATTTTATCAACAAATCTTACAGACATGTTCCCATCAAGGGCAAT 769
QY 665 TGGCCTGTTTGTGGGATGAACAACCTCGAATTTCTGGGCTTCTCACTGTCTTCAAGGGCT 724
DB 770 CGGCTGTTTGTGAGATGAACAACCTCAGACTCTGGGCTTCTCACTGTCTTCAAGGGCT 829
QY 725 CAGAAATTCAGCAGGATCCATCTGGTGAACAAATGGAACGAGCTCAGCAAGATGATTA 784
DB 830 CCAGAACTTCAGCAAGATCCATCTGGTGAACAGATGGAATGGGCTCAGCAAGTCAACTA 889
QY 785 TTGGCAATTCAGAGCAGTGAACATGATCAATGGGACTTCCGGGAGATGTTGGGCACTT 844
DB 890 CTGGCAATTCAGAGCAGTGAACATGATCAATGGCACTTCCGGGAGATGTTGGGCACTT 949
QY 845 CATGACACCCGAATCCTCGCTGGAATTTCTTCAAGCCGGAGGATGAGGTCCATGAAGCT 904
DB 950 CATGACACCCGAATCCTCGCTGGAATTTCTTCAAGCCGGAGGCTTGCAGGTCTATGAAGCT 1009
QY 905 GACCTCAACGAATCAAGGGTGTGGAAGGCAATCCACGATATCGTTTCAGGCCCCCA 964
DB 1010 CACCTACCATGATCAGGGGTGTTTGAAGGCAATCCCACTATCGCTTCAAGCCCCCTAA 1069
QY 965 TACTCTGTTTGCACAGGCTCGTCTACCCACCAACAGAGGCTTCTGCGCATGCGCAGA 1024
DB 1070 AACTTGTGTTGCAATGGGCTCTGTTTACCACCAATGAAGTCTTCTGCGGCTGCTTGA 1129
QY 1025 GTCTGSCATTCAGAAATGTCAGCACCTGCAAGTGTGGTGGCCTCTGTCTTCTTCCACCC 1084
DB 1130 ATCCGSCATTCAGAAATGTCAGCACCTGCAAGTGTGGTGGCCTCTGTCTTCTTCCACCC 1189
QY 1085 CACTTTTCAACAGCGGACCTGTTGTGTCAGAGCTGTTCTTGTCTGAACCTTAACTT 1144
DB 1190 TCACTTCTCAATGCAAGACCTGTCATCAGAAAGCTTCTGGGCTGAAACCTGACCC 1249
QY 1145 AAGAGCAGTCTCTGTTCTTAGACATCCATCCGTCATCGGTCATCGGATCCCATGAAGTCT 1204
DB 1250 AAGGAGCAATCTTGTCTTCTTGAACATCCATCGGTCATCGGATCCCATGAAGTCTT 1309
QY 1205 TGTGAAGATGCAAGTCTTCTTCAAAATCTGTCAAGGGCATCGGGCAACACAGGAA 1264
DB 1310 TGTGAAGTTCAGATAAGCTCTTACATCAAGCTGTCAAGGGCATTTGGGCAACACAGGAA 1369
QY 1265 GATCGAGCAGTAGTCTGCGCTGCTGTTGTCGAAACAGAGCGGAGCAATGGGTGGCAA 1324
DB 1370 GATCGAGCAGTGGTCTCTCCATGCTGTTGTTGAGCAGAGCGGTGCCATGGGCGCGCA 1429
QY 1325 GCGCTTGCAGCAGTCTTCAACAGCAGCTGCTGTGATGCGCCAGGTTCTTCACTACCGCA 1384
DB 1430 GCGCTTGAACAGCTTCTACAGCAGCTGCTGCTGATGCGCCAGGTTACTTCAAGTGTGCA 1489
QY 1385 GTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1444
DB 1490 GTATGCTGCTGGGCTTGGAGGCTCTCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1549
QY 1445 CAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAAGGGTCCAGAGTAAGGA 1504
DB 1550 CAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAAGGGTCCAGAGTAAGGA 1609
QY 1505 GGCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAGGGCAGCGTGTGCA 1564
DB 1610 GGCATTCAGGCTACTCTGAGTCTCTGATGTCAACAGCTGCCAGGGCAGCGTGTGCA 1669
QY 1565 AGAAGCCAAAGCTATAGGCTCTGGAAGACATTAAGCCCCCCCCCAACCTGATAGCTGGTC 1624

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Db      1670 AGAGCCAAGCTGTAGSGTCCCAAGAGACACGACGAGCCCCCCCCAACTGATAGCTTGCTG 172
Qy      1625 AGACCAACCCAGCCAGTCCCTACACCCCGCTTTCTTTAGGACTCTCTCAGCCGACAGCC 1681
Db      1730 AGACCAAGCCATCCAGCCCTTACACCCCGCTTTCTTTAGGACTCTCTCAGCCGACAGTC 1786

RESULT 11
US-08-749-907-1
; Sequence 1, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 156..1683
; OTHER INFORMATION: /function= "Nucleotides 156 through 1683
; OTHER INFORMATION: encode the amino acid sequence for the Hamster Scavenger
; OTHER INFORMATION: B-I."
US-08-749-907-1

Query Match 76.7%; Score 1369.8; DB 2; Length 1788;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 148; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy      5 CTCCTTCAGTCTTCAGCCCGAGAGCCCTTCGCGCACGCGGACATGGCGGACAGTC 64
Db      110 CCCCTTCAGTCCCTTACGCCCCGAGCCCGGCGCGCACACGCGACATGGCGGACAGCGC 169
Qy      65 CAGGGCGCGCTGGGTGGCCCTTGGGGTTGGGGCCCTTGGGGCTGCTGTTTCTGGCTCGG 124
Db      170 CAGGGCGCGCTGGGTGGCGGTGGGGCTTGGGGCTGCTGTCGCGCTGTGCTCGG 229
Qy      125 CGTTGTTCATGATCCTCATGTTGCCCTCCCTCATCAAGCAGCAGTGCTCAAGAATGTCCG 184
Db      230 TGTGGTTATGATCTCTGTATGTCCTCGCTCATCAACAGCAGGACTCAAGAATGTCCG 289
Qy      185 CATAGACCCGAGCAGCCTGTCTTTCGGGGATGTGGAAGAGGATCCCCGTCCCTTTCTACTT 244

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965	QY	TACTCTGTTGGCCAA	CGGGTCGCTCTACCA	CCCAAGAAAGGCTTC	TGCCCACATGCCGAGA	1024
1070	Db	AACTTTGTTTGGCCAA	TGGGTCTGTTTACCA	CCCAATGAAGGTTTCT	TGCCCGTGCCTTGA	1129
1025	QY	GTCTGGCATTTCA	GAATGTCAGCACTT	CGAGGTTTGGTGC	CGCTCTGTTTCTCTCCACCC	1084
1130	Db	ATCCGGCAITCAA	AAATGTCAACCTT	GCAGGTTTGGTGC	ACCCCTGTTTCTGTCAACACC	1189
1085	QY	CCACTTTTAA	CAAGCCGACCCCTG	TGTTGTTCAGAAAGCTG	TTCTTGGTCTGAACCCCTAACCC	1144
1190	Db	TCACTTCTCA	ATGACAGCCCTGTGCTAT	CAGAAGCCGTTCT	GGGTCTGAACCCCTGACCC	1249
1145	QY	AAAGAGCATTC	CTTGTTCCTAGACAT	CCATCCGGTCACT	GGGATCCCCATGAACCTGTTT	1204
1250	Db	AAGGAGCATTC	TTTGTTCCTTGACAT	CCATCCGGTCACT	GGGATCCCCATGAACCTGTTT	1309
1205	QY	TGTGAAGATGC	AGCTGAGCCCTTACAT	CAAAATCTGTCA	AGGGCATCGGGCAAAACAGGGAA	1264
1310	Db	TGTGAAGATTG	CAGATAAGCCCTTACAT	CAAAAGCTGTCA	AGGGCATCGGGCAAAACAGGGAA	1369
1265	QY	GATCGAGCCAG	TAGTTCTTCGCGTTGCT	GTGTCGTTTCGAAC	CAGAGCGGACGAATGGTGCCAA	1324
1370	Db	GATCGAGCCCG	TGGTCTCTCCAT	TGCTGTGGTTTGA	CAGAGCGGTGCCATGGCGCGGA	1429
1325	QY	GCCTCTGAGCA	CGTTTCTTACACG	CAGCTGGTGTCTGAT	CCCCCAGGTTCTTCACTACGCGCA	1384
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1385	QY	GTATGTCTGCT	GGGGCTTGGAGCC	CTCTGTTGCTGTG	TGTCCTCATCTGCCAAGCTGG	1444
1490	Db	GTATGTGCTG	CTGGGCTGGGGCG	CCCTCTGCTGTG	TGTCCTCATCTACCAGTTGCG	1549
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1550	Db	CAGCCAGGAGAA	TGCTTTTATTTTGG	AGTGTAGTAAAA	AGGGCTTCGACAGATAAGGA	1609
1505	QY	GGCCATT	CAGGCCCTACTCT	CAGTCCCTGTATGT	CAACAGCTGCCAAGGGCACGGTGTGCA	1564
1610	Db	GGCCATT	CAGGCCCTACTCT	GAAGTCTCTGATGT	CACCAAGCTGCCAAGGGCACGGTGTGCA	1669
1565	QY	AGAAGCCAA	AGCTATAGGGTCT	CTGAAGACACTATA	AGCCCCCCCCAAACCTGATAGCTGGTCT	1624
1670	Db	AGAAGCCAA	AGCTATAGGGTCT	CTGAAGACACCA	CGAGCCCCCCCCAACTGATAGCTGGTCT	1729
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RESULT 13

US-08-265-428-3
; Sequence 3, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428
; FILING DATE:
; CLASSIFICATION: 530

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Qy 425 GTCCATGGCTCAGAGAGTACTATGATGACTGCTTAACATCTTGGTCTGGGGGGCTC 484
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Qy 530 GTCCACCGGCTCTGAGAGTACTATGATGACTGCTTAACATCTTGGTCTGGGGGGGCGC 589
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Qy 485 GATATTGATGAGAGACAGCCTGTGAGCCTGAAGCTGATGATGACCTTTGGCGCTGGTCAC 544
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Qy 1025 GTCTGGCAATCAGAAATGTCAGCACTGAGGCTGTTGGTGGGCTCTGTTCTCTCCACCC 1084
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RESULT 15

PCT-US95-07721-3

; Sequence 3, Application PC/TUS9507721

; GENERAL INFORMATION:

; APPLICANT: Massachusetts Institute of Technology

; TITLE OF INVENTION: Class BI and CI Scavenger Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/07721

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: MIT6620

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794

; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1788 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: 156..1683

; OTHER INFORMATION: /function= "Nucleotides 156 through

; OTHER INFORMATION: 1683 encode the amino acid sequence for

; OTHER INFORMATION: the Hamster Scavenger Receptor Class

; OTHER INFORMATION: B-I."

PCT-US95-07721-3

Query Match

Best Local Similarity 76.7%; Score 1369.8; DB 6; Length 1788;

Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 5 CTCTCTCAGTCTAGAGCCCGGAGAGCCCTTCGCGGACGCGGACATGGCGGAGCTC 64

Db 110 CCCCTTCAGTCTCAGAGCCCGGAGAGCCCGGCGGCGACATGGCGGAGCTC 169

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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 18:08:32 ; Search time 1474.76 Seconds
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Title: US-08-765-108-7
Perfect score: 1785
Sequence: 1 CCGTCTCTTCAGTCTCTGA.....TCAGGACGAGGACAGACC 1785

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134589005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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9: /cgn2_6/ptodata/1/pubnpa/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubnpa/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1785	100.0	1785	3	US-09-148-012-3
2	1785	100.0	1785	6	US-10-178-611-3
3	1785	100.0	1785	6	US-10-164-863-3
4	1785	100.0	1785	6	US-10-176-073-3
5	1785	100.0	1785	9	US-10-933-037-3
6	1785	100.0	2496	7	US-10-322-281-564
7	1607	90.0	1607	3	US-09-882-945A-285
8	1607	90.0	1607	8	US-10-807-114-285
9	1459.4	81.8	2497	7	US-10-152-319A-1909
10	1396.2	78.2	1825	3	US-09-779-152-3
11	1396.2	78.2	1825	5	US-10-023-610-3
12	1396.2	78.2	1825	3	US-10-212-848-3
13	1369.8	76.7	1788	3	US-09-148-012-1
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15	1369.8	76.7	1788	6	US-10-164-863-1
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17	1369.8	76.7	1788	9	US-10-933-037-1
18	1142.6	64.0	2558	7	US-10-276-774-1032
19	1142.6	64.0	2630	3	US-09-779-152-1
20	1142.6	64.0	2630	5	US-10-023-610-1
21	1142.6	64.0	2630	7	US-10-212-848-1
22	1141	63.9	2566	6	US-10-024-396-3
23	1141	63.9	2566	7	US-10-648-593-90

24 1141 63.9 2566 8 US-10-775-920-249 Sequence 249, App
25 1141 63.9 2566 8 US-10-794-198A-11 Sequence 11, Appl
26 1141 63.9 2566 9 US-10-956-157-1424 Sequence 1424, Ap
27 1133 63.5 2628 7 US-10-210-172-115 Sequence 115, App
28 1127.8 63.2 3144 7 US-10-322-281-567 Sequence 567, App
29 1047.6 58.7 1527 8 US-10-494-555-2 Sequence 2, Appli
30 959 53.7 2751 6 US-10-313-641-11 Sequence 11, Appl
31 959 53.7 2751 6 US-10-428-551-11 Sequence 11, Appl
32 959 53.7 2751 8 US-10-775-920-247 Sequence 247, App
33 959 53.7 2751 8 US-10-775-920-248 Sequence 248, App
34 869 48.7 2650 9 US-10-450-763-22308 Sequence 22308, A
35 849 47.6 1248 7 US-10-210-172-117 Sequence 117, App
36 389.4 21.8 1400 9 US-10-956-157-6659 Sequence 6659, App
37 283.6 15.9 444 3 US-09-918-995-11387 Sequence 11387, A
38 263.6 14.8 719 6 US-10-024-396-11 Sequence 11, Appl
39 208.2 11.7 84252 7 US-10-322-281-563 Sequence 563, App
40 185.8 10.4 485 6 US-10-024-396-12 Sequence 12, Appl
41 166.6 9.3 599 9 US-10-450-763-22306 Sequence 22306, A
42 163 9.1 1938 7 US-10-152-319A-2060 Sequence 2060, App
43 163 9.1 2064 6 US-10-388-934-120 Sequence 120, App
44 162.2 9.1 2329 7 US-10-794-899-107 Sequence 107, App
45 161.2 9.0 1988 9 US-10-764-420-2465 Sequence 2465, Ap

ALIGNMENTS

RESULT 1
US-09-148-012-3
; Sequence 3, Application US/09148012
; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Sr-Bi
; TITLE OF INVENTION: Antagonist And Use Thereof As Contraceptives And
; TITLE OF INVENTION: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: MIT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51)..(1577)
; OTHER INFORMATION: Encodes the amino acid sequence for the murine
; OTHER INFORMATION: Scavenger Receptor Class BI
US-09-148-012-3

Query Match 100.0%; Score 1785; DB 3; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCGTCTCTTCAGTCTCTGAGCCCGAGAGAGCCCTTCGCGCAGCGGACATGGGCGCA 60
Db 1 CCGTCTCTTCAGTCTCTGAGCCCGAGAGAGCCCTTCGCGCAGCGGACATGGGCGCA 60
Qy 61 GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTGGCGCCCTTCGCGCAGCGGACATGGGCGCA 120
Db 61 GCTCCAGGCGCGCTGGGTGGCCCTTGGGGTGGCGCCCTTCGCGCAGCGGACATGGGCGCA 120
Qy 121 TCGGCGTGTGTCATGATCTCTATGTCCTTCCTTCATCAAGCAGAGGTCCTCAAGATG 180
Db 121 TCGGCGTGTGTCATGATCTCTATGTCCTTCCTTCATCAAGCAGAGGTCCTCAAGATG 180
Qy 181 TCGGCATAGACCCGAGCAGCTGCTTCGGATGTGGAGGAGATCCCGTCCCTTCT 240
Db 181 TCGGCATAGACCCGAGCAGCTGCTTCGGATGTGGAGGAGATCCCGTCCCTTCT 240

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Db
241 ACTTGTCTGTCTACTTCTTGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAGC 300
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1261 GGAAGATCGAGCAGTAGTCTGCGGTTGCTGTTGTCGAACAGCGGAGCAATGGGTG 1320
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1741 ATGCCACGCTGTGCAAAAACAACTCAGGACCGGACAGACC 1785
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RESULT 2

US-10-178-611-3
; Sequence 3, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear


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; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1

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LENGTH: 1785

TYPE: DNA
ORGANISM: Mus musculus

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; FEATURE:

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; LOCATION: (51) .. (1577)

OTHER INFORMATION: Classification

US-10-164-863-3

Query Match

Matches 1785; Conservat:

Query Match	100.0%	Score 1785:	DB 6:	Length 1785:
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Best Local Similarity	100.0%;	Pred. No.	0;
Matches	1785;	Conservative	0;
		Mismatches	0;
		Indels	0;

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Qy	1	CGGTCTCTCTTCAAGTCTTGAGCCCGCAGAGCCCTTCCGCGCACGCGGACATGGGGCGCA	50
Db	1	CGGTCTCTCTTCAAGTCTTGAGCCCGCAGAGCCCTTCCGCGCACGCGGACATGGGGCGCA	60
Qy	61	GCTCCAGGCGCGCTTGGGTGGCCCTTGGGGTTGGGCGCCCTGGGGCTGCTGTTTGTCTGC	120
Db	61	GCTCCAGGCGCGCTTGGGTGGCCCTTGGGGTTGGGCGCCCTGGGGCTGCTGTTTGTCTGC	120
Qy	121	TGCGGGTTGTCATGATCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180
Db	121	TGCGGGTTGTCATGATCTCATGTGTGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAATG	180
Qy	181	TCCGATAGACCCGAGCAGCTGTCTTCGCGATGTGGAAGAGATGCCCGTCCCTTTCT	240
Db	181	TCCGATAGACCCGAGCAGCTGTCTTCGCGATGTGGAAGAGATGCCCGTCCCTTTCT	240
Qy	241	ACTTGTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCAGAAAGC	300
Db	241	ACTTGTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCAGAAAGC	300
Qy	301	CAGTAGTCCGGAGCGTGGACCTATGTCTACAGGGAGTTTACAGCAAAAGGTCAACATCA	360
Db	301	CAGTAGTCCGGAGCGTGGACCTATGTCTACAGGGAGTTTACAGCAAAAGGTCAACATCA	360
Qy	361	CCTTCATAGCAACGACACCGGTCTTCTGTCGTCGAGAAACCGAGCCTCCATTTCCAGCCTG	420
Db	361	CCTTCATAGCAACGACACCGGTCTTCTGTCGTCGAGAAACCGAGCCTCCATTTCCAGCCTG	420
Qy	421	ACAAGTCGATGGCTCAGAGTAGTCACTATGTCCTTACATCTTACATCTTGGTCTCTGGGG	480
Db	421	ACAAGTCGATGGCTCAGAGTAGTCACTATGTCCTTACATCTTACATCTTGGTCTCTGGGG	480
Qy	481	GCTCGATATTTGATGGAGCAGCAAGCTGTGAGCCCTGGAAGCTTGATGATGACCTTGGCGCTGG	540
Db	481	GCTCGATATTTGATGGAGCAGCAAGCTGTGAGCCCTGGAAGCTTGATGATGACCTTGGCGCTGG	540
Qy	541	TCAACATGGGCGAGCGTCTTTTATGAAACCGCACAGTTGGTGAGATCTGTGTGGGGCTATG	600
Db	541	TCAACATGGGCGAGCGTCTTTTATGAAACCGCACAGTTGGTGAGATCTGTGTGGGGCTATG	600
Qy	601	ACGATCCCTTGGTGCAATTTTCTCAACAGTACCTCCAGACATGCTTCCCATTAAGGGCA	660
Db	601	ACGATCCCTTGGTGCAATTTTCTCAACAGTACCTCCAGACATGCTTCCCATTAAGGGCA	660
Qy	661	AAATTTGGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCA	720
Db	661	AAATTTGGCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCACTGTCTTCA	720
Qy	721	GGTCCAGAAATTTACAGCAGGATCCATCTGTGGTGGCAAAATGGAACCGGACTCAGCAAGATCG	780
Db	721	GGTCCAGAAATTTACAGCAGGATCCATCTGTGGTGGCAAAATGGAACCGGACTCAGCAAGATCG	780

Qy	781	ATTATTGGCAATT	CAGAGCAGTGTAACATGATCAATGGGACTTC	CGGGCAGATGTGGGCAC	840
Db	781	ATTATTGGCAATT	CAGAAGCAGTGTAACATGATCAATGGGACTTC	CGGGCAGATGTGGGCAC	840
Qy	841	CCTTTCATGACAC	CCCGAATCCTCGCTGGAAATTCCTTCAGCCCGAGGAGCATG	CAGGTCATGA	900
Db	841	CCTTTCATGACAC	CCCGAATCCTCGCTGGAAATTCCTTCAGCCCGAGGAGCATG	CAGGTCATGA	900
Qy	901	AGCTGACCTAAC	ACGAATCAAGGGGTGTTTGAAGGCATTC	CCACGATATCGCTTCACGGCCCC	960
Db	901	AGCTGACCTAAC	ACGAATCAAGGGGTGTTTGAAGGCATTC	CCACGATATCGCTTCACGGCCCC	960
Qy	961	CCGATATCTGTT	TGCCAACAGGGTTCGCTCTAACCCACCCAAACGAAGGCTTC	TGCGCCATGCC	1020
Db	961	CCGATATCTGTT	TGCCAACAGGGTTCGCTCTAACCCACCCAAACGAAGGCTTC	TGCGCCATGCC	1020
Qy	1021	GAGAGTCTGCA	TTTTCAGAAATGTCAGACACCTGCAGGTTTGTGTGCGCCTCTCTGTTTCTCTCCC		1080
Db	1021	GAGAGTCTGCA	TTTTCAGAAATGTCAGACACCTGCAGGTTTGTGTGCGCCTCTCTGTTTCTCTCCC		1080
Qy	1081	ACCCCCACTTTT	TACACCGCCAGCCCTCTGTGTGTGCAGAAAGCTGTTTCTTGGTCTGAAACCCCTA		1140
Db	1081	ACCCCCACTTTT	TACACCGCCAGCCCTCTGTGTGTGCAGAAAGCTGTTTCTTGGTCTGAAACCCCTA		1140
Qy	1141	ACCCAAAGGAG	CAATCCTTGTTCCTAGACATCAATCCGGTCACTGGGATCCCCATGAAC		1200
Db	1141	ACCCAAAGGAG	CAATCCTTGTTCCTAGACATCAATCCGGTCACTGGGATCCCCATGAAC		1200
Qy	1201	GTTCCTGTGA	AGATGTCAGCTGAGCCTCTACATCAAACTCTGTCAAGGGGCATCGGGCAACAG		1260
Db	1201	GTTCCTGTGA	AGATGTCAGCTGAGCCTCTACATCAAACTCTGTCAAGGGGCATCGGGCAACAG		1260
Qy	1261	GGAAAGTCG	AGCAGTAGTTCTCCGTTGCTGTGGTTTCGAACAGAGCGGAGCAATGGGTG		1320
Db	1261	GGAAAGTCG	AGCAGTAGTTCTCCGTTGCTGTGGTTTCGAACAGAGCGGAGCAATGGGTG		1320
Qy	1321	GCAAGCCCTTG	AGCAGTCCTTACACGCACTGGTGTGTATGCCCCAGGTTCTTCACTACG		1380
Db	1321	GCAAGCCCTTG	AGCAGTCCTTACACGCACTGGTGTGTATGCCCCAGGTTCTTCACTACG		1380
Qy	1381	CGCAGTATG	CTGCTGGGGCTTTGGAGCCCTCCTGTGTGCTGGTGCCCATCATCTGCCAAC		1440
Db	1381	CGCAGTATG	CTGCTGGGGCTTTGGAGCCCTCCTGTGTGCTGGTGCCCATCATCTGCCAAC		1440
Qy	1441	TGCGCAGCC	AGGAGAAATGCTTTTGTGAGTGAGTAGTAAAGGGCTCCACAGATA		1500
Db	1441	TGCGCAGCC	AGGAGAAATGCTTTTGTGAGTGAGTAGTAAAGGGCTCCACAGATA		1500
Qy	1501	AGGAGGCCAT	TACAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCAACAGGGCAGCGTGC		1560
Db	1501	AGGAGGCCAT	TACAGGCTACTCTGAGTCCCTGATGTACACAGCTGCCAACAGGGCAGCGTGC		1560
Qy	1561	TGCAAGAAG	CCAAAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCCCCAAACCTGATAGCTT		1620
Db	1561	TGCAAGAAG	CCAAAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCCCCAAACCTGATAGCTT		1620
Qy	1621	GGTCAGAC	CCAGCCACCGAGTCCCTTACACCCCGCTTCTTTGAGGACTCTCTCAGCGGAGCAGC		1680
Db	1621	GGTCAGAC	CCAGCCACCGAGTCCCTTACACCCCGCTTCTTTGAGGACTCTCTCAGCGGAGCAGC		1680
Qy	1681	CCACAGTG	CCATGGCTGAGGCCACCCAGATGTACACCTGTCCGACGCAAGGCACATGG		1740
Db	1681	CCACAGTG	CCATGGCTGAGGCCACCCAGATGTACACCTGTCCGACGCAAGGCACATGG		1740
Qy	1741	ATGCCCA	CGCATGTGCAAAAACAACTCCAGGGACCGAGACC		1785
Db	1741	ATGCCCA	CGCATGTGCAAAAACAACTCCAGGGACCGAGACC		1785

RESULT 4
US-10-706-073-3
: Sequence 3. Application US/10706073

Db 1741 ATGCCACGATGTGCAAAAACAACTCAGGACCCAGGACAGACC 1785

RESULT 5

US-10-933-037-3
; Sequence 3, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,037
; FILING DATE: 02-Sep-2004

CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:

NAME/KEY: CDS
; LOCATION: 51..1577
; OTHER INFORMATION: /Function = "Nucleotides 51 through 1577
; encode the amino acid sequence for the murine Scavenger Receptor Class B1.
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-933-037-3

Query Match 100.0%; Score 1785; DB 9; Length 1785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTCTCTCAGTCTGAGCCCGGAGAGCCCTTCGGGCGACGCGGACATGGGCGGCA 60
Db 1 CCGTCTCTCAGTCTGAGCCCGGAGAGCCCTTCGGGCGACGCGGACATGGGCGGCA 60
Qy 61 GCTCCAGGGCGCTGGGTGGCTTGGGTTGGGCGCCCTGGGCTGCTGTTGCTCGCG 120
Db 61 GCTCCAGGGCGCTGGGTGGCTTGGGTTGGGCGCCCTGGGCTGCTGTTGCTCGCG 120
Qy 121 TCGGCGTTGTCATGATCCTCATGGTGGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG 180
Db 121 TCGGCGTTGTCATGATCCTCATGGTGGCCCTCCCTCATCAAGCAGCAGGTGCTCAAGAAATG 180
Qy 181 TCCGCATAGACCCGAGCAGCTGCTTCCGCGATGTGAAGAGATCCCGTCCCTTCT 240
Db 181 TCCGCATAGACCCGAGCAGCTGCTTCCGCGATGTGAAGAGATCCCGTCCCTTCT 240

Qy 241 ACTTGTCTGTCTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAC 300
Db 241 ACTTGTCTGTCTACTTCTTTCGAAAGTGTCAACCCAAACGAGGTCTCTCAACGGCCAGAAC 300
Qy 301 CAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTTCAGACAAAAGGTCAACATCA 360
Db 301 CAGTAGTCCGGAGCGTGACCCCTATGTCTACAGGAGTTTCAGACAAAAGGTCAACATCA 360
Qy 361 CCTTCAATGACAACGACACCGTGTCTTCTGTGAGAACCGCAGCCTCCATTTTCCAGCCTG 420
Db 361 CCTTCAATGACAACGACACCGTGTCTTCTGTGAGAACCGCAGCCTCCATTTTCCAGCCTG 420
Qy 421 ACAAGTCGATGGCTCAGAGAGTACTACATTTGTACTGTCTAAACATCTTGGTCTCTGGGG 480
Db 421 ACAAGTCGATGGCTCAGAGAGTACTACATTTGTACTGTCTAAACATCTTGGTCTCTGGGG 480
Qy 481 GCTCGATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGATGATGATGATG 540
Db 481 GCTCGATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGATGATGATGATG 540
Qy 541 TCACCATGGGCCAGCGTCTTTTATGAACCGCACAGTTGCTGTGAGATCCTGTGGGGCTATG 600
Db 541 TCACCATGGGCCAGCGTCTTTTATGAACCGCACAGTTGCTGTGAGATCCTGTGGGGCTATG 600
Qy 601 ACGATCCCTTCTGTGCAATTTTCTCAACACACGCTACCTCCAGACATGCTTCCCATAAAGGCA 660
Db 601 ACGATCCCTTCTGTGCAATTTTCTCAACACACGCTACCTCCAGACATGCTTCCCATAAAGGCA 660
Qy 661 AATTGGCCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCTACTGCTTTCACGG 720
Db 661 AATTGGCCTGTTTGTGGGATGAACAACTCGAATTTCTGGGGTCTTCTACTGCTTTCACGG 720
Qy 721 GCGTCCAGAAATTCAGCAGSATCCATCTGCTGTGACAAATGGAACGAGCTCAGCAAGATCG 780
Db 721 GCGTCCAGAAATTCAGCAGSATCCATCTGCTGTGACAAATGGAACGAGCTCAGCAAGATCG 780
Qy 781 ATTATTGGCATTTCAGAGCAGTGTAAATGAGGACTTCCCGGCGAGATGTGGGCGAC 840
Db 781 ATTATTGGCATTTCAGAGCAGTGTAAATGAGGACTTCCCGGCGAGATGTGGGCGAC 840
Qy 841 CTTTCATGACACCCGAATCTCTGCTGGAATTTCTTACGCCGAGGAGCATGAGGTCATGA 900
Db 841 CTTTCATGACACCCGAATCTCTGCTGGAATTTCTTACGCCGAGGAGCATGAGGTCATGA 900
Qy 901 AGCTGACCTACACGAATCAAGGCTGTTTGAAGGCAATCCCGATCGCTTTCACGCGCC 960
Db 901 AGCTGACCTACACGAATCAAGGCTGTTTGAAGGCAATCCCGATCGCTTTCACGCGCC 960
Qy 961 CCGATACTCTGTTTGCACACGGGTCCGCTCTACCCACCAACGAGGCTTCTGCCCATGCC 1020
Db 961 CCGATACTCTGTTTGCACACGGGTCCGCTCTACCCACCAACGAGGCTTCTGCCCATGCC 1020
Qy 1021 GAGAGTCTGGCATTCAGAAATGTGACCACTGAGGTTTGGTGGCCCTCTGTTTCTCTCCC 1080
Db 1021 GAGAGTCTGGCATTCAGAAATGTGACCACTGAGGTTTGGTGGCCCTCTGTTTCTCTCCC 1080
Qy 1081 ACCCCACATTTTACACGGCGACCTGTGTGTCAGAACTGTTCTTGGTCTCAACCCCTA 1140
Db 1081 ACCCCACATTTTACACGGCGACCTGTGTGTCAGAACTGTTCTTGGTCTCAACCCCTA 1140
Qy 1141 ACCCAAGGAGCATTCCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCCCATGAAC 1200
Db 1141 ACCCAAGGAGCATTCCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCCCATGAAC 1200
Qy 1201 GTTCTGTGAAGATGACAGTGAAGCTCTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1260
Db 1201 GTTCTGTGAAGATGACAGTGAAGCTCTACATCAAAATCTGTCAAGGGCATCGGGCAACAG 1260
Qy 1261 GGAAGATCGAGCAGTAGTCTGCGCTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
Db 1261 GGAAGATCGAGCAGTAGTCTGCGCTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
Qy 1321 GCAAGCCCTGAGCACGTTCTTACACGAGCTGTGTGCTGATGTCGCCCGAGGTTCTTCTACTACG 1380

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Db 1321 GAAAGCCCTGAGCAGCTTCTACAGCAGCTGGTGTCTGATGCCCAAGGTTCTCACTACG 1380
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Db 1381 CGCAGTATGTGTCTGCTGGGGCTTGAGGCGCTCCTGTGTCTGGTGCCTCATCTGCGCAAC 1440
Qy 1441 TGGCAGCAGCAGAGAAATGCTTTTGTGTTTGGAGTGTGTAGTAAAGGGCTCCAGGATA 1500
Db 1441 TGGCAGCAGCAGAGAAATGCTTTTGTGTTTGGAGTGTGTAGTAAAGGGCTCCAGGATA 1500
Qy 1501 AGGAGGCAATTCAGGCTTACTCTGAGTCCCTGATGTACAGCTGCCAAGGCGACGCTGC 1560
Db 1501 AGGAGGCAATTCAGGCTTACTCTGAGTCCCTGATGTACAGCTGCCAAGGCGACGCTGC 1560
Qy 1561 TGCAGAGCAGCAGCTATAGGCTCTGAAGACACTATATAAGCCGCCCAACCTGATAGCTT 1620
Db 1561 TGCAGAGCAGCAGCTATAGGCTCTGAAGACACTATATAAGCCGCCCAACCTGATAGCTT 1620
Qy 1621 GGTGAGCAGCAGCAGCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1680
Db 1621 GGTGAGCAGCAGCAGCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGC 1680
Qy 1681 CCACAGTGCATGCGCTGAGCCCGCCAGATGTACACCTGTCCGACGCGCAGCAGATGG 1740
Db 1681 CCACAGTGCATGCGCTGAGCCCGCCAGATGTACACCTGTCCGACGCGCAGCAGATGG 1740
Qy 1741 ATGCCCAGCAGTGTGCAAAAACAACTCAGGACACGAGGACAGACC 1785
Db 1741 ATGCCCAGCAGTGTGCAAAAACAACTCAGGACACGAGGACAGACC 1785

RESULT 6
US-10-322-281-564
; Sequence 564, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 2496
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-281-564

Query Match 100.0%; Score 1785; DB 7; Length 2496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTCTCCTTCAGTCTCTGAGCCCGCAGAGCCCTTCGCGCAGCAGCGACATGGCGCGCA 60
Db 143 CCGTCTCCTTCAGTCTCTGAGCCCGCAGAGCCCTTCGCGCAGCAGCGACATGGCGCGCA 202
Qy 61 GCTCAGGCGCGCTGGGTGCGCTTGGGTTGGGCGCCCTGGGCGCTGTGTTGCTGCGC 120
Db 203 GCTCAGGCGCGCTGGGTGCGCTTGGGTTGGGCGCCCTGGGCGCTGTGTTGCTGCGC 262
Qy 121 TCGGCGTGTGATGATCTCATGTGTCCTTCCCTCATCAGCAGCAGGTGCTCAAGATG 180
Db 263 TCGGCGTGTGATGATCTCATGTGTCCTTCCCTCATCAGCAGCAGGTGCTCAAGATG 322
Qy 181 TCCGATAGACCCGAGCAGCTGTCTTGGGATGTGGAAGGAGATCCCGCTTCTTCT 240
Db 323 TCCGATAGACCCGAGCAGCTGTCTTGGGATGTGGAAGGAGATCCCGCTTCTTCT 382
Qy 241 ACTTGTCTGTCTACTTCTTGAAGTGTGTCAACCAAGAGGTCTCTCAAGCGGACAGC 300
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Db 383 ACTTGTCTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCCTCAACGGCCAGAACG 442
Qy 301 CAGTAGTCCGGGAGCGTGGAGCCCTATGTCTACAGGAGATTTCAGACAAAGGTCAACATCA 360
Db 443 CAGTAGTCCGGGAGCGTGGAGCCCTATGTCTACAGGAGATTTCAGACAAAGGTCAACATCA 502
Qy 361 CTTTCAATGACAAACGACACCCGTGTCTTCTGTGAGAAACCGCAGCCTCCATTTCCAGCTG 420
Db 503 CTTTCAATGACAAACGACACCCGTGTCTTCTGTGAGAAACCGCAGCCTCCATTTCCAGCTG 562
Qy 421 ACAAGTCGATGCTCAGAGAGTACTACATTGTACTGCTTACATCTTGGTCTCTGGGG 480
Db 563 ACAAGTCGATGCTCAGAGAGTACTACATTGTACTGCTTACATCTTGGTCTCTGGGG 622
Qy 481 GCTCGATATTGATGGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGACCTTTGGCGCTGG 540
Db 623 GCTCGATATTGATGGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGACCTTTGGCGCTGG 682
Qy 541 TCACCATGGGCCAGCGTGTCTTTTATGAACCGCAAGTTGTGTGAGATCCTGTGGGCTTATG 600
Db 683 TCACCATGGGCCAGCGTGTCTTTTATGAACCGCAAGTTGTGTGAGATCCTGTGGGCTTATG 742
Qy 601 AGCATCCCTTCTGTGCTATTTCTCAACAGTACTCTCCAGACATGCTTCCCATTAAGGGCA 660
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Qy 661 AATTGGCCCTGTGTGTTGGGATGAACAACTCGAATCTTGGGGTCTTCACTGTCTTCAAG 720
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Qy 721 GCGTCCAGAAATTCAGCAGGATCCATCTGTGTGAACAAATCGAACCGGACTCAGCAAGATCG 780
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Qy 841 CTTTATGACACCCGGAATCCTCGCTGGAATTTCTTACGCCCGGAGGATGAGGTTCCATGA 900
Db 983 CTTTATGACACCCGGAATCCTCGCTGGAATTTCTTACGCCCGGAGGATGAGGTTCCATGA 1042
Qy 901 AGCTGACCTTCAACGAATCAAGGTTGTGTAAGGCAATTCACGATATCGTTCACGCGCC 960
Db 1043 AGCTGACCTTCAACGAATCAAGGTTGTGTAAGGCAATTCACGATATCGTTCACGCGCC 1102
Qy 961 CCGATCTCTGTTTGCACAGCGGTCCGTCTACCCACCAAGAGGCTTCTGCCCATGCC 1020
Db 1103 CCGATCTCTGTTTGCACAGCGGTCCGTCTACCCACCAAGAGGCTTCTGCCCATGCC 1162
Qy 1021 GAGAGTCTGGCAATTCAGAATGTGAGACCTGAGGTTTGGTGGCGCTCTGTTTCTCTCCC 1080
Db 1163 GAGAGTCTGGCAATTCAGAATGTGAGACCTGAGGTTTGGTGGCGCTCTGTTTCTCTCCC 1222
Qy 1081 ACCCCCACTTTTACACGCGGACCCCTGTGTGTGTCAGAAGCTGTTCTTGGTCTGAACCCCTA 1140
Db 1223 ACCCCCACTTTTACACGCGGACCCCTGTGTGTGTCAGAAGCTGTTCTTGGTCTGAACCCCTA 1282
Qy 1141 ACCCAAGAGAGCATTCCTTGTCTTAGACATCATCATCCGCTCACTGGGATCCCATGAACCT 1200
Db 1283 ACCCAAGAGAGCATTCCTTGTCTTAGACATCATCATCCGCTCACTGGGATCCCATGAACCT 1342
Qy 1201 GTTCTGTGAAGATGACGCTGAGCCTCTACATCAAAATCTGTCAAGGGGATCGGGCAACAG 1260
Db 1343 GTTCTGTGAAGATGACGCTGAGCCTCTCTACATCAAAATCTGTCAAGGGGATCGGGCAACAG 1402
Qy 1261 GGAAGATTCAGAGCAGTAGTTCCTGCGGTGCTGTGGTTTCGAACAGAGCGGAGCAATGGGTG 1320
Db 1403 GGAAGATTCAGAGCAGTAGTTCCTGCGGTGCTGTGGTTTCGAACAGAGCGGAGCAATGGGTG 1462
Qy 1321 GCAAGCCCTGAGACAGTTCCTACACGAGTGTGTGTGATGTCGCCAGGTTCTTCACTACG 1380
Db 1463 GCAAGCCCTGAGACAGTTCCTACACGAGTGTGTGTGATGTCGCCAGGTTCTTCACTACG 1522
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Db 1321 CUCCAGGAUAAGGAGCCAUUUCAGGCCUACUCUGAGUCCUGAUGUACACGAGCUGGCCAA 1380
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Db 1381 GGGCAACGGTGTGCAAGAGCCAAAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAA 1440
Qy 1610 CCTCATAGCTTGGTTCAGACAGCCAGCCAGCCAGTCCCTACACCCGGCTTCTTGAAGACTCTCT 1669
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Qy 1670 CAGCGGACAGCCACCAAGTCCATGGCTGAGCCGCGGAGTGTGACACCTGTGCGCAGCC 1729
Db 1501 CAGCGGACAGCCACCAAGTCCATGGCTGAGCCGCGGAGTGTGACACCTGTGCGCAGCC 1560
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Db 1561 ACGGACATGATGCCACGCGATGTGCAAAACAACTCAGGACGAC 1607

RESULT 8
US-10-807-114-285
; Sequence 285, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 285
; LENGTH: 1607
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-807-114-285

Query Match 90.0%; Score 1607; DB 8; Length 1607;
Best Local Similarity 77.3%; Pred. No. 0;
Matches 1243; Conservative 364; Mismatches 0; Indels 0; Gaps 0;

Qy 170 GCTCAAGATGTCGCGATAGACCCGAGCAGCTGCTCTTGGGATGTGGAAGGATCCC 229
Db 1 GCUCAGAAUGUCCGCAUAGACCCGAGCAGCUGUCUUCGCGAUGUGGAGGAGUCCC 60
Qy 230 CGTCCCTTTCTACTTGTCTACTTCTTCTGAGTGTCAACCAACGAGGTCTCAA 289
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Qy 290 CGGCGAGAAGCCAGTAGTCCGCGAGCGTGGACCTATGTCTACAGGAGTTCAGACAAA 349
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Db 241 UUUCCAGCUGAAGCGCAGGCGUACAGAGUGACUACAUUGUACUGCCUAAACUUCU 300
Qy 470 GGTCTGGGGGCTCGATATTGATGAGAGCAGCAGCTGTGAGCTGAGCTGATGATGAC 529
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Qy 530 CTTGGCGCTGCTACACATGGGCCAGCGTGTCTTTATGAACCGCAGTGTGTGATCTCT 589
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Qy 650 CATAAAGGGCAAAATTTGGCCCTGTTTGTGGATGAGAACATCGAATTTCTGGGTCTTCC 709
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Qy 890 CAGTCCATGAAGTCACTTACACGAAATCAAGGGTGTGTTGAAGGCAATTCACGATCG 949
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Qy 950 CTTTCAACGGGGCCCGATACTCTGTTTTCACAGGGTCTGTCTACCCACCAACGAGGCTT 1009
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Qy 1370 TCTTCACTACGCGAGTATGCTGTGCTGGGGCTTGGAGGCTCTCTGTGTGTGCTCCAT 1429
Db 1201 UCUUACUACGCGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1260
Qy 1430 CATCTGCCAACTCGCGACCGCAGGAGAAATGCTTTTGTGAGTGTGATGATGATGATGAT 1489
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Db 1381 GGGCAACGGTCTGCAAGAGCCAGCTATAGGGTCTTGAAGACACTATAAGCCCCCAAA 1440
Qy 1610 CTTGATAGTGTGTGACAGCAGCAGCCAGTCCCTTACACCCCGCTTCTTGAAGACTCTCT 1669
Db 1441 CTUGAUGCUGGUGCAGACCCAGCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1500

Qy 1265 GATCAGCCAGTAGTTCTGCGGTTGCTGTGTTGAAACAGAGCGAGCAATGGGTGGCAA 1324
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Qy 1370 GATCAGCCCGTGGTCTCTCCATGCTGTGTTGAGCAGAGCGGTGCCATGGCGGCGA 1429
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Qy 1325 GCCCTGAGCAGCTTCTACACGACGCTGGTCTGATGCCCGCAGGTTCTTCACTACGCGCA 1384
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Qy 1505 GGCCATTGAGCCCTACTCTGAGTCCCTGATGCTCAACGCTGCCAAGGCGAGGTGCTGCA 1564
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Qy 1670 AGAAGCCAAAGCTATAGGCTCTCTGAGACACTATAGGCCCCCAACCTGATAGCTTGGTC 1729
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Qy 1790 CAGTGCCATGGCCTGAG-CCCCAGATGTCAACCTGT 1825
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RESULT 12
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; Sequence 3, Application US/10212848
; Publication No. US2004002325A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Jeanette
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RISK FACTORS
; TITLE OF INVENTION: FOR ABNORMAL LIPID LEVELS AND THE DISEASES AND DISORDERS
; TITLE OF INVENTION: ASSOCIATED THEREWITH
; FILE REFERENCE: MMI-012
; CURRENT APPLICATION NUMBER: US/10/212,848
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1682)
US-10-212-848-3

Query Match 78.2%; Score 1396.2; DB 7; Length 1825;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

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Qy 65 CAGGGCGGCTGGGTGGGCTTGGGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 124
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Qy 170 CAGGGCGGCTGGGTGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 229
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Qy 125 CGTTGTATGATCTCTATGTTGGTGGCTCCCTCATCAGCAGCAGGTGCTCAGATGTCCG 184
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Qy 230 TGTGGTTATGATCTCTGATGTCCTCGCTCATCAACAGCAGGATCTGAGAAATGTCCG 289
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Qy 1130 ATCGGCAATCAAAATGTGAGCACTTGCAGGTTTGTGCAACCCCTGTTTCTGTCAACACC 1189
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Qy 1085 CCATTTTACACCGCGACCTCTGTGTGTGTCAGAAAGCTGTGTGGTCTGAACCTTAAACCC 1144
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Qy 1190 TCATCTTCAATGACAGACCTCTGTGCTATCAGAAGCGGTTCTGGTCTGAACCTTGAACCC 1249
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Qy 1265 GATCGAGCCAGTAGTTCTGCGGTTGCTGTGTTTCGAAACAGAGCGGCAATGGGTGGCAA 1324
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GenCore version 5.1.7
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1455.6	82.1	2497	12	US-11-136-527-2943
2	1369.8	76.7	1788	12	US-11-128-049-1074
3	1369.8	76.7	1788	12	US-11-128-049-1074
4	1291	72.3	1531	9	US-11-222-745-3
5	1142.6	64.0	2569	8	US-10-821-234-66
6	1141	63.9	2566	9	US-11-072-175-90
7	1141	63.9	2566	12	US-11-055-309A-11
8	1048.4	58.7	1530	9	US-11-222-745-8
9	694.6	38.9	1400	12	US-11-136-527-7039
10	513.2	28.8	600	12	US-11-128-061-4716
11	513.2	28.8	600	12	US-11-128-049-4716
12	163.8	9.2	2076	12	US-11-136-527-1803
13	127	7.1	1400	12	US-11-136-527-5899
14	97.2	5.4	496	12	US-11-128-061-2632
15	97.2	5.4	496	12	US-11-128-061-2632
16	97.2	5.4	496	12	US-11-128-049-2632
17	97.2	5.4	496	12	US-11-128-049-6274
18	82.2	4.6	506	6	US-09-925-065A-515554
19	69.6	3.9	2675	12	US-11-136-527-2950
20	64.8	3.6	1910	12	US-11-128-061-1101

21	64.8	3.6	1910	12	US-11-128-049-1101	Sequence 1101, Ap
22	58.6	3.3	2216	8	US-10-909-125-1747	Sequence 1747, Ap
23	57.8	3.2	645	6	US-09-925-065A-675492	Sequence 675492, Ap
24	43.6	2.4	586	6	US-09-925-065A-593691	Sequence 593691, Ap
25	43.6	2.4	586	6	US-09-925-065A-593692	Sequence 593692, Ap
26	43.6	2.4	595	6	US-09-925-065A-840891	Sequence 840891, Ap
27	43	2.4	2024	12	US-11-004-762-21	Sequence 21, Appl
28	41.4	2.3	2718	6	US-09-925-065A-701020	Sequence 701020, Appl
29	41.4	2.3	2828	12	US-11-004-762-22	Sequence 22, Appl
30	41	2.3	4192	7	US-10-826-585-36	Sequence 36, Appl
31	41	2.3	4646	8	US-10-775-169-198	Sequence 198, Appl
32	41	2.3	4646	12	US-11-045-578-5	Sequence 5, Appl
33	38.8	2.2	6264	12	US-11-075-185-58	Sequence 58, Appl
34	38.8	2.2	78869	12	US-11-075-185-1	Sequence 1, Appl
35	38.2	2.1	2060	12	US-11-122-329-8	Sequence 8, Appl
36	38.2	2.1	2060	12	US-11-169-041-66	Sequence 66, Appl
37	37.8	2.1	1400	12	US-11-128-061-4097	Sequence 4097, Ap
38	37.8	2.1	1400	12	US-11-128-049-4097	Sequence 4097, Ap
39	37.8	2.1	3958	12	US-11-128-061-455	Sequence 455, App
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41	36.8	2.1	2043	12	US-11-000-688-1033	Sequence 1033, Ap
42	36.8	2.1	2048	12	US-11-226-701-16	Sequence 16, Appl
43	36.6	2.1	6615	12	US-11-052-554A-518	Sequence 518, App
44	36.4	2.0	564	6	US-09-925-065A-331637	Sequence 331637, Ap
45	36.4	2.0	564	6	US-09-925-065A-331639	Sequence 331639, Ap

ALIGNMENTS

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US-11-136-527-2943
; Sequence 2943, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2943
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2943

Query Match	82.1%	Score	1465.6	DB	12	Length	2497
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Qy	121	TCGCGGTGTCATGATCTCTGATGCTCTCTTCATCAAGCAGGAGGCTCTCAAGATG	180				
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453 CAGTAGTCCGGAGCGCGGACCTTATGTCTACAGGAGATTTCAGACAAAAGGTTCACATCA 512
361 CTTTCAATGACAAACGACACCGTGTCTCTGGTGGAGAACCGCGCTCCATTTCCAGCGCTG 420
513 CTTTCAATGACAAACGACACCGTGTCTCTACATAGAGAACCGAGCTTCRTTTCAGCCAG 572
421 ACAAGTCCGATGGCTCAGAGAGTGAATCAATGTAATGTAATGTAATGTAATGTAATGTA 480
573 ACAGTCCAGGCGCTCAGAGAGTGAATCAATGTAATGTAATGTAATGTAATGTAATGTA 632
481 GCTCGATATTGATGAGAGAACCGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 540
633 GGGCAGTGAATGATGAGAGAACCGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 692
541 TCACCATGGGCGAGCGTGTCTTATGAAACCGCACAGTTGGTGAATCCTGTGGGGCTATG 600
693 TCACCATGGGCGAGCGCGCTTATGAAACCGCACAGTTGGTGAATCCTGTGGGGCTATG 752
601 ACGATCCCTGTGTGATTTCTCAACAGCTACCTCCAGACATGCTTCCCATAAAGGCGCA 660
753 ARGATCCGTTTGTGAAATTTCTCAGCAAAATATTTCCAGACATGTTCCCATCAAAAGGCA 812
661 AATTGGCCTGTTTGTGGGATGAACTCGAATTTCTGGGTTCTTCACTGTCTTCAAGG 720
813 AATTGGCCTGTTTGTGGGATGAACTCGAATTTCTGGGTTCTTCACTGTCTTCAAGG 872
721 GCGTCCAGAAATTTCCAGCAGGATCATCTGGTGGACAAATGGAACGGACTCAGCAAGATCG 780
873 GTGTCCAGAAATTTCCAGCAGGATCATCTGGTGGATAGTGAACGGCTCAGCAGATCA 932
781 ATTAATGGCATTTCCAGCAGGATGTAATGATCAATGAGGACTTCGGGCGAGATGTGGCGAC 840
933 AWTATTGGCATTTCCAGCAGGATGTAATGATCAATGAGGACTTCGGGCGAGATGTGGCGAC 992
841 CTTTCATGACACCGGATCTCGCTGGAATTTCTCAGCCCGGAGGATGAGGCTTCATGA 900
993 CAITTCATGACACCGGATCTCGCTGGAATTTCTCAGCCCGGAGGATGAGGCTTCATGA 1052
901 AGCTGACCTTACAGCAATCAAGGCTGTTTGAAGGCAATTTCCACGATATGCTTCAAGCGCC 960
1053 AGCTGACCTTACAGCAATCAAGGCTGTTTGAAGGCAATTTCCACGATATGCTTCAAGCGCC 1112
961 CCGATATCTGTTTGGCAAGCGGTCGCTACACCAACCAAGAGGCTTCTGCCCATGCC 1020
1113 CCGATATCTGTTTGGCAAGCGGTCGCTACACCAACCAAGAGGCTTCTGCCCATGCC 1172
1021 GAGAGTCCGATTCAGATGTCAGACCTGACGTTTGGTGGGCTCTGTTTCTCTCC 1080
1173 GCGAGTCCGATTCAGATGTCAGACCTGACGTTTGGTGGGCTCTGTTTCTCTCC 1232
1081 ACCCCCACTTTTACAAAGCGGACCTGTTGTTGTCAGAAAGCTGTTTGGTCTGAACCCCTA 1140
1233 AGCCCACTTTTACAAAGCGGACCTGTTGTTGTCAGAAAGCTGTTTGGTCTGAACCCCTG 1292
1141 ACCCAAGGAGCATTTCTGTTTCTAGACATCCATCCGGTCACTGGGATCCCATGAAC 1200
1293 ACCCAAGGAGCATTTCTGTTTCTAGACATCCATCCGGTCACTGGGATCCCATGAAC 1352
1201 GTTCTGTGAGATCAGCTGAGCTTACATCAATCTGTCAAGGGCATCGGGCAACAG 1260
1353 GTTCCGTGAAGATCAGCTGAGCTTACATCAATCTGTCAAGGGCATCGGGCAACAG 1412
1261 GGAAGATCGAGCAGTAGTCTGCGGTTGCTGTTGTCGAACAGAGCGGAGCAATGGGTG 1320
1413 GGAAGATCGAGCAGTAGTCTGCGGTTGCTGTTGTCGAACAGAGCGGAGCAATGGGTG 1472
1321 GCAAGCCCTGAGCAGCTTCTACAGCAGCTGGTGTGATGCCCGCAGGTTCTTCACTACG 1380
1473 GCAAGCCCTGAGCAGCTTCTACAGCAGCTGGTGTGATGCCCGCAGGTTCTTCACTACG 1532

1381 CGCAGTATGTGCTGCTGGGCTTGGAGGCTCCTGCTGTTGTTGTTGTTGTTGTTGTTGTTG 1440
1533 CGCAGTATGTGCTGCTGGGCTTGGAGGCTCCTGCTKCTGTTGTTGTTGTTGTTGTTGTTG 1592
1441 TGCGCAGCCAGGAGAAATGCTTTTGTGTTTGGAGTGTAGTAAAGGGCTCCAGGATA 1500
1593 TGCGCAGCCAGGAGAAATGCTTTTATTTTGGAGTGTAGTAAAGGGCTCCAGGATA 1652
1501 AGAGGCGCATTTAGGCGTACTCTGAGTCCCTGATGTCACAGCTGCCAAGGGCACGCTGC 1560
1653 AGAGGCGCATTTAGGCGTACTCTGAGTCTCTGATGTACACAGCTGCCAAGGGCACGCTAS 1712
1561 TGCAAGAGCCAGCTATAGGCTCTCTGAGACACTATAAGCCCCCAAACTCTGATAGCTT 1620
1713 TGCAAGAGCCAGCTATAGGCTCTCTGAGACACTATAAGCCCCCAAACTCTGATAGCTT 1772
1621 GGTTCAGACAGCCAGCCAGTCCCTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGC 1680
1773 GGTTCAGACAGCCAGCCAGTCCCTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGC 1832
1681 CACAGAGTCCAGTGGCTGAGCCCCCAGATGTACACCTGTCCGAGCGGACAGGACATGG 1740
1833 CGCCAGTGCASGTCTGAGCCCCCAGATGTACACCTGTCCMCAAGGACATAGTGTGC 1892
1741 ATGCCACGCGCATGTCAA 1758
1893 GGAACACTCAGGACCA 1910

RESULT 2
US-11-128-061-1074
; Sequence 1074, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1074
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-1074

Query Match 76.7%; Score 1369.8; DB 12; Length 1788;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

5 CTCTTCAGTCTGAGCCCGGAGAGCCCTTTCGGCGCAGCGGACATGGCGGACGCTC 64
110 CCCTTCAGTCTGAGCCCGGAGAGCCCTTTCGGCGCAGCGGACATGGCGGACGCTC 169
65 CAGGCGCGCTGGGTGGCGCTTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 124
170 CAGGCGCGCTGGGTGGCGCTTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT 229
125 CGTGTGATGATCCTCATGTTGCTTCCCTTCATCAAGCAGCAGGCTGCTCAAGATGTCG 184
230 TGTGGTATGATCCTCGTGTGCTTCCCTTCATCAAGCAGCAGGCTGCTCAAGATGTCG 289

Qy	185	CATAGACCGGAGCAGCCTGTCTCTTCGGGATGTGGAAGAGATCCCGTCCCTTTCTACTT	244
Db	290	CATAGACCCGAGCAGCCTGTCTTTTGCATGTGGAAGGAGATCCCTGTACCTTCTACTT	349
Qy	245	GTCTGTCTACTTCTTCGAAGTGGTCAACCGAAACGAGGTCTCTCAAGCGCAGAGCCAGT	304
Db	350	GTCCGTCTACTTCTTCGAGGTGGTCAATCCAGCGAGATCCTAAGGCTGAGAGCCAGT	409
Qy	305	AGTCCGGAGCGTGGACCTATGTCTACAGGAGTTTCAACAAGGTCAACATCACCCTT	364
Db	410	AGTCCGGAGCGTGGACCTATGTCTACAGGGAATTCAGACATAAGGCAACATCACCTT	469
Qy	365	CAATGACAAACGACACCGGTCTCTTCGTGGAGAACCGCAGCCTCCATTTCCAGCCTGCACAA	424
Db	470	CAATGACAAATGTAATCTGTGTCTTTGTGGACACCGCAGCCTCCATTTCCAGCCGGACAG	529
Qy	425	GTCCGATGGCTCAGAGATGACTACATTTGTATCTGCTAAACATCTTGGTCTCTGGGGGGCTC	484
Db	530	GTCCACCGGCTCTGAGAGTGACTACATTTATCTGCTAAACATCTTGGTCTTGGGGGGCGC	589
Qy	485	GATATTGATGAGAGCAAGCCTGTGAGCCTGAAGCTGATGATGATGACTTTGGCGCTGGTCA	544
Db	590	AGTAATGATGAGAGCAAGTCTGCAGGCTCTGAAGCTGATGATGACCTTTGGGGCTGGCCAC	649
Qy	545	CATGGCCAGCGTGCCTTTTATGAACCGCACAGTTGGTGAGATCCTGGGGCTATGACGA	604
Db	650	CTTGGGCCAGCGTGCCTTTTATGAACCGAACAGTTGGTGAGATCCTTGGGGCTATGAGGA	709
Qy	605	TCCCTTCGTGCATTTTCTCAACAGGTACTCTCCACAGATGCTCTCCCATAAAGGGCAATTT	664
Db	710	TCCCTTCGTGTAATTTATCAACAATACTTACCAGACATGTTCCCATCAAGGGCAGATT	769
Qy	665	TGGCTCTGTTGTTGGGATGAACAACTCGAATCTTGGGCTTTCACTGCTTTCACGGGCGT	724
Db	770	CGGCTCTGTTTGTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTTACGGGCGT	829
Qy	725	CCGAATTTACGACGAGTCCATCTGGTGGACAAATGGAACGGACTCAGCAGATCGATTATTA	784
Db	830	CCGAATTTACGACGAGTCCATCTGGTGGACAAATGGAATGGGCTCAGCAAGGTCACACTA	889
Qy	785	TTGGCATTCAGACGAGTGTAATCATGATCAATGGGACTTTCGGGCGAGATGTGGGCAACCTT	844
Db	890	CTGCAATTCAGACGAGTGCAACATGATCAATGGCACCTTCGGGCGAGATGTGGGCAACCAT	949
Qy	845	CATGACACCGAATCTCTCGCTGGAATTTCTTACGCCGAGGCAATGCAGGTCATGAAAGCT	904
Db	950	CATGACACCCAGTCTCTCGCTGGAAATTTCTTCAGTCCGGAAGCCTGCAGGTCTATGAAAGCT	1009
Qy	905	GACCTACAAACGAATCAAGGCTGTTTGAAGGCAATTCACAGTATCGTTCACGGCCCCGA	964
Db	1010	CACCTACATGATTCAGGGGTGTTTGAAGGCATTCGCCACCTATCGTTCACAGCCCCCTAA	1069
Qy	965	TACTCTGTTTGCACACGGGTCCTCTACCCACCAACGAAGGCTTCTGCCATCCGAGGA	1024
Db	1070	AACCTTGTGTGCCAATGGTCTGTTTACCACCCCAATGAAGTTCCTGCCCGTGCCTTGA	1129
Qy	1025	GTCTGGCATTCAGAAATGTACAGACCTGACAGTGTGGTGGCCTCTGTTTCTCTCCACCC	1084
Db	1130	ATCCGGCATTCAAAATGTGCAGCACTTGCAAGTGTGGTGCACCCCTGTTTCTGTCAACACC	1189
Qy	1085	CCACTTTTACAAACCGACCTGTGTGTGTGACAGAGCTGTTCTTGGTCTGAAACCTTAACC	1144
Db	1190	TCATTTCTACANTGAGACCTGTGTCTATCAGAAGCGGTTCTGGGTCTGAAACCTTGACCC	1249
Qy	1145	AAAGGAGCATTCCTTGTTCCTTAGACATCCATCCGGTCACTGGGATCCCATGAACCTGTTT	1204
Db	1250	AAGGGAGCATTCCTTGTTCCTTGACATCCATCCGGTCACTGGGATCCCATGAACCTGTT	1309
Qy	1205	TGTGAAGATGACGTGAGCCTCTACATCAAAATCTGTCAAGGGCAATCGGGCAACAGGGAA	1264
Db	1310	TGTGAAGTTCAGATTAAGCCTCTACATCAAAAGCTGTCAAGGGCAATGGGCAACAGGGAA	1369

Qy	1265	GATCGAGCCAGTAGTTCCTGCGGTTCGAGACGAGCGGAGCAATGGGTGGCAA	1324
Db	1370	GATCGAGCCCGTGTCCTCCCATTCGTGTGGTTTGAGCAGAGCGGTGCCATGGCGCGCGA	1429
Qy	1325	GCCTCTGAGCACGTTCTACACGACGCTGGTGCTGATGCCCCCAGGTTCTTCACTACGCGCA	1384
Db	1430	GCCTCTGAACACGTTCTACACGACGCTGGTGCTGATGCCCCCAGGTACTTCAGTATATGCA	1489
Qy	1385	GTATGTGCTCTGGGCGCTTGGAGGCCCTCTGTGTTGCTGGTGCCCATCATCTGCCAACTGGG	1444
Db	1490	GTATGTGCTCTGGGCGCTGGGCGGCTCTCTGCTGCTGCTGGTGCCTCATCTACCACTTGGC	1549
Qy	1445	CAGCCAGGAGAAATGCTTTTTTGTGTTTGGAGTGTGTAGTAAAGGGCTCCCGAGATAAGGA	1504
Db	1550	CAGCCAGGAGAAATGCTTTTTTATTTTGGAGTGTGTAGTAAAGGGCTCGCAGGATAAGGA	1609
Qy	1505	GGCATTTCAGGCTTACTCTCAGTCCCTGATGTCCACAGCTGCCAAAGGGACGGTGTCTGCA	1564
Db	1610	GGCCATTTCAGGCTTACTCTCAGTCTCTGATGTCTCAGTGTCCACAGCTGCCAAGGGACGGTGTCTGCA	1669
Qy	1565	AGAAGCCCAAGCTATAGGGTCTCTGAAGACACTATAAGCCCCCCCCAAACCTGATAGCTTGGTC	1624
Db	1670	AGAAGCCCAAGCTGTAGGGTCCCCAAGACACCAAGGCCCCCCCCAACTGATAGCTTGGTC	1729
Qy	1625	AGACCAAGCCACCAAGTCCCTTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGCC	1681
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RESULT 3

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US-11-128-049-1074
; Sequence 1074, Application US/11128049
; Publication No. US20060010513A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
;
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
;
; FILE REFERENCE: 01997.027700
;
; CURRENT APPLICATION NUMBER: US/11/138,049
;
; CURRENT FILING DATE: 2005-05-11
;
; PRIOR APPLICATION NUMBER: US 60/570,425
;
; PRIOR FILING DATE: 2004-05-11
;
; NUMBER OF SEQ ID NOS: 7285
;
; SOFTWARE: PatentIn version 3.3
;
; SEQ ID NO 1074
;
; LENGTH: 1788
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; TYPE: DNA
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; ORGANISM: Cricetulus griseus
;
US-11-128-049-1074

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Query Match	76.7%	Score 1369.8;	DB 12;	Length 1788;
Best Local Similarity	88.6%;	Pred. No. 0;		
Matches 1485; Conservative	0;	Mismatches 192;	Indels 0;	Gaps 0;

QY	185	CATAGACCCGAGCAGCCTGTCTCCTTCGGGATGTGGAAGAGATCCCGTCCCTTTCTACTTT	244
DB	290	CATAGACCCGAGCAGCCTGTCTCCTTTGCAATGTGTGAAGAGAGATCCCTGTACTCTTTACTTT	349
QY	245	GTCTGTCTTACTCTTTCTGGAAGTGGTCAACCCAAACGAGGTCTCTCAACGGCCAGAACCCAGT	304
DB	350	GTCCGTCTACTCTTTCTGAGGTGGTCAATCCACGGAGATCCTTAAGGTGGAAGCCAGT	409
QY	305	AGTCCGGAGCGTGGACCCCTATGTCTACAGGAGTTCAGACAAAGGTCAACATCACCTTT	364
DB	410	AGTGGGGAGCGTGGACCCCTATGTCTACAGGAAATTCAGACATTAAGGCCAATCACCTTT	469
QY	365	CAATGACAAACGACACCGTGTCTTCGTGGAGAAACCGACGCTTCATTTCCAGGCTTGACAA	424
DB	470	CAATGACAAATGATACTGTGTCTTTGTGGAGCACCGCAGGCTTCCATTTCCAGCGGACAG	529
QY	425	GTCCGATGGCTCAGAGAGTGACTACATTTGTACTGSCCTAAACATCTTGATCTCTGGGGGGCTC	484
DB	530	GTCCCCACGGCTCTCAGAGTGACTACATTTACTGCTCCCTAAACATTTCTGGTCTTTGGGGGGCGC	589
QY	485	GATATTTGATGTGAGAGCAAGCCCTGTGAGCTCTGAAGCTGATGATGACCTTTGCGGCTTGGTCCAC	544
DB	590	AGTAATGATGTGAGAGCAAGTCTGCAGGCTTGAAGCTGATGATGACCTTTGGGGCTTGGCCAC	649
QY	545	CATGGCCAGCGTGTCTTTATGAAACCGGACAGTTGGTGAGATCCTGTGGGGCTATGACGA	604
DB	650	CTTGGGCCAGCGTGTCTTTATGAAACCGAACAGTTGGTGAGATCCTGTGGGGCTATGAGGA	709
QY	605	TCCCTTCGTGCAATTTCTCAACAGTACTCTCCAGACATGCTTTCCCATTAAGGGCAATTT	664
DB	710	TCCCTTCGTGAAATTTTATCAACAAATACTTACCAGACATGTGTTCCCATCAAGGGCAAGTT	769
QY	665	TGGCTGTGTTGTGGAGTGAACAACTCGAATTTCTGGGGTCTTCACTGCTTTACGGGCGT	724
DB	770	CGGCTGTGTTGTGAGATGAACAACTCAGACTCTGGGCTCTTCACTGTGTTACGGGCGT	829
QY	725	CCAGAAATTCAGCAGGATCCATCTGGTGGACAAATGGAACGGACTCAGCAAGATCGAATTA	784
DB	830	CCAGAAATTCAGCAAGATCCACCTGGTGGACAGATGGAATGGGCTCAGCAAGGTCAACTA	889
QY	785	TTGGCATTCAGACAGTGTAATCATGATCAATGGGACTTCCGGGCAGATGTGGGCAACCTTT	844
DB	890	CTGGCATTCAGACAGTGTCAAATGATCAATGGCACTTCCGGGCAGATGTGGGCAACCATTT	949
QY	845	CATGACACCCGAATCTCTCGCTGGAAATTTCTCAGCCCGGAGGCAATGCAAGTCCATGAAGCT	904
DB	950	CATGACACCCGAGTCTCTCGCTGGAAATTTCTCAGTCCGGAAGCTTGCAGGTTCTATGAAGCT	1009
QY	905	GACCTTAAACGAATCAAGGGTGTGTTGAAGGCATTTCCACGCTATCGCTTCACGGCCCCCGA	964
DB	1010	CACCTACCATGATTCAGGGTGTGTTGAAGGCATCCCCACCTATCGCTTCACAGCCCCCTAA	1069
QY	965	TACTCTGTTTGCACAGGGTCCGTCTACCCACCAACGAAGGCTTTCGCCCATGCGGAGAA	1024
DB	1070	AACTTTGTTTGCACATGGGTCTGTTTACCCACCCCAATGAAGGTTTCTGCCCCGTGCTTTGA	1129
QY	1025	GTCTGGGCATTCAGAAATGTCACACCTGCAGGTTTGTGGCGCTCTGTTTCTCTCCCAACC	1084
DB	1130	ATCCGGCATTCACAAATGTGACAGCTTGCAGGTTTGTGGTCAACCCCTGTTTCTGTCAACACC	1189
QY	1085	CCACTTTTAAACCGCGACCCCTGTGTTGTTCAGAAAGCTGTTCTTGGTCTGAACCCCTAACCC	1144
DB	1190	TCACTTCTACAATGCAGACCCCTGTGCTATCAGAAAGCCGTTCTGGGTCTGAAACCTTGACCC	1249
QY	1145	AAAGGAGCATTCCTTGTTCCTAGACATCCATCCGGTCACTGGGATCCCCATGAACTGTTTC	1204
DB	1250	AAGGGAGCATTCCTTGTTCCTTGACATCCATCCGCTCACTGGGATCCCATGAACTGTTTC	1309
QY	1205	TGTGAAGATGCAGTCAAGCTCTACATCAAAATCTGTCAAGGGCATCGGGCAACACAGGAA	1264
DB	1310	TGTGAAGTTGCAGATGAAGCTCTACATCAAAAGCTGTCAAGGGCATTTGGGCAACACAGGAA	1369
QY	1265	GATCGAGCCAGTAGTTCCTGCGGCTGTGCTGTGTTGTGAAACAGAGCGGAGCAATGGGTGGCAA	1324

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301 GGTAAACATCACCTTCAATGACATGACACCGTGTCTACATAGAGAACGAGCCTTCA 360
410 TTTCAGCCTGACAGTGCATGCTCAGAGAGTGAATACATTGTACTGCTTAAACATCTT 469
361 TTTCAGCAGACAGTCCAGAGGCTCAGAGAGTGAATACATTGTACTGCTTAAACATCTT 420
470 GGTCTGGGGGCTCGATATTGATGAGAGCAGAGCTGTGAGCTGAAGCTGATGATGAC 529
421 GGTCTGGAGGGGAGTGATGATGAGAGCAGAGCTGAAGCTGAAGCTGCTAATGAC 480
530 CTGGCGCTGTCACTATGGGCGACGCTGCTTTATGAACCGCACAGTTGTGTGATGATCCT 589
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710 TGTCTTCAAGGGCTGACAGATTTTCAAGAGATCCATCTGTGTGACAAATGGAACGACT 769
661 CGTCTTACAGGGTGTCCAGAAATTTCAAGAGATCCATCTGTGTGATGATGNAACGACT 720
770 CAGCAAGATCGAATTTTGGCAATTTCAAGAGATGTAACATGATCAATGGAATTTCCGGGCA 829
721 CAGCGAGTCAAAATTTGGCAATTTGGCAATTTGGCAATTTGGCAATTTGGCAATTTGG 780
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781 GATGTGGGACCTTTCATGACACCGGAATCTCGTGTGAATTTTTCAGCCCGGAGGATG 840
890 CAGGTCCATGAAGCTGACCTTCAAGATCAAGGCTGTTTCAAGGCAATTTCCACGATCG 949
841 CAGATCTATGAAGCTGACCTTCAAGATCAAGGCTGTTTCAAGGCAATTTCCACGATCG 900
950 CTTCAAGGCCCCGATACTGTTTGGCAAGGCTCGTCTACCCACCCCAAGAGGCTT 1009
901 CTTCAAGGCCCCGATACTGTTTGGCAAGGCTCGTCTACCCACCCCAAGAGGCTT 960
1010 CTGGCCATGCCAGAGTCTGCAATTCAGATGTGACACCTGCAAGGTTTGTGCGCTCT 1069
961 CTGGCCGTCGCGAGTCCGCAATTCAGATGTGACACCTGCAAGGTTTGTGCGCTCT 1020
1070 GTTCTCTCCACCCCACTTTTCAAGCGGACCTGCTGTGTGCAAGGCTTCTTGG 1129
1021 GTTCTCTCCACCCCACTTTTCAAGCGGACCTGCTGTGTGCAAGGCTTCTTGG 1080
1130 TCTGAACCTTAACCAAGGAGCATTTCTGTTCTAGACATCATCCGCTCACTGGGAT 1189
1081 TCTGAACCTTAACCAAGGAGCATTTCTGTTCTGACATCATCCGCTCACTGGGAT 1140
1190 CCCCATGAATCTGTTGTAAGATGACGCTGAGCTCTTACATCAAAATCTGTAAGGGCAT 1249
1141 CCCCATGAATCTGTTGTAAGATGACGCTGAGCTCTTACATCAAAATCTGTAAGGGCAT 1200
1250 CGGCAACAGGAGATGACGAGCAGTGTGCTGCTGCTGTGCTGCTGCAAGAGCGG 1309
1201 CGGCAACAGGAGATGACGAGCAGTGTGCTGCTGCTGCTGCTGCTGCAAGAGCGG 1260
1310 AGCAATGGGTGGCAAGCCCTGAGCAGCTTCTACAGCAGCTGTGTGCTGATGCCCCAGGT 1369
1261 GATGATGGGTGGCAAGCCCTGAGCAGCTTCTACAGCAGCTGTGTGCTGATGCCCCAGGT 1320
1370 TCTTCACTACGCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGCTGCTGCT 1429
1321 TCTTCACTACGCGAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGCTGCTGCT 1380
1430 CATCTGCCAATCTGCGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAGAGG 1489
1381 CATTTACCACTGCGCAGCAGGAGAAATGCTTTTGTGAGTGTGTAGTAAGAGG 1440

Qy 1490 CTCCAGGATAAGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAA 1549
Db 1441 CTCGAGGATAAGAGGCCATTCAGGCTACTCTGAGTCCCTGATGTCAACAGCTGCCAA 1500
Qy 1550 GGGCACGGTGTGCAAGAGCCAGCTATAG 1580
Db 1501 GGGCACGGTGTGCAAGAGCCAGCTATAG 1531

RESULT 5

US-10-821-234-66/c
; Sequence 66, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIORITY FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIORITY FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 66
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-66

Query Match 64.0%; Score 1142.6; DB 8; Length 2569;

Best Local Similarity 79.7%; Pred. No. 0;

Matches 134; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

Qy 14 GTCCTGAGCCCCGAGAGCCCCCTTCCGCGCACGCGGACATGCGCGGAGCTCCAGGGCGG 73
Db 2537 GCCCTGAGCGCGCGGTGGGCCCCAGCGCGGACATGCGCGGAGCTCCAGGCGG 2478
Qy 74 CTGGTGGCTTGGGGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 133
Db 2477 CTGGGCTGCGGGGCGCTGCGGGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 2418
Qy 134 GATCCTCATGTCCTCCCTCATCAAGCAGCAGGCTGCTCAAGAAATGTCGCGCATAGACC 193
Db 2417 GATCGTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2358
Qy 194 GAGCAGCTGCTCTTCCGAGTGTGGAGAGATCCCGTCCCTTCTTCTGCTGCTGCTA 253
Db 2357 CAGTAGCTGCTCTTCAACATGTGGAAGGAGATCCCTATCCCTTCTTCTGCTGCTA 2298
Qy 254 CTTCTTCGAAGTGTGCAACCCAAACAGGCTCTCAACGCGCAGAGCAGCTAGTCCGGA 313
Db 2297 CTTCTTTGAGCTCATGAACCCAGCAGAGATCTGGAAGGCGGAGAGCGGAGTCCGGA 2238
Qy 314 GCGTGGACCTATGCTACAGGGGTTGAGCAAAAGGTCAACATCACTCAATGACAA 373
Db 2237 GCGCGGCCCTTACGCTGACAGGGAGTCCAGGCAAAAAGCAACATCACTTCAACAA 2178
Qy 374 CGACACCGTGTCTTCTGAGAGAACCGCAGCTCTCAATTCAGGCTGCAAGTCCGATGG 433
Db 2177 CGACACCGTGTCTTCTGAGTACCGCACTTCCAGTTCAGGCTCCAGTCCGCG 2118
Qy 434 CTCAGAGTGAATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
Db 2117 CTCGAGAGGAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2058
Qy 494 GAGAGCAAGCTGTGAGCCTGAGCTGATGATGACCTTGGCGCTGCTGCTGCTGCTGCT 553
Db 2057 GGAGTAATAGCCCATGACCTTGAAGCTCATGACCTTGGCATTCACCACTCCGCGGA 1998

QY 554 GCCTGCTTTATGAACCGCAGTGTGGTGGATCTCTGTGGGGCTATGACGATCCCTTCGT 613
Db |||||
QY 1997 ACCTGCTTCATGACCGCACTGTGGTGAGATCATGTGGGGCTACAGGACCCCTTGT 1938
Db |||||
QY 614 GCATTTTCTCAACACGCTACCTCCAGACATGCTTCCCATAAAGGGCAAAATTTGGCCTGTT 673
Db |||||
QY 1937 GAATCTCATCAACAAGTACTTTCAGGCATGTTCCCTTCAAGGACAAGTTGGATTATT 1878
Db |||||
QY 674 TGTGGGATGAACCAACTCGAATTTCTGGGTCTTCACTGTCTTCAAGGGGCTCAGAAATTT 733
Db |||||
QY 1877 TGTGAGCTCAACAACCTCCGACTCTGGGCTCTTCAAGGTGTTCAAGGGGCTCAGAAACAT 1818
Db |||||
QY 734 CAGCAGATCCATCTGTGTGACAAATGGAACGCACTCAGCAAGATCAATATTGGCAATC 793
Db |||||
QY 1817 CAGCAGATCCATCTGTGTGACAAATGGAACGCACTCAGCAAGATCAATATTGGCAATC 1758
Db |||||
QY 794 AGAGCAGTGAACATGATCAATGGAATCTCCGGCAGATGTGGGCAACCTTTCATGACACC 853
Db |||||
QY 1757 CGATCAGTGCAACATGATCAATGGAATCTCCGGCAGATGTGGGCAACCTTTCATGACTCC 1698
Db |||||
QY 854 CGAATCCCTCGCTGGAATTTCTTACGCGGAGGATGCGAGTCCATGAGCTGACCTACAA 913
Db |||||
QY 1697 TGAATCTCTGCTGAGTCTTACAGCCGAGGCTGCCGATCCATGAGCTAATGTACAA 1638
Db |||||
QY 914 CGAATCAAGGCTGTTTGAAGGCAATCCACGATATCGCTTCAAGGCGCCCGATCTCTGT 973
Db |||||
QY 1637 GGAGTCAGGGGTGTTTGAAGGCAATCCCACTATCGCTTCTGTGGCTCCCAAAACCTGTT 1578
Db |||||
QY 974 TGCACAGGCTCGCTTACCCACCAAGAGGCTTCTGCCCATGCGGAGGCTGTGGCAT 1033
Db |||||
QY 1577 TGCACAGGCTCGCTTACCCACCAAGAGGCTTCTGCCCATGCGGAGGCTGTGGCAT 1518
Db |||||
QY 1034 TCAGATGTCAGCACTGCGAGGTTTGGTGGCTCTGTCTTCTCCACCCCACTTTA 1093
Db |||||
QY 1517 TCAGAACCTCAGCACTGCGAGGTTTCAAGTCCCTGTTTCTCTCCCATCTCCTTCT 1458
Db |||||
QY 1094 CAACGCGACCTGCTGTGTGTCAGAGCTGTTCTGGTCTGAACCTTAAACCAAGGAGCA 1153
Db |||||
QY 1457 CAACGCGACCTGCTGTGTGTCAGAGCTGTTCTGGTCTGAACCTTAAACCAAGGAGCA 1398
Db |||||
QY 1154 TTCCTGTTCTTACATCCATCGGTCATCGGATCCCATGAACCTGTTCTGTGAAGAT 1213
Db |||||
QY 1397 CTCCTGTTCTTGAACATCCACCGGTCACGGGAATCCCATGAACCTGCTGTGAACT 1338
Db |||||
QY 1214 GCAGCTGAGCTCTACATCAATCTGTCAAGGCACTCGGCAACAGGAGAGATCGAGCC 1273
Db |||||
QY 1337 GCAGCTGAGCTCTACATCAATCTGTCAAGGCACTCGGCAACAGGAGAGATCGAGCC 1278
Db |||||
QY 1274 AGTAGTTCTGCGGTTGCTGTGTCGAACAGAGCGAGCAATGGGTGGCAAGCCCTGAG 1333
Db |||||
QY 1277 TGTGGTCTGCGGCTGCTGTGTTGACAGAGCGGGGCCATGGAGGGGAGACTCTTCA 1218
Db |||||
QY 1334 CAGCTTCTACACGAGCTGTGTGATGCCCCAGGTTCTTCACTPACGCGCAGTATGCT 1393
Db |||||
QY 1217 CACATTTCTACACTCAGCTGTGTGATGCCCCAGGTTGATGCACTATGCCCAGTACGCT 1158
Db |||||
QY 1394 GCTGGGCTTGGAGGCTCTCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1453
Db |||||
QY 1157 CTTGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
Db |||||
QY 1454 GAAATGCTTTTGTGTTGGAGTGTGTGTTGAAAGGGCTCCAGGATAGGAGGCACTTCA 1513
Db |||||
QY 1097 GAAATGCTTTTGTGTTGGAGTGTGTGTTGAAAGGGCTCAAAGGATAGGAGGCACTTCA 1038
Db |||||
QY 1514 GGCCTACTCTGAGTCTCTGATGTCACAGCTGTCGAAGGCAAGGCTGCTGCAAGAGCCAA 1573
Db |||||
QY 1037 GGCCTACTCTGAAATCCCTGATGATCAGCTGCCCAAGGCTGCTGTGCTGCGAGGAGCAA 978
Db |||||
QY 1574 GCTATAGGCTCTCAAGACACTATAAGCCCCCAAACTGATAGCTTGGTCAGACAGGCC 1633
Db |||||
QY 977 ACTGTAGGGTCTGAGGACCCGTGAGCCAGGCTTGGCGCTGAGCCGCTGAGCCGCT 918
Db |||||
QY 1634 ACCCAGTCCCTACACCCCGCTTCTTGGAGTCTCTCAGCGGACAGCCACCCAGTGCAT 1693
Db |||||

Db 917 CCCAGCCCTACACCCGCTTCTCCCGACTCTCCAGCGACAGCCCCCAGCCCCAC 858
QY 1694 GGCCTGAGCCCC 1706
Db 857 AGCCTGAGCCTCC 845
RESULT 6
US-11-072-175-90
; Sequence 90, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 2566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-90
Query Match 63.9%; Score 1141; DB 9; Length 2566;
Best Local Similarity 79.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 345; Indels 0; Gaps 0;
QY 14 GTCTCAGAGCCCGAGAGCCCTTCCGCGCACGCGGACATGGGCGGAGCTCCAGGGCGCG 73
Db 33 GCCTCGAGAGCGCGGGTGGGCCCGGCGGAGACATGGGCTGCTCGGCCAAGGGCG 92
QY 74 CTGGGTGGCTTGGGGTGGGGCCCTGGGGCTGTGTTTGTGCGCTCGGCTGTGCTAT 133
Db 93 CTGGGCTGCGGGGCGCTGGGGCTGTGCGGGCTGTGCTGCGCTGTGCTGCGGCTGTCT 152
QY 134 GATCCTCATGCTGCTCCCTCATCAAGCAGCAGGCTCTCAAGAAAGTCCGATAGACCC 193
Db 153 GATCGTGATGGTGGCTGCTCATCAAGCAGCAGGCTCTTAAGAACGTGGCGCATCGACCC 212
QY 194 GAGCAGCTGTCTTCCGGATGTGGAAGAGATGCCCGCTCCCTTTCTACTTGTCTGTCTA 253
Db 213 CAGTAGCCTGTCTTCAACATGTGGAAGAGATCCCTATCCCTTCTATCTCTCCGTCTA 272
QY 254 CTCTCTCGAAGTGGTCAACCCAAACGAGGTCTCAACCGGCGAGAGCAGTATGTCGGGA 313
Db 273 CTCTCTTGAAGTCAATCAACCCAGCGAGATCTCTGAAGGGCGAGAGCGCAGGTGGGA 332
QY 314 GCGTGACCCCTATGTCTACAGGAGTTTCAAGAAAGTCAACATCACTTCAATGACAA 373
Db 333 GCGCGGGCCCTACGTGTACAGGAGTCCAGGGCAAAAGCAACATCACCTTCAACACAA 392
QY 374 CAGACCGTGTCTTCCGTGGAGAACCGCAGCTCCATTTCCAGCCTGACAAGTCGATGG 433
Db 393 CGACACCGTGTCTTCTCGAGTACCGCAGCTTCCAGTTCAGCCCTCCCAAGTCCACGG 452
QY 434 CTGAGAGTGAATCAATGTACTGTCTTAATCAATCTTGGTCTCTGGGGGCTCGATATGAT 493
Db 453 CTGAGAGAGCGACTACATGCTCATGTGCCCAACATCTGCTTGGGTCTGGGCTGGTATGAT 512
QY 494 GAGAGCAAGCTGTGAGGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATG 553
Db 513 GGAGATAAGCCCATGACCTGAACTCATCATGATGATGATGATGATGATGATGATGATG 572
QY 554 GCCTGCTTTTATGAACCGCAGTGTGGTGGATCTCTCAGCGGACAGCCACCCAGTGCAT 613
Db |||||

Qy	494	GGAGGCAAGCCTGTGAGCCTGAGACCTGATGATGACCTTGGCGCTGTGTCACCATCGGGCA	553
Db	513	GGAGAAATGAAGCCATGAGCCCTGAAGACTCATCATGACCTTGGCATTCACACCCCTCGGCGA	572
Qy	554	CGGTGCTTTTATGAACCGCAGATGTGGTGAGATCCTGTGGGGCTATGACGATCCCTTCGT	613
Db	573	ACGTGCCCTTCATGAACCCGCATGTGGGTGAGATCANTGTGGGGCTACAAAGGACCCCTTGT	632
Qy	614	GCATTTTCTCAACAGCTACCTCCACAGACATGCTTCCCATAAAGGCGCAAAATTTGGCCCTGTT	673
Db	633	GAATCTCATCAACAGTACTTTCCAGGCATGTTCCCTTCAAGGACAAGTTCGGAATATT	692
Qy	674	TGTTGGGATGAACAACTCTCGAATCTTGGGGTCTTCACTGTCTTTCACGGCGTGCAGAAATTT	733
Db	693	TGCTGAGCTCAACAACTCCGACTCTGGGCTCTTCACGGTGTTCACGGGTTCACGGGGTCCAGAACAT	752
Qy	734	CAGCAGGATCCATCTGGTGGGCAAAATGGAACGGGACTCAGCAAGATCGATTAATTGGCATTC	793
Db	753	CAGCAGSATTCCACTCTGTGGGCAAGTGGAAACGGGCTGAGCAAGGTTGACTTCTCGGCATTC	812
Qy	794	AGAGCAGTGTAAACATGATCAATGGGACTTCCGGGCAGATGTGGGCACCCCTTCATGACACC	853
Db	813	CGATCAGTGCACATGATCAATGGAACTTCTGGGGCAATGTGGCGGCCCTTCATGACTCC	872
Qy	854	CGAATCTCTCGCTGGAAATTTTTCAGCCGGAGGCATGCAAGTCCATGAAGCTGACCTACAA	913
Db	873	TGAGTCTCTCGCTGGAGTTTCTACAGCCGGAGGCCCTGCCGATCCATGAAGCTAATGTACAA	932
Qy	914	CGAATCAAGGGTGTTTGAAGGCATTCACACGTATCGCTTTCAGGGCCCCCGATCTCTGTT	973
Db	933	GGAGTCAGGGGTGTTTGAAGGCATCCCAACCATATCGCTTCGTGGCTCCCAAAACCCCTGTT	992
Qy	974	TGCCAAACGGGTCCGTCTACCCACCAACGAAGGCTTCTGCCCATGCGAGAGTCTGGCAT	1033
Db	993	TGCCAAACGGGTCCATCTACCCACCAACGAAGGCTTCTGCCCGTGCCTGGAGTCTGGAA	1052
Qy	1034	TCAGAAATCTCAGCACTGACAGTGTGGTGGCCCTCTGTGTTCTCTCCCAACCCCACTTTTA	1093
Db	1053	TCAGAAACGTGACGACCTCAGGTTCAAGTGCCCTTGTGTTCTCTCCCATCTCATCTTCC	1112
Qy	1094	CAACGCCAGCCCTGTGTGTGTCAGAACTGTGTTGGTCTGAACCTTAACCAAGGAGCA	1153
Db	1113	CAACGCCAGCCCGTCTCGGCAGAAAGCGGTGACTGGCCCTGCACCCCTAAACGAGGAGCA	1172
Qy	1154	TTCTCTGTCTTAGACATCCATCCGGTCACTGGGATCCCATGAATCTGTTCTGTGTAAGAT	1213
Db	1173	CTCTCTGTCTTGGNATCCACCGGTCAACGGAAATCCCCATGAATCTGCTCTGTGAAACT	1232
Qy	1214	GCAGTGAACCTCTACATCAAACTGTCAAGGGCATCGGGCAAAACAGGGAAGATCGAGCC	1273
Db	1233	GCAGTGAACCTCTACATGAATCTGTGCGAGGCATTTGGAACAACCTGGGAAGATTGAGCC	1292
Qy	1274	AGTAGTTCTGCGGTTCTGTGGTTCGAACAGAGCGGAGCAATGGGTGGCAAGCCCTTGAG	1333
Db	1293	TGTGTCTCTGCGCTGCTCTGTGTTGCAAGAGCGGGGCCCATGGAGGGGGAGACTCTTCA	1352
Qy	1334	CACGTTCTTACACGACGCTGTGCTATGTCGCCCGGCTTCTTCACTACCGCGCATGTGCT	1393
Db	1353	CACATTTCTACACTCAGCTGGGTGTGATGCCCAAGGTGATGACATATGCCCAAGTACGTCT	1412
Qy	1394	GCTGGGGCTTGGAGCCCTCTGTTGCTGGTGCCCATCATCTGCCAACTGCCGACGACGGA	1453
Db	1413	CCTGGCGCTGGGCTGGCTCTGTGCTGTGTTCCCTGTCTATCTGCCCAATCCGAGGCCAAGA	1472
Qy	1454	GAATGTCTTTTGTGTTGGAGTGTGTGTAATAAAGGGCTCCAGGATTAAGGAGGCCATTC	1513
Db	1473	GAATGTCTATTATTTTGGAGTAGTAGTAATAAAGGGCTCAAAGGATAAGGAGGCCATTC	1532
Qy	1514	GGCTACTCTGAGTCCCTGTATGTACACAGCTGCCAAAGGCGAGGTGCTGCAAGAGCCAA	1573
Db	1533	GGCTATTCTGAATCCCTGTATGACATAGCTTCCCAAGGGCTCTGTGCTGCAAGGAAGCAA	1592
Qy	1574	GCTATAGGGTCTCTGAAGACACTATAAGCCCCCCCCAAACCTGATAGTGTGGTCAGACGACC	1633

Db	1593	ACTGTAGGTCCTGAGGACACCGGTGAGCCAGCCAGGCCTGGCGCCTGGGGCTTGACCGGCC	1652
Qy	1634	ACCAGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGCCACCACAGTGCAT	1693
Db	1653	CCCAGCCCTACACCCCGCTTCTCCGGACTCTCCAGCAGACAGCCCCCAGCCCCAC	1712
Qy	1694	GGCTGAGCCCCC	1706
Db	1713	AGCTGAGCTCC	1725
RESULT 8			
US-11-222-745-8			
; Sequence 8, Application US/11222745			
; Publication No. US20060035834A1			
; GENERAL INFORMATION:			
; APPLICANT: Karin, Nathan			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AN			
; TITLE OF INVENTION: INFLAMMATION			
; FILE REFERENCE: 30441			
; CURRENT APPLICATION NUMBER: US/11/222,745			
; CURRENT FILING DATE: 2005-09-12			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 8			
; LENGTH: 1530			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-222-745-8			
Query Match 58.7%; Score 1048.4; DB 9; Length 1530;			
Best Local Similarity 80.3%; Pred. No. 7e-289;			
Matches 1229; Conservative 0; Mismatches 301; Indels 0; Gaps 0;			
Qy	51	ATGGCGGCGAGCTCCAGGGCGCGCTGGTGGCTTTGGGGTTGGCGGCCCTTGGGGCTGCTG	110
Db	1	ATGGGCTGCTCCGCAAGCGCGCTGGGCTGCCGGGGCGCTGGGGCGCTCGCGGGCTACTG	60
Qy	111	TTTGTGCGCTCGCGTTGTTCATGATCCTCATGGTGCCCTCCCTCATCAAGCAGCAGGTG	170
Db	61	TGGCTGTGTGTGGCGCTGTTCATGATCGTATGGTGCCGCTCATCAAGCAGCAGGTG	120
Qy	171	CTCAAGAAATGTCGGCATAGACCCGAGCAGCGCTGTCTTCCGGATGTGGAAGGAGATCCCC	230
Db	121	CTTAAAGACGTGGCATCGACCCAGTAGCCTGTCTTCAACATGTGGAAGGAGATCCCT	180
Qy	231	GTCCCTTTCTATTGTGTGTCTACTTCTTCGAAGTGGTCAACCCAAACGAGGTCTCTCAAC	290
Db	181	ATCCCCCTTCTATCTCTCCGTCTACTTCTTTGACGTATGAACCCAGCAGAGATCCTGAAG	240
Qy	291	GGCCAGAGCCAGTAGTCCGGGAGCTGGACCTATGTCTACAGGGAGTTTCAGACAAAG	350
Db	241	GGCGAGAAGCCGAGGTGCGGGAGCGGGGCCCTTACGTGTACAGGGAGTCCAGGCACAA	300
Qy	351	GTCAACATCACCTTCAATGACACGACACCGTGTCTTCTGTGGAGAACCGCAGCTCCAT	410
Db	301	AGCAACATCACCTTCAACAAACGACACCGTGTCTTCTTCAGTATCCGACCTTCCAG	360
Qy	411	TTCCAGCCTGACAAGTCGCATGGCTCAGAGGTGACTTACATTTGTACTGCTTAACATCTTG	470
Db	361	TTCCAGCCCTCCAAGTCCCAAGCTCCGAGAGCGACTTACATCGTCATGCTGCCCAACATCCTG	420
Qy	471	GTCTGGGGGGCTCGATATTGATGGAGAGCAAGCTGTGAGCCTGAGAGCTGATGATGAC	530
Db	421	GTCTTGGGTGCGGGGTGATGATGGAGATTAAGCCCATGACCTCGAAGCTCATCATGACC	480
Qy	531	TTGGCGCTGTGTCACCAATGGGCCAGCGTGTCTTTATGAACCGCAGTGTGTGTGATCCTG	590
Db	481	TTGGCATTCACCACTTCGGCGAAGTGCCTTCATGAACCGCACTGTGGGTGAGATCATG	540
Qy	591	TGGGGCTATGACGATCCCTTCGTGCAATTTCTCAACACGTACCTCCAGACATGCTTCCC	650

Db 541 TGGGGCTACAGGACCCCTTGTGAATCTCATCAAGTACTTTTCAGGAGTGTTCCTCC 600
Qy 651 ATAAAGGCAAAATTTGGCTGTTTGGGATGAACAACTCGAATCTGGGGTCTTCACT 710
Db 601 TTCAAGGACAAATTTGGCTGTTTGGGATGAACAACTCGAATCTGGGGTCTTCACT 660
Qy 711 GTCTTTCAGGGGCTCAGAAATTTTCAGGAGTTCATCTGGTGGGCAATGGAAGGACTC 770
Db 661 GTGTTCAGGGGGTCCAGAAATTTTCAGGAGTTCATCTGGTGGGCAATGGAAGGACTC 720
Qy 771 AGCAAGATTCAGTATTTGGCTTTCAGAGCAGTGAATCAATGAGTCAATGAGTCAATGAGTCA 830
Db 721 AGCAAGTTCAGTATTTGGCTTTCAGAGCAGTGAATCAATGAGTCAATGAGTCAATGAGTCA 780
Qy 831 ATGTGGGACCCCTTCATGACACCCGAAATCTCTGCTGGAATTTTCAGCCCGGAGGATGC 890
Db 781 ATGTGGGCGCCCTTCATGACTCTCTGAGTCTCTGCTGAGTTCATGAGTTCATGAGTTCATGAG 840
Qy 891 AGTTCATGAGCTGACCTCAACGAATCAAGGCTGTTTGAAGGCAATTCACGATTCGC 950
Db 841 CGATTCATGAGCTGAATGTAAGAGGAGTCAAGGCTGTTTGAAGGCAATTCACGATTCGC 900
Qy 951 TTCAAGGCGCCCGGATCTCTGTTTGGCAAGCGGCTCTGCTGAGTTCATGAGTTCATGAGTTC 1010
Db 901 TTCTGCTCCCAAAACCTGTTTGGCAAGCGGCTCTGCTGAGTTCATGAGTTCATGAGTTCATGAG 960
Qy 1011 TGCCCATGCGGAGTCTGCGATTCAGAAATGTCAGACCTGCGAGTTCGAGTTCGAGTTCGAGTTC 1070
Db 961 TGCCCGTGGCTGAGTCTGGAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTC 1020
Qy 1071 TTTCTCTCCACCCCACTTTTCAAGCGGACCTGTTGTTGTCAGAAATTCAGAAATTCAGAAATTCAG 1130
Db 1021 TTTCTCTCCACCTTCTCTCAAGCGGACCTGTTGTTGTCAGAAATTCAGAAATTCAGAAATTCAG 1080
Qy 1131 CTGAACCTTAACCAAGGAGTCTCTGTTTCTGAGACATCCATCCGCTGAGTTCAGTTCGAGTTC 1190
Db 1081 CTGACCTTAACCAAGGAGTCTCTGTTTCTGAGACATCCATCCGCTGAGTTCAGTTCGAGTTCAG 1140
Qy 1191 CCCATGAATCTGTTGTAAGATGAGCTGAGCTCTACATCAATCTGTAAGGCTATC 1250
Db 1141 CCCATGAATCTGTTGTAAGATGAGCTGAGCTCTACATCAATCTGTAAGGCTATC 1200
Qy 1251 GGGCAAAACAGGAAAGATGAGCTGAGTTCGCTGCTGAGTTCGAGTTCGAGTTCGAGTTCGAG 1310
Db 1201 GGAACAAATGGAAGATGAGCTGAGTTCGCTGCTGAGTTCGAGTTCGAGTTCGAGTTCGAG 1260
Qy 1311 GCATGGGTGCGAGCCCTGAGCACTGTCAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 1370
Db 1261 GCCATGAGGGGAGAGCTCTTCAACATTCATCACTCAGCTGAGTTCGAGTTCGAGTTCGAG 1320
Qy 1371 CTTCACTACGCGAGTATGCTGCTGGGGCTGAGGCTCTCTGTTGCTGTTGCTGCTGCTGCTGCT 1430
Db 1321 ATGCACTATGCGCAAGTACCTCTCTGCGCTGGGCTGAGTTCGCTGCTGCTGCTGCTGCTGCT 1380
Qy 1431 ATCTGCAACTGCGCAGCAGGAGAAATGCTTTTGTGAGTGGTGTAGTAAAGGGC 1490
Db 1381 ATCTGCAAAATCCGAGCAGGAGAAATGCTTTTGTGAGTGGTGTAGTAAAGGGC 1440
Qy 1491 TCCAGGATTAAGAGGAGGCTATCAGGCTCTCTGAGTCCCTGATGTCACAGCTGCCAAG 1550
Db 1441 TCAAGGATTAAGAGGAGGCTATCAGGCTCTCTGAGTCCCTGATGTCACAGCTGCCAAG 1500
Qy 1551 GGCAAGTGTGCAAGAGGAGGCTATGAG 1580
Db 1501 GGCTCTGTGTCAGGAGGAGGAGGCTATGAG 1530

RESULT 9

US-11-136-527-7039

; Sequence 7039, Application US/11136527

; Publication No. US2005028750A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7039
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-7039

Query Match 38.9%; Score 694.6; DB 12; Length 1400;

Best Local Similarity 89.8%; Pred. No. 64e-188;

Matches 730; Conservative 12; Mismatches 71; Indels 0; Gaps 0;

Qy 946 ATCGTTTCACGGCCCCCGATCTCTGTTTGGCAACGGGTCCGTACCCACCAAGG 1005
Db 1 ATCGTTTCACGGCCCCCGATCTCTGTTTGGCAACGGGTCCGTACCCACCAAGG 60
Qy 1006 GCTTCTGCCATCGCAGAGTCTGGCATTCAGAAATGTCAGCAGCTGCGAGTTGGTGGC 1065
Db 61 GCTTCTGCCATCGCAGAGTCTGGCATTCAGAAATGTCAGCAGCTGCGAGTTGGTGGC 120
Qy 1066 CTCTGTTTCTCTCCACCCCTCTTTTACAAAGCCGACCTGTTGTTCAGAAAGTGTTC 1125
Db 121 CCCTGTTTCTCTCCAGCCCTCTTCTACAAAGTGTGACCCGCTGTTGTTCAGAAAGTGTTC 180
Qy 1126 TTGGTCTGAACCTAAACCCAAAGGAGCATTCCTTGTTCCTAGACATCCATCCGCTCACTG 1185
Db 181 TTGGTCTGAACCTAAACCCAAAGGAGCATTCCTTGTTCCTAGACATCCATCCGCTCACTG 240
Qy 1186 GATTCCTCACTGATCTTGTGAAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1245
Db 241 GATTCCTCACTGATCTTCCGTGAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 300
Qy 1246 GCATCGGGCAACAGAGGAGATCGAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1305
Db 301 GCATCGGGCAACAGAGGAGATCGAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 360
Qy 1306 GCGGAGCAATGGGTGGCAAGCCCTGAGCAGCTGTTCTACAGCAGCTGGTCTGATGCCCC 1365
Db 361 GCGGAGTATGGGTGGCAAGCCCTGAGCAGCTGTTCTACAGCAGCTGGTCTGATGCCCC 420
Qy 1366 AGTTCTTCACTACGCGCAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGGTGC 1425
Db 421 AGTTCTTCACTACGCGCAGTATGCTGCTGGGCTTGGAGGCTCTCTGTTGCTGGTGC 480
Qy 1426 CCATCATCTGCCAATCGCCAGCCAGGAGAAATGCTTTTGTGAGTGGTGTAGTAAAA 1485
Db 481 CCATCATTTTACCACCTGCGCAGCAGGAGAAATGCTTTTGTGAGTGGTGTAGTAAAA 540
Qy 1486 AGGGCTCCCAAGATAAGGAGGCCATTCAGGCTTCTCTGAGTCCCTGATCTCACCAGCTG 1545
Db 541 AGGGCTCGCAGATTAAGGAGGCCATTCAGGCTTCTCTGAGTCTCTGATGTCTCACCAGCTG 600
Qy 1546 CCAAGGCGCAGGTGCTGCAAGAAAGCAAGCTATAGGGTCTCTGAGGACCTATTAAGGCCCTC 1605
Db 601 CCAAGGCGCAGGTGCTGCAAGAAAGCAAGCTATAGGGTCTCTGAGGACCTATTAAGGCCCTC 660
Qy 1606 CAAACCTGATGCTTGGTTCAGACCCAGCCAGCTCCCTACACCCGCTCTCTGAGGACT 1665
Db 661 CAAACCTGATGCTTGGTTCAGACCCAGCCAGCTCCCTACACCCGCTCTCTGAGGACT 720
Qy 1666 CTCTCAGCGGACAGCCCAACAGTGCATGGCTGAGCCCTGAGCCCTGAGCTGCACCTGTCGCG 1725
Db 721 CTCTCAGCGGACAGCCCAACAGTGCATGGCTGAGCCCTGAGCTGCACCTGTCGCG 780
Qy 1726 ACCCAGCGCAGTGGATGCCACGCTATGCA 1758

Db 541 CAGACGACCATCCAGCCCTACACCCCGCTTCTTGGAGACTCTCTCAGCGGACAGTC 598

RESULT 12
US-11-136-527-1803
; Sequence 1803, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1803
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1803

Query Match 9.2%; Score 163.8; DB 12; Length 2076;
Best Local Similarity 47.1%; Pred. No. 2.3e-36;
Matches 572; Conservative 2; Mismatches 629; Indels 12; Gaps 2;

Qy 97 CCCGCGGCGCTGCTTTGCTGCGCTCGCGGTGTGCATGATCCTCATGGTGCCTCCCTCA 156
Db 271 CTCCTGCTGCTGCTGGTACAGAGTGTACGCTGTAGTGGCTCGAGTCTTTTCAGAGGCGAG 330
Qy 157 TCAAGCAGCAGGTGCTCAAGAAATGTCCGCATAGACCCGAGCAGGCTGTCTTCCGGGATGT 216
Db 331 TGGACACAGCATCAGAGAGATATGTTATTAACAAATGGTACCAAGTCTTTGATTCCT 390
Qy 217 GGAAGGAGATCCCGCTCCCTTTCTACTTGTCTGTCTACTTCTCGAAGTGTCAACCCAA 276
Db 391 GGGAGAGCGCCCTCTACTCTGTGTACATCCAGTATTTATTTCTCAATGTCCACCAATCCAG 450
Qy 277 ACAGGTCTCTCAAGCGCAGAGCCAGTGTGCGGCGGTGGACCTGTCTTACACAGG 336
Db 451 AGGAGATCTCTCAAGGAGAAATCCCTCTGTAGAGAGTGGGCGGTACACCTACACAGG 510
Qy 337 AGTTTCAGACAAAAGGTCAACATCACTTTCAATGACACGACACCGTGTCTTCTGTGGAGA 396
Db 511 AGCTCAGGACAGGACCAAGCTTCAGTTGGAGAAATGGACCAACATATCTCCCTCA 570
Qy 397 ACCGACGCTCCATTTCCAGCTGACACAGTGCATGGCTCAGAGAGTGACTTACATTTGTAC 456
Db 571 CCAATAAGGCATATATTTTGAACGAAACCAAGTCTGTTGGAGACCCCTACCGTTGACTTGA 630
Qy 457 TGCCTAACATCTGGTCTCTGGGGGCTCGATATTGATGGAGAGCAAGCTGTGAGCCCTGA 516
Db 631 TTGAACAATAAATATTTCTCTGTTGACTGTGTGGAAATGGCCGAGCAGCCCTTCTCTCA 690
Qy 517 AGCTGATGATGACCTTGGCGCTGTCTACCATGGCGCAGCGCTTTTATGAACGACAG 576
Db 691 GGGAGATCATCGAGCCCATGCTGAAGCTTATCAGCAGACGCTGTTGTCTACTCACACTG 750
Qy 577 TTGGTGAGATCCTGTGGGGCTATGACGATCCCTTCTCGTCATTTTCTCAACAGCTACCTCC 636
Db 751 TACATGAATCTCTCTGGGGCTTACAAAGATGAGTCTGTGCTGTCTCATATTTTCAGAC 810
Qy 537 CAGACATGCTTCCCATTAAGGGCAATTTGGCGCTGTTTGGTGGATGACAACTCGAATT 696
Db 811 CTGACGCTCTCCC-----TAACTTTGGCGCTGTTCTATGAGAGAAATGGAACATAATG 861
Qy 697 CTGGGCTCTTCACTGTCTTCAAGGCGCTCCAGAAATTTTCAGCAGGATCCATCTGTGGACA 756
Db 862 ATGGGAGATGTTTCTGACTGAGAGGACAAATTAACCTGAACTTTTACAAAATTTGGG 921
Qy 757 AATGGAACGGACTCAGCAAGATCGATTATTGGCATTTCAGAGCAGTGAACATGATCAATG 816

Db 922 AGTGGAAATGAAAAACGTCGCTGGACTGGTGGACGCGACACGTGCAATATGATCAACG 981
Qy 817 GGACTTCCGGGAGATGTGGGCAACCTTTCATGACACCCGAATCTGCTCGAATTTCTTCA 876
Db 982 GGACAGAGGAGATCTTTTTCACCCATTATAGCAAGGATGAGACCTGTACATCTTCC 1041
Qy 877 GCGCGAGGAGCATGAGGTCCATGAAGTGCACCTACACGAATCAAGGTTGTTGAAGGCA 936
Db 1042 CATCTGACTTCTCAGGTCCGTCTATATAACTTTTCAGTAGCTTTGAGAACGTAGAGGAC 1101
Qy 937 TTCCACGATATGCTTTCACGCGCCCGCATACTCTGTTTGGCAAGGCTGCTTACCCAC 996
Db 1102 TGCTGCTTTTTCGGTATAAGGTGCTGSCAGAAATACCTAGCCAAATTCCTCGAAAAACGCTG 1161
Qy 997 CCAAC---GAAGGCTTCTGCCCATGCCGAGAGTCTGCAATTCAGAAATGTCAGCACTGCA 1053
Db 1162 GCTTCTGTATACCGGAGGAAATGTCATGACGCGGGAGTCTGACGTGACGATTTGCA 1221
Qy 1054 GGTGCGCTGCTGCTTCTTCTCCACCCCACTTTTACAAAGCGGACCCCTGTGTGT 1113
Db 1222 AGAATGCTGCGCCATTTATCATGCTTTTCCACACTTTTACCAAGCGGACGAGAAGTTCG 1281
Qy 1114 CAGAGCTGTTCTGCTCTGAACCTTAACCCAAAGGAGCATTCCTTCTTCTAGACATCC 1173
Db 1282 TTTGCGCCATAAAGGCGCATGCTCCAAACAAAGGAAGAACATGAGTCAATTTGTGGACATTA 1341
Qy 1174 ATCCGCTCAGTGGATCCCATGAACTGTTCTGTGAAGATGCAGCTGAGCTCTACATCA 1233
Db 1342 ATCTTTGACAGAAATTTTAAAGGSCCAAGAGATTCCAAAATCAACACGATGATTA 1401
Qy 1234 AATCTGTCAAGGATCGGGCAACAGGGAAGATCGAGCCAGTAGTTCTCCGTTGCTGT 1293
Db 1402 AGAAGCTGGATGACTTTGTGAAACGGGAAACATTAGGCTATGKTTTCCAGTGATGT 1461
Qy 1294 GGTTCGACAGAGCG 1308
Db 1462 ATCTCAATGAGAGTG 1476

RESULT 13
US-11-136-527-5899
; Sequence 5899, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5899
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5899

Query Match 7.1%; Score 127; DB 12; Length 1400;
Best Local Similarity 49.9%; Pred. No. 6.3e-26;
Matches 375; Conservative 2; Mismatches 362; Indels 12; Gaps 2;

Qy 561 TTTATGAACCGCAGTGTGTGAGATCCTGTGGGCTATGACGATCCCTTCGTGCAATTT 620
Db 59 TTTGTCACTCACACTGTACATGAACCTGCTCTGGGCTTACAAAGATGAGGTCTTGTGCTC 118
Qy 621 CTCACACGCTACCTCCAGACATGCTTCCATFAAGGGCAAAATTTGGCTGTTTGTGGG 680
Db 119 GTCCATATTTTCAGACCTGACGCTCTCC-----TAACTTTGGCTGTTCTATGAG 169

QY 681 ATGAACAACACTCGAATTCCTGGGGTCTTCACTGTCTTCCACGGCGCTCCAGAAATTTTCAGCAGG 740
Db 170 AGAAATCGAACTAATGATGGGAGTAGTGTCTTCTGACTGGAGAGGACAATTAACCTGAAC 229
QY 741 ATCCATCTGGTGGCAAAATGGAACGGACTCAGCAAGATCGAATTAATGGCAATTCAGAGCAG 800
Db 230 TTTTCAAAAAATTTGGAGTGGAAATGGAAAAACGCTGCTGGACTGGTGGAGCAGCGACAG 289
QY 801 TGTAACATGATCAATGGGACTTCGGGCGAGATGGGCGACCTTCATGACACCGGATCC 860
Db 290 TGCATATGATCAACGGGACAGCGGAGATCTTTTCCACCATTAATAAGCAAGGATGAG 349
QY 861 TCGCTGGAATTTCTTCAGCCCGGAGCATGAGGTCCATGAAGTGCATCAACGCAATCA 920
Db 350 ACCCTGTACATCTTCCCATCTGACTCTGCGAGGTCCGCTCTATATAACTTTTCAGTAGCTTT 409
QY 921 AGGTGTTTGAAGCATTCACAGTATCGCTTCAAGGCCCCCGGATCTGTTTGGCCAAAC 980
Db 410 GAGAACGTAGAGGACTCGCTGCTTTTCGGTATAAGGTGCTGCAGAAATACTAGCCAAAT 469
QY 981 GGGTCGCTTACCCACCCAAAC---GAAGGCTTCTGCCCATGCGGAGAGTCTGGCATTTCAG 1037
Db 470 TCCTCCGAAACGCTGCTCTGATACCGAGGAAACTGSCATGGACGGGAGTCTG 529
QY 1038 AATGTACGACCTCTGAGGTTTGGTGGCCCTCTGTTTCTCTCCACCCCGGACTTTTACAAAC 1097
Db 530 AACGTACGATTTGCAAGATGGTGGCCCATATCATGTCTTCCACACTTTTACCAA 589
QY 1098 GCCGACCTGTGTTGTGAGAGCTGTTTGGTGTGAACCTTAACCCAAAGGAGCATTC 1157
Db 590 GCCGACGAGAAGTTGCTTGGCCCATAAAGGCGATGGCTCCAAACAGGAAGAACATGAG 649
QY 1158 TTGTTCTAGACATCCATCGGTCACTGGGATCCCATGAACTGTTCTGTAAGATGCG 1217
Db 650 TCAATTTGGACATTAATCTTTGACAGGAATTAATTTAAGAGGGSCTAAGAGATTCCAA 709
QY 1218 CTGAGCCTCTACATCAAAATCTGTCAGGGCATCGGCAAAACAGGGAAGATCGAGCCAGTA 1277
Db 710 ATCAACACGTACGTTAAGAGCTGGATGACTTTGTGGAAACGGGAACATTAGMCTATG 769
QY 1278 GTTCTGGCTGTGTTGGTTCGAACACAGCG 1308
Db 770 KTTTTCCAGTGATGTCTCAATGAGAGTG 800

RESULT 14
US-11-128-061-2632
; Sequence 2632, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2632
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-2632

Query Match 5.4%; Score 97.2; DB 12; Length 496;
Best Local Similarity 87.8%; Pred. No. 1.4e-17;
Matches 130; Conservative 0; Mismatches 13; Indels 5; Gaps 2;
QY 1638 AGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGCCACCGATGGCC 1697
Db 1 AGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCGCCAGTGCATGGCC 60
QY 1698 TGAGCCCCCAGATGTCAACCTGTTCGCGACGCGACATGGATGCCACCGCATGTGCA 1757
Db 61 TGAGCCCCCAGATGTCAACCTGTTC---TGCACAGCACACATGCGCCCGGCGTGTGCA 116
QY 1758 AAAACAACCTCAGGACACGAGGACAGACC 1785
Db 117 AATC-ACTCAGGACACGAGGACAGACC 143
RESULT 15
US-11-128-061-6274
; Sequence 6274, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6274
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-6274

Query Match 5.4%; Score 97.2; DB 12; Length 496;
Best Local Similarity 87.8%; Pred. No. 1.4e-17;
Matches 130; Conservative 0; Mismatches 13; Indels 5; Gaps 2;
QY 1638 AGTCCCTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGCCACCGATGGCC 1697
Db 1 AGCCCTTACACCCCGCTTCTTGAGGACTCTCTCAGCGGACAGTCCGCCAGTGCATGGCC 60
QY 1698 TGAGCCCCCAGATGTCAACCTGTTCGCGACGCGACATGGATGCCACCGCATGTGCA 1757
Db 61 TGAGCCCCCAGATGTCAACCTGTTC---TGCACAGCACACATGCGCCCGGCGTGTGCA 116
QY 1758 AAAACAACCTCAGGACACGAGGACAGACC 1785
Db 117 AATC-ACTCAGGACACGAGGACAGACC 143

Search completed: February 23, 2006, 18:46:02
Job time : 549.539 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 23, 2006, 12:34:44 ; Search time 152 Seconds
(without alignments)
1471.341 Million cell updates/sec

Title: US-08-765-108-8
Perfect score: 2681
Sequence: 1 MGSSRRARWALGALGALL.....YSESLMSPAAGTGVLEAKL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	2	AAW93575 Mouse sca
2	2681	100.0	509	2	AAW93575 Mouse sca
3	2681	100.0	509	5	Abb57092 Mouse isc
4	2681	100.0	509	5	Aae21525 Murine sc
5	2681	100.0	509	8	Adj53337 Murine SR
6	2681	100.0	509	9	Adz13455 Murine ca
7	2681	100.0	509	9	Aeb03940 Murine SC
8	2681	100.0	519	8	Abo84950 Murine ca
9	2681	100.0	519	8	Adr67033 Murine ca
10	2677	99.9	509	8	Adu51468 Mouse sca
11	2504	93.4	509	8	Adu51466 Rat scave
12	2504	93.4	510	7	Ades56446 Rat Prote
13	2504	93.4	510	7	Ades56442 Rat Prote
14	2479	92.5	509	7	Ades55241 Rat Prote
15	2468	92.1	506	9	Adz13453 Murine ca
16	2447	91.3	509	2	Ar88465 Hamster s
17	2447	91.3	509	2	AAW93574 Hamster s
18	2447	91.3	509	2	AAW93574 Hamster s
19	2447	91.3	509	5	Abg33056 Hamster S
20	2447	91.3	509	5	Aae21523 Murine s
21	2447	91.3	509	6	Abo27241 Human sca
22	2447	91.3	509	8	Adj46121 Human sca
23	2447	91.3	509	8	Adj53335 Hamster S
24	2447	91.3	509	8	Adu51467 Hamster s

25	2296	85.6	509	9	AEB03938	Aeb03938 Hamster S
26	2200	82.1	509	6	ABO27240	ABO27240 Human sca
27	2200	82.1	509	6	ADJ46119	ADJ46119 Human sca
28	2200	82.1	509	9	ADZ13464	ADZ13464 Human can
29	2200	82.1	509	9	ADZ13458	ADZ13458 Human can
30	2200	82.1	514	9	ADZ13466	ADZ13466 Human can
31	2193	81.8	509	2	AAW97899	AAW97899 Human SR-
32	2193	81.8	509	2	AAW97900	AAW97900 Human SR-
33	2193	81.8	532	4	ABE12012	ABE12012 Human SR-
34	2193	81.8	532	7	ABE09273	ABE09273 Novel pro
35	2192	81.8	509	2	AAW49573	AAW49573 Human CLA
36	2192	81.8	509	6	AAO31106	AAO31106 Human CD3
37	2192	81.8	509	8	ADL61295	ADL61295 Human sca
38	2192	81.8	510	7	ADE56448	ADE56448 Human Pro
39	2192	81.8	510	7	ADE56444	ADE56444 Human Pro
40	2160	80.6	509	7	ADE40210	ADE40210 Human NOV
41	2068.5	77.2	537	4	ABG22317	ABG22317 Novel hum
42	2051	76.5	481	7	ADE08291	ADE08291 Novel pro
43	2022.5	75.4	552	6	ABR62035	ABR62035 Human SR-
44	2022.5	75.4	552	7	ADE55243	ADE55243 Human Pro
45	2022.5	75.4	552	8	ADP23287	ADP23287 PRO polyp

ALIGNMENTS

RESULT 1
AAW93575
ID AAW93575 standard; protein; 509 AA.
XX
AC AAW93575;
XX
DT 17-JUN-1999 (first entry)
XX
DE Mouse scavenger receptor class B-I protein.
XX
KW Scavenger receptor class B type I; mouse; steroid production; HDL; cholesterol; cholesteryl ester transport; high-density lipoprotein; lipoprotein; liver; steroidogenic tissue; SR-BI; contraception; treatment; disorder; overproduction; underproduction; menopause; breast cancer; prostate cancer; endometriosis; fibroid tumour.
XX
OS Mus sp.
XX
PN WO9911288-A1.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US018463.
XX
PR 05-SEP-1997; 97US-0057943P.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Krieger M;
XX
PI WPI; 1999-204984/17.
XX
DR N-PSDB; AAX23404.
XX
DR Modification of steroid production in mammals - by administering modulator of SR-BI expression or activity.
XX
PT Disclosure; Page 81-82; 86pp; English.
XX
CC This invention describes a method for modifying steroid production in a mammal which comprises administering a compound that alters cholesterol or cholesteryl ester transport from high-density lipoprotein (HDL) or other lipoproteins to liver or steroidogenic tissues via SR-BI (scavenger receptor class B type I). This method is useful for female contraception, for treating disorders characterised by overproduction of steroids, for treating disorders characterised by underproduction of steroids, especially menopause, for treating disorders that can be treated by decreasing steroid production, especially breast cancer, prostate cancer, CC

```
CC endometriosis or fibroid tumours
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFLSYVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENRSLH 120
QY 121 FQPKSHGSES DYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Db 121 FQPKSHGSES DYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
QY 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMMNSNGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMMNSNGVFTVFTGVQNFRIHLVDKWNGL 240
QY 241 SKIDYWHSEQNMINGTSGQMWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYWHSEQNMINGTSGQMWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
Db 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
QY 361 LNPDPKSHLSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLLWPFQSG 420
Db 361 LNPDPKSHLSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLLWPFQSG 420
QY 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQEKCFLFWSGSKG 480
Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQEKCFLFWSGSKG 480
QY 481 SQDKEAIQAYSESILMSPAAGTGLVQEAQL 509
Db 481 SQDKEAIQAYSESILMSPAAGTGLVQEAQL 509

RESULT 2
AAY44020
ID AAY44020 standard; protein; 509 AA.
XX
AC AAY44020;
XX
DT 18-JAN-2000 (first entry)
XX
DE Mouse Scavenger receptor class BI protein.
XX
KW Hamster; scavenger receptor; modulation; cholesterol transport; lipid;
KW lipoprotein; mammalian cell; plasma; expression; clearance rate; HDL;
KW high density lipoprotein; ester; blood.
XX
OS Mus sp.
XX
PN US5962322-A.
XX
PD 05-OCT-1999.
XX
PF 15-NOV-1996; 96US-00749907.
XX
PR 15-NOV-1996; 96US-00749907.
XX
PA (UTPE-) UNIV PENNSYLVANIA.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Krieger M, Rigotti A, Kozarsky K;
```

```
XX
DR WPI; 1999-589717/50.
DR N-PDB; AA230616.
XX
FT Modulating cholesterol transport for the control of cholesterol levels in
PT blood.
XX
PS Disclosure; Col 29-32; 23pp; English.
XX
CC This sequence represents the mouse scavenger receptor class BI (SR-BI)
CC which is used in a method of modulating cholesterol transport. The method
CC comprises selectively altering the transport of lipid, cholesterol and/or
CC lipoproteins (or their components) into and out of mammalian cells to
CC alter plasma cholesterol levels, by administering a compound which alters
CC the expression or activity of the SR-BI scavenger protein receptor. This
CC alters the rate of clearance of the protein component of high density
CC lipoprotein (HDL) as compared to the ester component of HDL. The method
CC may be used to control cholesterol levels in the blood plasma of mammals
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFLSYVFFVFNPNVNEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSFVENRSLH 120
QY 121 FQPKSHGSES DYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Db 121 FQPKSHGSES DYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
QY 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMMNSNGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMMNSNGVFTVFTGVQNFRIHLVDKWNGL 240
QY 241 SKIDYWHSEQNMINGTSGQMWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYWHSEQNMINGTSGQMWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
Db 301 FTAPDTLIFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYADPVLSEAVLG 360
QY 361 LNPDPKSHLSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLLWPFQSG 420
Db 361 LNPDPKSHLSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLLWPFQSG 420
QY 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQEKCFLFWSGSKG 480
Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQEKCFLFWSGSKG 480
QY 481 SQDKEAIQAYSESILMSPAAGTGLVQEAQL 509
Db 481 SQDKEAIQAYSESILMSPAAGTGLVQEAQL 509

RESULT 3
ABB57092
ID ABB57092 standard; protein; 509 AA.
XX
AC ABB57092;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related protein sequence SEQ ID NO:202.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
```

vasospastic ischaemia; ischaemic condition; ischaemic disease.

Mus musculus.

WO200188188-A2.

22-NOV-2001.

18-MAY-2001; 2001WO-JP004192.

18-MAY-2000; 2000JP-00145977.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

WPI; 2002-034733/04.

N-PSDB; AB199330.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

Claim 2; Page 576-579; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in AB57020 to AB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention

Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVWILVPSLIKQVILKNVRIDPSSLSFGWKKEIP 60
Dy 1 MGSSRRARWALGALGALLFAALGVVWILVPSLIKQVILKNVRIDPSSLSFGWKKEIP 60
Qy 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGPVYVREPRQKVNITFNDNDTVSFVENSRLH 120
Dy 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGPVYVREPRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSSSDYILVPLNVLGSSILMESKPVSLKLMNTLALVTMGQAFMNTVGEIL 180
Dy 121 FQPKSHGSSSDYILVPLNVLGSSILMESKPVSLKLMNTLALVTMGQAFMNTVGEIL 180
Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNPRIHLVDKNGL 240
Dy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNPRIHLVDKNGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPMTPESSLEPSPPEACHSMKLTYNESRVFEGIPYR 300
Dy 241 SKIDYHSEQCNMINGTSGQWAPMTPESSLEPSPPEACHSMKLTYNESRVFEGIPYR 300
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Dy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSLEFLDIHPTVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVVPLPLWFEOSG 420

Db 361 LNPMPKHSLEFLDIHPTVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVVPLPLWFEOSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGIGLLLVPIICQLRSQEKCFLFWSGSKG 480
Dy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGIGLLLVPIICQLRSQEKCFLFWSGSKG 480
Qy 481 SODKEATQAYSESLMSPAAGKTVLQEAKL 509
Dy 481 SODKEATQAYSESLMSPAAGKTVLQEAKL 509

RESULT 4

AAE21525

ID AAE21525 standard; protein; 509 AA.

AC AAE21525;

DT 16-JUL-2002 (first entry)

DE Murine scavenger receptor type B-I (SR-BI).

KW Scavenger receptor protein type BI; low density lipoprotein; LDL; murine; SR-BI.

XX Mus sp.

XX US6350859-B1.

XX 26-FEB-2002.

XX 02-FEB-1999; 99US-00241581.

XX 23-JUN-1994; 94US-00265428.

XX 27-MAR-1997; 97US-00765108.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Krieger M, Acton SL, Rigotti A;

XX WPI; 2002-314680/35.

XX N-PSDB; AAD33917.

PT Antibody specific for scavenger receptor protein type BI useful for detection, characterization or isolation of receptor proteins, as well as inhibiting scavenger protein binding to low density lipoprotein.

XX Claim 1; Col 49-52; 41pp; English.

XX The invention relates to an antibody specific for scavenger receptor protein type B-I (SR-BI) derived from murine and hamster. Antibodies of the invention are useful for detection, characterisation and isolation of receptor proteins and for inhibiting scavenger protein binding to low density lipoprotein (LDL). The present sequence is murine SR-BI protein

Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.8e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVWILVPSLIKQVILKNVRIDPSSLSFGWKKEIP 60
Dy 1 MGSSRRARWALGALGALLFAALGVVWILVPSLIKQVILKNVRIDPSSLSFGWKKEIP 60
Qy 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGPVYVREPRQKVNITFNDNDTVSFVENSRLH 120
Dy 61 VPFLSVYFVFEVNPNEVLNGQKPVVRERGPVYVREPRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSSSDYILVPLNVLGSSILMESKPVSLKLMNTLALVTMGQAFMNTVGEIL 180
Dy 121 FQPKSHGSSSDYILVPLNVLGSSILMESKPVSLKLMNTLALVTMGQAFMNTVGEIL 180
Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNPRIHLVDKNGL 240

Db 181 WGYDDPFVHFLNTYLPDMLPIKGRGFLVGMNNSGVFTVFTGVQVFSRIHLVDKWNGL 240
 Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300
 Db 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300
 Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Qy 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKGIGQTKIEBPVVLPLLWPFQSG 420
 Db 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKGIGQTKIEBPVVLPLLWPFQSG 420
 Qy 421 AMGGKPLSTFTQVLMPQVLYHQAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
 Db 421 AMGGKPLSTFTQVLMPQVLYHQAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
 Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509
 Db 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 5

ADJ53337 ID ADJ53337 standard; protein; 509 AA.
 XX AC ADJ53337;
 XX DT 06-MAY-2004 (first entry)
 XX DE Murine SR-BI scavenger receptor polypeptide.
 XX KW Mouse; SR-BI; scavenger receptor; HDL receptor; lipid; cholesterol;
 KW lipoprotein; bile acid; steroid hormone; vitamin A; atherosclerosis;
 KW adipocyte fat uptake; endocrine disorder; antiarteriosclerotic; receptor;
 KW scavenger receptor class BI.
 XX OS Mus sp.
 XX FN US2003167475-A1.
 XX PD 04-SEP-2003.
 XX PF 24-JUN-2002; 2002US-00178611.
 XX PR 15-NOV-1996; 96US-00749907.
 XX PR 30-AUG-1999; 99US-00385799.
 XX PA (KOZA/) KOZARSKY K.
 XX PA (RIGO/) RIGOTTI A.
 XX PA (KRIE/) KRIEGER M.
 XX PI Kozarsky K, Rigotti A, Krieger M;
 XX DR WPI: 2004-246237/23.
 XX DR N-PSDB; ADJ53336.
 XX PT Screening for agents that influence lipid transport, useful e.g. for
 PT treating or preventing atherosclerosis, based on modulation of the SR-BI
 PT scavenger receptor.
 XX PS Disclosure; SEQ ID NO 4; 22pp; English.

CC The invention relates to a method for screening compounds that alter
 CC transport of lipids, cholesterol, lipoproteins or their components,
 CC mediated by the SR-BI scavenger receptor (SR-BI HDL receptor) or a
 CC homologue. The test compound is administered to an animal and cholesterol
 CC or bile acid levels, production levels of steroid hormones or alterations
 CC in chemical composition of lipids, lipoproteins, cholesterol, steroid
 CC hormones, bile acids and vitamin A is measured. Agents that alter
 CC transport of lipids, cholesterol or lipoproteins are potentially useful

CC for the treatment or prevention of atherosclerosis, fat uptake by
 CC adipocytes and some endocrine disorders. This sequence represents the
 CC murine SR-BI scavenger receptor of the invention.
 XX SQ Sequence 509 AA;
 Query Match 100.0%; Score 2681; DB 8; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGSSRARWALGIGALGALLFAALGVVIMLVPSLIKQVLLKVRIDPSSLSFGMMKEIP 60
 Db 1 MGSSRARWALGIGALGALLFAALGVVIMLVPSLIKQVLLKVRIDPSSLSFGMMKEIP 60
 Qy 61 VPYLSVYFEVYNPNVNLNGQKPVYRERGYPYVYRFRQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPYLSVYFEVYNPNVNLNGQKPVYRERGYPYVYRFRQKVNITFNDNDTVSFVENRSLH 120
 Qy 121 FQDKSHGSES DYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFNMRTVGEIL 180
 Db 121 FQDKSHGSES DYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFNMRTVGEIL 180
 Qy 181 WGYDDPFVHFLNTYLPDMLPIKGRGFLVGMNNSGVFTVFTGVQVFSRIHLVDKWNGL 240
 Db 181 WGYDDPFVHFLNTYLPDMLPIKGRGFLVGMNNSGVFTVFTGVQVFSRIHLVDKWNGL 240
 Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300
 Db 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVPEGIPTYR 300
 Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
 Qy 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKGIGQTKIEBPVVLPLLWPFQSG 420
 Db 361 LNPMPKESLFLDIHPVTGIPMNCVVKQSLYIKSVKGIGQTKIEBPVVLPLLWPFQSG 420
 Qy 421 AMGGKPLSTFTQVLMPQVLYHQAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
 Db 421 AMGGKPLSTFTQVLMPQVLYHQAQVLLGLGGLLLVPIICQLRSQEKCFLEWGSKKG 480
 Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509
 Db 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 6

ADZ13455 ID ADZ13455 standard; protein; 509 AA.
 XX AC ADZ13455;
 XX DT 16-JUN-2005 (first entry)
 XX DE Murine cancer-associated protein #109.
 XX KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
 KW cytosolic.
 XX OS Mus sp.
 XX FN WO2005031001-A2.
 XX PD 07-APR-2005.
 XX PF 23-SEP-2004; 2004WO-US031617.
 XX PR 23-SEP-2003; 2003US-00669920.
 XX PA (CHIR) CHIRON CORP.
 XX PI Morris DW, Malandro MS;

XX WPI; 2005-273395/28.
 DR N-PSDB; ADZ13454.
 XX
 PT Nucleic acid array useful for detecting cancer associated nucleic acid,
 PT comprises two or more nucleic acid probes.
 XX
 PS Disclosure; SEQ ID NO 975; 198pp; English.
 XX
 CC The invention relates to a nucleic acid array for detecting a cancer
 CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
 CC The invention also relates to a peptide array comprising two or more
 CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
 CC that binds to a polypeptide, an isolated antibody or its fragment which
 CC binds to a polypeptide, which is prepared by immunizing a host animal
 CC with a composition comprising the polypeptide or its antigen binding
 CC fragment and collecting cells from the host expressing antibodies against
 CC the antigen or its antigen binding fragment, a composition comprising the
 CC antibody and a carrier, a method of screening for anticancer activity, a
 CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
 CC method of treating cancer and a method of inhibiting expression of a CA
 CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
 CC nucleic acids. The antibody is useful for detecting the presence or
 CC absence of cancer cells in an individual which involves contacting cells
 CC from the individual with the antibody and detecting a complex of a CA
 CC protein from the cancer cells and the antibody, where the detection of
 CC the complex correlates with the presence of cancer cells in the
 CC individual. The composition is useful for inhibiting growth of cancer
 CC cells in an individual or for delivering a therapeutic agent to cancer
 CC cells in an individual. The invention is also useful for diagnosing
 CC cancer, for treating cancer and for inhibiting expression of a CA gene in
 CC a cell. This sequence represents a murine cancer-associated protein of
 CC the invention.
 XX
 SQ Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 9; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRAEWALGICGALLFAALGVMLVPSLIKQVLKNVRIDPSSISFGWKKEIP 60
 Db 1 MGSSRAEWALGICGALLFAALGVMLVPSLIKQVLKNVRIDPSSISFGWKKEIP 60
 Qy 61 VPFFYLVVFFVWVNEVNLGQKPVRRGPGVYVREFRQKNITFNDNDTVSFVENRSLH 120
 Db 61 VPFFYLVVFFVWVNEVNLGQKPVRRGPGVYVREFRQKNITFNDNDTVSFVENRSLH 120
 Qy 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMNTLALVTMGQAFMNRVTGSEIL 180
 Db 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMNTLALVTMGQAFMNRVTGSEIL 180
 Qy 181 WGYDDPFVHFLNTLPDMLPIKGFGLVGMNNSGVFTTGTQVNFSTRHLVDKWNGL 240
 Db 181 WGYDDPFVHFLNTLPDMLPIKGFGLVGMNNSGVFTTGTQVNFSTRHLVDKWNGL 240
 Qy 241 SKIDYWHSEQCNMINGTSGQWAPMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
 Db 241 SKIDYWHSEQCNMINGTSGQWAPMTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
 Qy 301 FTPADTLFANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVIG 360
 Db 301 FTPADTLFANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVIG 360
 Qy 361 LNPDPKHSFLDHPVTGIPMNCVSKQLSYIKSVKIGIQGTGKIEPVVPLPLWFEQSG 420
 Db 361 LNPDPKHSFLDHPVTGIPMNCVSKQLSYIKSVKIGIQGTGKIEPVVPLPLWFEQSG 420
 Qy 421 AMGGKPLSTFTQVLVMPQVLYHAYVLLGGLLLVPIICQLRSQEKCFLFWSGSKKG 480
 Db 421 AMGGKPLSTFTQVLVMPQVLYHAYVLLGGLLLVPIICQLRSQEKCFLFWSGSKKG 480
 Qy 481 SQDKEAIOAYSESLMSPAAGTGLVQEA 509

DB 481 SQDKEAIOAYSESLMSPAAGTGLVQEA 509
 RESULT 7
 AEB03940
 ID AEB03940 standard; protein; 509 AA.
 AC AEB03940;
 XX
 DT 25-AUG-2005 (first entry)
 DE Murine Scavenger Receptor Class B-1, SEQ ID 4.
 KW Antilipemic; transgenic animal; Scavenger Receptor Class B-1;
 KW high density lipoprotein receptor; cholesterol; lipid.
 OS Mus sp.
 XX
 PN US2005136005-A1.
 XX
 PD 23-JUN-2005.
 XX
 PF 02-SEP-2004; 2004US-00933037.
 XX
 PR 23-JUN-1994; 94US-00265428.
 PR 19-JUN-1995; 95WO-US007721.
 PR 15-NOV-1996; 96US-00749907.
 PR 27-MAR-1997; 97US-00765108.
 PR 30-AUG-1999; 99US-00385799.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Kozarsky K, Rigotti A, Krieger M;
 XX
 DR WPI; 2005-457475/46.
 DR N-PSDB; AEB03939, AEB03942.
 XX
 PT New genetically engineered mouse or derivative cells with inactivated SR-
 PT BI gene expression or activity, useful as a model for designing drugs
 PT that can modulate cholesterol transport.
 XX
 PS Disclosure; SEQ ID NO 4; 21pp; English.
 XX
 CC The present invention relates to a novel genetically engineered mouse, or
 CC cells derived from it, where Scavenger Receptor Class B-1 (SR-BI) gene
 CC expression or SR-BI activity has been inactivated. SR-BI is a high
 CC density lipoprotein (HDL) receptor. It was found that estrogen
 CC downregulates SR-BI under conditions of upregulation of the low density
 CC lipoprotein (LDL)-receptor, and estrogen also upregulates SR-BI in rat
 CC adrenal membranes and other non-placental steroidogenic tissues from
 CC animals treated with estrogen, but not in other non-placental non-
 CC steroidogenic tissues. Also, overexpression of the SR-BI in the hepatic
 CC tissue causes a decrease in blood cholesterol levels. The animal is
 CC useful as a model for designing drugs that can modulate cholesterol
 CC transport or that can stimulate or inhibit the binding to and lipid
 CC movements mediated by SR-BI and redirect uptake and metabolism of lipids
 CC and cholesterol by cells. The present sequence is SR-BI, which was used
 CC to illustrate the invention. Note: The SEQ ID 3 given in the sequence
 CC listing (the sequence shown in AEB03939) is stated to be 1785 nucleotides
 CC in length. However, there appears to be a 1 to 3 nucleotide deletion at
 CC the end of each line of the sequence shown in the sequence listing.
 CC resulting in a sequence that is 1761 nucleotides in length. Therefore a
 CC corrected version of the sequence has been produced with Ns added to
 CC replace the missing nucleotides (the sequence shown in AEB03942). SEQ ID
 CC 3 is stated to encode SEQ ID 4 (given in AEB03940).

Sequence 509 AA;

Query Match 100.0%; Score 2681; DB 9; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Db |||||
Qy 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Db |||||
Qy 61 VPFLSYVFFVVPVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
Db |||||
Qy 61 VPFLSYVFFVVPVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
Db |||||
Qy 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMTLALVTMGORAFMNRVTGGEIL 180
Db |||||
Qy 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMTLALVTMGORAFMNRVTGGEIL 180
Db |||||
Qy 181 WGYDDPPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db |||||
Qy 181 WGYDDPPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db |||||
Qy 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
Db |||||
Qy 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
Db |||||
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db |||||
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db |||||
Qy 361 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIGQTKIHPVVLPLLWPFQSG 420
Db |||||
Qy 361 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIGQTKIHPVVLPLLWPFQSG 420
Db |||||
Qy 421 AMGGKPLSTFTYQLVLMQVLYHYAQQVLLGLGILLVPIICQLRSQEKCFLFWSGSKKG 480
Db |||||
Qy 481 SODKEATQAYSESIMSPAAGTIVLQEA 509
Db |||||
Qy 481 SODKEATQAYSESIMSPAAGTIVLQEA 509
Db |||||

RESULT 8
AB084950
ID AB084950 standard; protein; 519 AA.
XX
AC AB084950;
XX
DT 18-NOV-2004 (first entry)
XX
DE Murine cancer-associated protein (CAP) MP07-081.
XX
KW Mouse; cancer-associated protein; CAP; cancer; cytostatic.
XX
OS Mus musculus.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-499109/47.
XX
DR N-ESDB; ABD33431.
XX
PT Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Disclosure; SEQ ID NO 565; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-

CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene, and
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a murine CAP of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 519 AA;
Query Match 100.0%; Score 2681; DB 8; Length 519;
Best Local Similarity 100.0%; Pred. No. 3.9e-261;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Db |||||
Qy 11 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQVVKVNRIDPSSLSFGMWKEIP 70
Db |||||
Qy 61 VPFLSYVFFVVPVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 120
Db |||||
Qy 71 VPFLSYVFFVVPVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENRSLH 130
Db |||||
Qy 121 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMTLALVTMGORAFMNRVTGGEIL 180
Db |||||
Qy 131 FQPKSHGSESDYIVLPNIIVLGSSILMESKPVSLKMTLALVTMGORAFMNRVTGGEIL 190
Db |||||
Qy 181 WGYDDPPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db |||||
Qy 191 WGYDDPPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFPSRIHLVDKWNGL 250
Db |||||
Qy 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 300
Db |||||
Qy 251 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPTYR 310
Db |||||
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db |||||
Qy 311 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 370
Db |||||
Qy 361 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIGQTKIHPVVLPLLWPFQSG 420
Db |||||
Qy 371 LNPMPKESLFLDIHPVTGIPMNCVVMQSLYIKSVKGIGQTKIHPVVLPLLWPFQSG 430
Db |||||
Qy 421 AMGGKPLSTFTYQLVLMQVLYHYAQQVLLGLGILLVPIICQLRSQEKCFLFWSGSKKG 480
Db |||||
Qy 431 AMGGKPLSTFTYQLVLMQVLYHYAQQVLLGLGILLVPIICQLRSQEKCFLFWSGSKKG 490
Db |||||
Qy 481 SODKEATQAYSESIMSPAAGTIVLQEA 509
Db |||||
Qy 491 SODKEATQAYSESIMSPAAGTIVLQEA 519
Db |||||
RESULT 9
ADR67033
ID ADR67033 standard; protein; 519 AA.
XX
AC ADR67033;
XX
DT 18-NOV-2004 (first entry)
XX
DE Mouse cancer associated protein sequence SEQ ID NO:79.
XX
KW cancer; cancer associated nucleic acid; cancer associated gene;
KW cancer associated protein; CAP; cytostatic; vaccine; gene therapy;
KW lymphoma; leukaemia; mouse.
XX

OS Mus sp.
 FN WO2004074321-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US005000.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 23-SEP-2003; 2003US-00669920.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 FA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652915/63.
 DR N-PSDB; ADR67031, ADR67032.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS Disclosure; SEQ ID NO 79; 166pp; English.
 XX
 CC The present invention describes an isolated cancer associated (CA)
 CC nucleic acid (I). Also described: (1) an expression vector comprising (I)
 CC ; (2) a host cell comprising (I) or the expression vector; (3) a
 CC microarray for detecting a CA nucleic acid; (4) an isolated cancer
 CC associated protein (CAP) polypeptide, encoded within an open reading
 CC frame of a CA sequence; (5) an isolated antibody, or its antigen binding
 CC fragment, that binds to the above polypeptide; (6) a hybridoma that
 CC produces the above monoclonal antibody; (7) a pharmaceutical composition
 CC comprising the above antibody and a pharmaceutical excipient; (8) a kit
 CC for detecting cancer cells, comprising the (monoclonal) antibody
 CC described above; (9) methods for diagnosing cancer or for detecting the
 CC presence or absence of cancer cells in an individual; (10) a method for
 CC inhibiting growth of cancer cells in an individual; (11) a method for
 CC delivering a therapeutic agent to cancer cells in an individual; (12) an
 CC electronic library comprising the above polynucleotide or polypeptide, or
 CC their fragments; (13) methods of screening for anticancer activity or for
 CC a bioactive agent capable of modulating the activity of a CAP; (14)
 CC methods for detecting cancer associated with expression of a polypeptide
 CC in a test cell sample, or with the presence of an antibody in a test
 CC serum sample; (15) a method for treating cancers; and (16) a method for
 CC inhibiting the expression of CA gene in a cell. The CA sequences have
 CC cytostatic activity, and can be used in vaccines, and in gene therapy.
 CC The composition and methods are useful for detecting, diagnosing,
 CC preventing and treating cancers, especially lymphoma and leukaemia. They
 CC may also be used in screening for agents that modulate cancer. The
 CC present sequence represents a cancer associated protein (CAP) sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 519 AA;

Query Match 100.0%; Score 2681; DB 8; Length 519;
 Best Local Similarity 100.0%; Pred. No. 3.9e-261;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60
 Db 11 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 70
 Qy 61 VPFVLSVYFFVFNVEVNGKPVVRERGPVVRERQKVNITFNDNDTVSFVNRSLH 120
 Db 71 VPFVLSVYFFVFNVEVNGKPVVRERGPVVRERQKVNITFNDNDTVSFVNRSLH 130
 Qy 121 FOPDKSHGSESDYIVLPNVLVGGSLMESKPSVSLKAMTIALVTMGORAFNNRTVGIL 180
 Db 131 FOPDKSHGSESDYIVLPNVLVGGSLMESKPSVSLKAMTIALVTMGORAFNNRTVGIL 190
 Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLVGMNNSGVFTFTGQVNFRIHLVDKWNGL 240

Db 191 WGYDDPFFVHFLNTYLPDMLPIKGFGLVGMNNSGVFTFTGQVNFRIHLVDKWNGL 250
 Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
 Db 251 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 310
 Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 360
 Db 311 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFNADPVLSEAVLG 370
 Qy 361 LNPKEHSLFLDHPVTGIPMNCVGMQSLYIKSVKGIQOTCKIPIPVLPILWFQSG 420
 Db 371 LNPKEHSLFLDHPVTGIPMNCVGMQSLYIKSVKGIQOTCKIPIPVLPILWFQSG 430
 Qy 421 AMGGKPLSTFTQVLMPQVLAQYVLLGLGGLLLVPIICQLRSQEKCLFWSGSKG 480
 Db 431 AMGGKPLSTFTQVLMPQVLAQYVLLGLGGLLLVPIICQLRSQEKCLFWSGSKG 490
 Qy 481 SQDKEAIOAYSESLSMSPAAGTIVLQEA 509
 Db 491 SQDKEAIOAYSESLSMSPAAGTIVLQEA 519

RESULT 10
 ADUS1468
 ID ADUS1468 standard; protein; 509 AA.
 XX
 AC ADUS1468;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Mouse scavenger receptor class B type I-related protein - SEQ ID 3.
 XX
 KW Monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
 KW SR-BI; spermatogenesis.
 XX
 OS Mus musculus.
 XX
 PN JP2004331633-A.
 XX
 PD 25-NOV-2004.
 XX
 PF 29-MAY-2003; 2003JP-00152800.
 XX
 PR 10-MAR-2003; 2003JP-00063407.
 XX
 FA (UYKA-) UNIV KANAZAWA TLO YG.
 XX
 DR WPI; 2004-810031/80.
 XX
 PT Novel monoclonal antibody which belongs to mouse IgG1/kappa subclass and
 PT which specifically binds to scavenger receptor class B type I (SR-BI) of
 PT rat origin, useful for functional analysis of SR-BI.
 XX
 PS Disclosure; SEQ ID NO 3; 21pp; Japanese.
 XX
 CC The invention comprises a monoclonal antibody that belongs to the mouse
 CC IgG1/kappa subclass which specifically binds to scavenger receptor class
 CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
 CC is useful for the detection and analysis of SR-BI. The monoclonal
 CC antibody of the invention is useful for analysing the influence of SR-BI
 CC on spermatogenesis in testis. The present amino acid sequence represents
 CC a mouse SR-BI-related protein.
 XX
 SQ Sequence 509 AA;

Query Match 99.9%; Score 2677; DB 8; Length 509;
 Best Local Similarity 99.8%; Pred. No. 9.6e-261;
 Matches 508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60

Db 1 MGSRRARWALGALGALLPAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
 QY 61 VPFFLSVYFVFNPNVNEVLNGOKVVRERGYPVYRERQKVNITFNNDNTVSFVENRSLH 120
 Db 61 VPFFLSVYFVFNPNVNEVLNGOKVVRERGYPVYRERQKVNITFNNDNTVSFVENRSLH 120
 QY 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGGEIL 180
 QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 QY 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
 Db 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
 QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 QY 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIGQTKIBPVVPLLLWFSQSG 420
 Db 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIGQTKIBPVVPLLLWFSQSG 420
 QY 421 AMGKPLSTFTYTLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480
 Db 421 AMGKPLSTFTYTLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480
 QY 481 SQDKEAIQAYSESLMSPAAGTGLVQEAKL 509
 Db 481 SQDKEAIQAYSESLMSPAAGTGLVQEAKL 509

RESULT 11
 ADU51466
 ID ADU51466 standard; protein; 509 AA.
 XX AC ADU51466;
 XX DT 10-FEB-2005 (first entry)
 XX DE Rat scavenger receptor class B type I (SR-BI)-related protein - SEQ ID 1.
 XX KW monoclonal antibody; IgG1/kappa; scavenger receptor class B type I;
 XX KW SR-BI; spermatogenesis.
 XX OS Rattus norvegicus.
 XX PN JP2004331633-A.
 XX XX 25-NOV-2004.
 XX PD 29-MAY-2003; 2003JP-00152800.
 XX PF 10-MAR-2003; 2003JP-00063407.
 XX PR (UYKA-) UNIV KANAZAWA TILO YG.
 XX FA WPI; 2004-810031/80.
 XX DR Novel monoclonal antibody which belongs to mouse IgG1/kappa subclass and
 XX PT which specifically binds to scavenger receptor class B type I (SR-BI) of
 XX PT rat origin, useful for functional analysis of SR-BI.
 XX PS Disclosure; SEQ ID NO 1; 21pp; Japanese.

CC The invention comprises a monoclonal antibody that belongs to the mouse
 CC CC IgG1/kappa subclass which specifically binds to scavenger receptor class
 CC CC B type I (SR-BI) of rat origin. The monoclonal antibody of the invention
 CC CC is useful for the detection and analysis of SR-BI. The monoclonal
 CC antibody of the invention is useful for analysing the influence of SR-BI

CC on spermatogenesis in testis. The present amino acid sequence represents
 CC a rat SR-BI-related protein.
 XX Sequence 509 AA;
 SQ Query Match 93.4%; Score 2504; DB 8; Length 509;
 Best Local Similarity 92.3%; Pred. No. 2.9e-243;
 Matches 470; Conservative 23; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MGSRRARWALGALGALLPAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
 Db 1 MGSRRARWALGALGALLPAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
 QY 61 VPFFLSVYFVFNPNVNEVLNGOKVVRERGYPVYRERQKVNITFNNDNTVSFVENRSLH 120
 Db 61 VPFFLSVYFVFNPNVNEVLNGOKVVRERGYPVYRERQKVNITFNNDNTVSFVENRSLH 120
 QY 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMMTLALVTMGORAFMNRVTGGEIL 180
 QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFRIHLVDKWNGL 240
 QY 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
 Db 241 SKIDYHSEOCNMGNTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
 QY 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDPVLSEAVLG 360
 QY 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIGQTKIBPVVPLLLWFSQSG 420
 Db 361 LNPMPKHSFLDHPVTGIPMNCVVKMQLSLYIKSVKGIGQTKIBPVVPLLLWFSQSG 420
 QY 421 AMGKPLSTFTYTLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480
 Db 421 AMGKPLSTFTYTLVLMPOVLHYAQVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480
 QY 481 SQDKEAIQAYSESLMSPAAGTGLVQEAKL 509
 Db 481 SQDKEAIQAYSESLMSPAAGTGLVQEAKL 509

RESULT 12
 ADE56446
 ID ADE56446 standard; protein; 510 AA.
 XX AC ADE56446;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein D89655, SEQ ID NO 2299.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 510 AA;

Query Match 93.4%; Score 2504; DB 7; Length 510;
Best Local Similarity 92.3%; Pred. No. 2.9e-243;
Matches 470; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGGSSRRARWALGALGALLFAALGVVMIILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGVSSRRARWALGVLGGLLCAALGVMIILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVYFFVVPNEVNLQKVPVRRGPGVYVRRFRQKVNITFNDNDTVSFVNRSLH 120
Db 61 VPFYLSVYFFVVPNEVNLQKVPVRRGPGVYVRRFRQKVNITFNDNDTVSYIENSLR 120
QY 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGQRAFMRNRTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGQRAFMRNRTVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLIHLVDKWNGL 240
QY 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SEVNYHSEOCNMINGTAGQWAPFMTPESSLEFFSPEACRSKMLTYQESRVFEGIPTYR 300
QY 301 FTAPDTLFPANGSVYPPNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFPANGSVYPPNEGFCPCRESGIONVSTCRFCGAPLFLSQPHFYNADPVLSEAVLG 360
QY 361 LNPDKHSLFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGOTGKIBPVVPLLLWFSQSG 420
Db 361 LNPDKHSLFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGOTGKIBPVVPLLLWFSQSG 420
QY 421 AMGGKPLSTFTYTQVLVMPQVLYHYAYVLLGLGGLLLVPIICQLRSQEKCFLWFSQSGK 480
Db 421 AMGGKPLSTFTYTQVLVMPQVLYHYAYVLLGLGGLLLVPIICQLRSQEKCFLWFSQSGK 480
QY 481 SODKEATQAYSESLSMSPAAGTIVLOEAKL 509
Db 481 SODKEATQAYSESLSMSPAAGTIVLOEAKL 509

RESULT 14

AD55241
ID AD55241 standard; protein; 509 AA.

AC AD55241;

DT 29-JAN-2004 (first entry)

DE Rat Protein AAC23892, SEQ ID NO 1055.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS WO2003016475-A2.

FN 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; AAC23892.

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 509 AA;

Query Match 92.5%; Score 2479; DB 7; Length 509;

Best Local Similarity 91.2%; Pred. No. 9.7e-241;

Matches 464; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGGSSRRARWALGALGALLFAALGVVMIILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGGSSRRARWALGVLGGLLCAALGVMIILMVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVYFFVVPNEVNLQKVPVRRGPGVYVRRFRQKVNITFNDNDTVSFVNRSLH 120
Db 61 VPFYLSVYFFVVPNEVNLQKVPVRRGPGVYVRRFRQKVNITFNDNDTVSYIENSLH 120
QY 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGQRAFMRNRTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPVSLKLMNTLALVTMGQRAFMRNRTVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSLIHLVDKWNGL 240
QY 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SEVNYHSEOCNMINGTAGQWAPFMTPESSLEFFSPEACRSKMLTYQESRVFEGIPTYR 300
QY 301 FTAPDTLFPANGSVYPPNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFPANGSVYPPNEGFCPCRESGIONVSTCRFCGAPLFLSQPHFYNADPVLSEAVLG 360
QY 361 LNPDKHSLFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGOTGKIBPVVPLLLWFSQSG 420
Db 361 LNPDKHSLFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGOTGKIBPVVPLLLWFSQSG 420
QY 421 AMGGKPLSTFTYTQVLVMPQVLYHYAYVLLGLGGLLLVPIICQLRSQEKCFLWFSQSGK 480

Db 421 MWGGKTLNFTYQLVLMPOVHLHYAQVLLGGGLLVPITIIYQLRSQKCFLWGSKKG 480
Qy 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEAMQAYSESLMSPAAGTIVVQEAKL 509

RESULT 15

ID ADZ13453 standard; protein; 506 AA.
XX AC ADZ13453;
XX 16-JUN-2005 (first entry)
XX Murine cancer-associated protein #108.
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasia;
KW cytostatic.
XX OS Mus sp.
XX WO2005031001-A2.
XX 07-APR-2005.
XX 23-SEP-2004; 2004WO-US031617.
XX 23-SEP-2003; 2003US-00669920.
XX (CHIR) CHIRON CORP.
XX Morris DW, Malandro MS;
XX WPI; 2005-273395/28.
XX N-PSDB; ADZ13452.

Nucleic acid array useful for detecting cancer associated nucleic acid,
comprises two or more nucleic acid probes.

Disclosure; SEQ ID NO 973; 198pp; English.

The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a murine cancer-associated protein of the invention.

Sequence 506 AA;

Query Match 92.1%; Score 2468; DB 9; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIILWVPSLIKQQLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMIILWVPSLIKQQLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVREGRGPVYVREKVNITFNNDNTVSFVENRSLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVREGRGPVYVREKVNITFNNDNTVSFVENRSLH 120
Qy 121 FQDKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFNMRTVGEIL 180
Db 121 FQDKSHGSESDYIVLPNIIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFNMRTVGEIL 180
Qy 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGMNNSNSGVFTFTGVQVNFRIHLVDKWNGL 240
Db 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGMNNSNSGVFTFTGVQVNFRIHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMGNTSGOMWAPFMTPESSLEFFSPSEACRSKMLTYNESRVPEGIPTYR 300
Db 241 SKIDYHSEOCNMGNTSGOMWAPFMTPESSLEFFSPSEACRSKMLTYNESRVPEGIPTYR 300
Qy 301 FTAPDTLFAANGSVYPPNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFAANGSVYPPNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSLEFLDIHPVTGIPMNCVVMQVLSLYIKSVKGIGQTKIEFPVVLPLLWFEQSG 420
Db 361 LNPMPKHSLEFLDIHPVTGIPMNCVVMQVLSLYIKSVKGIGQTKIEFPVVLPLLWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVHLHYAQVLLGGGLLVPITIIYQLRSQ 467
Db 421 AMGGKPLSTFTYQLVLMPOVHLHYAQVLLGGGLLVPITIIYQLRSQ 467

Search completed: February 23, 2006, 12:40:06
Job time : 153.5 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:40:25 ; Search time 26 Seconds
(without alignments)
1883.628 Million cell updates/sec

Title: US-08-765-108-8
Perfect score: 2881
Sequence: 1 MGSSRRARWALGALGALL.....YSESLMSPAAGTGLQAKL 509
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2484	92.7	529	2 JC5533	scavenger receptor
2	2447	91.3	509	1 A53920	scavenger receptor
3	2192	81.8	509	1 A48528	membrane glycoprot
4	742.5	27.7	478	1 A56525	lysosomal integral
5	734	27.3	478	1 JH0241	85K lysosomal memb
6	732	27.3	478	2 JC5670	lysosomal membrane
7	677	25.3	472	1 A54870	cell adhesion rece
8	662	24.7	472	2 I49590	CD36 antigen - mou
9	645	24.1	472	1 A47402	fatty acid binding
10	633	23.6	519	1 S38957	epithelial membran
11	587	21.9	457	1 S43137	D-CD36 protein - f
12	490.5	18.3	534	2 T27054	hypothetical prote
13	472	17.6	525	2 A59259	sensory neuron mem
14	401	15.0	536	2 T24000	hypothetical prote
15	393	14.7	531	2 T20763	hypothetical prote
16	379	14.1	590	2 T20537	hypothetical prote
17	363.5	13.6	552	2 T27424	hypothetical prote
18	345	12.9	562	2 T15396	hypothetical prote
19	115.5	4.3	1573	2 T50113	3-dehydroquinatase
20	105.5	3.9	592	2 E70488	cycochrome-c oxida
21	104.5	3.9	924	2 B95192	hypothetical prote
22	104	3.9	1003	2 T05898	hypothetical prote
23	101.5	3.8	1026	2 T18220	chitin synthase (E
24	99.5	3.7	570	2 T38489	helicase - fission
25	99.5	3.7	924	2 G98058	hypothetical prote
26	98	3.7	303	2 AC1087	PTS system mannose
27	98	3.7	303	2 AB1451	hypothetical prote
28	96.5	3.6	273	2 AB1551	hypothetical prote
29	96.5	3.6	1835	2 S46082	urea carboxylase (

30 3.6 224 2 AP0851 secretory protein
31 96 955 2 T39765 probable nuclear m
32 95 224 2 T11207 spap protein - Sal
33 95 224 2 S37308 spap protein - Sal
34 95 695 2 D90468 copper-transportin
35 94.5 411 2 H69158 LPS biosynthesis R
36 94.5 3.5 2211 1 KPB05 coagulation factor
37 94 3.5 366 2 C89875 hypothetical prote
38 94 3.5 670 2 T32221 hypothetical prote
39 94 3.5 1661 2 S64800 probable membrane
40 93 901 2 T03726 capsid polypeptide
41 92.5 3.5 605 2 AC1139 internalin protein
42 92 3.4 398 2 S74347 hypothetical prote
43 92 3.4 427 2 C87232 probable integral
44 92 3.4 448 2 T44869 probable membrane
45 92 3.4 543 2 F91067 hypothetical prote

ALIGNMENTS

RESULT 1

JC5533
scavenger receptor class B type I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5533
R;Mizutani, T.; Sonoda, Y.; Minegishi, T.; Wakabayashi, K.; Miyamoto, K.
Biochem. Biophys. Res. Commun. 234, 499-505, 1997
A;Title: Cloning, characterization, and cellular distribution of rat scavenger receptor (C) to ovarian theca interna cells or to corpus luteum.
A;Reference number: JC5533; MUID: 97320450; PMID: 9177301
A;Accession: JC5533
A;Molecule type: mRNA
A;Residues: 1-529 <MTZ>
A;Cross-references: UNIPROT:P97943; UNIPARC:UP10000177A34
A;Experimental source: ovary
C;Comment: This protein is a specific receptor for high density lipoprotein. It plays a role to ovarian theca interna cells or to corpus luteum.
C;Genetics:
A;Gene: srbi
C;Superfamily: lysosomal integral membrane protein II
F;1-25/Domain: signal sequence #status predicted <Sig>
F;466-482/Domain: transmembrane #status predicted <TM>

Query Match 92.7%; Score 2484; DB 2; Length 529;
Best Local Similarity 88.8%; Pred. No. 2.8e-188;
Matches 470; Conservative 23; Mismatches 16; Indels 20; Gaps 1;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIILMFSLIKQQLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVMIILMFSLIKQQLKNVRIDPSSLSFGMWKEIP 60

Qy 61 VPFLSYVFEVNVNPEVLNGQKPVVRERGPVYVREPRQKVNITFDNDTVSFVENSRLH 120
Db 61 VPFLSYVFEVNVNPEVLNGQKPVVRERGPVYVREPRQKVNITFDNDTVSFVENSRLH 120

Qy 121 FQPKSHGSSSDYIVLPNIIVLGSSIIILMESKPSVSLKLMMTLALVTMGORAFMNTVGEIL 180
Db 121 FQPKSHGSSSDYIVLPNIIVLGSSIIILMESKPSVSLKLMMTLALVTMGORAFMNTVGEIL 180

Qy 181 WGVDPPVHFLNTYLPDMLPIKGFGLFVGNNNSNGVFTVFTGVQNFRIHLVDKNGL 240
Db 181 WGVDPPVHFLNTYLPDMLPIKGFGLFVGNNNSNGVFTVFTGVQNFRIHLVDKNGL 240

Qy 241 SKIDYWHSEQCNNMGTSGQWAPFMTPESSLSBFFSPSEACRSKMLTYNEGRVFEIGIPTYR 300
Db 241 SEVNYWHSEQCNNMGTSGQWAPFMTPESSLSBFFSPSEACRSKMLTYNEGRVFEIGIPTYR 300

Qy 301 FTAPDITLFPANGSVYPPNPEGCPCEGIONVYTCRECAPLFLSHPHFYNDPVLSEAVLG 360
Db 301 FTAPDITLFPANGSVYPPNPEGCPCEGIONVYTCRECAPLFLSHPHFYNDPVLSEAVLG 360

Qy 361 -----LNPNPKHSLFLDIHPVTGIPMNCVKNQSLSLYIKSVKGI 400

Query Match 27.4%; Score 734; DB 1; Length 478;
Best Local Similarity 31.7%; Pred. No. 4.2e-50;
Matches 152; Conservative 106; Mismatches 198; Indels 24; Gaps 9;

QY 15 GAGLLGFAALGVVMIL--WVPSLLKQVLKKNVRIDPSSLSFGMWKKEIPVPFYLVSVPFEV 72
DB 10 GTLSLLLVTSVLVARVFKQADVDTIEKNMWLQNGTKVFDSEKPEPLPVYIQIFYFN 69

QY 73 VNPNEVLNGQKPVVRERGPVYTYREFROKVNITFNDN-DTVSFVENRSLHFQPKSHGES 131
DB 70 TNPEEILQGEIPLLEEVPYTYRELNRKANVQFGENGTTISAVTNKAYIFERNQSVGDPT 129

QY 132 -DIVLVPNIIVLGGSILMESKPSVSLKLMNTLALVTMGQRAFMRNTVGEIILWGYDDPPVHF 190
DB 130 VDLIRTNIPILL--TVVEMAQQPFRLRIEAMLKAYQQTLFVTHVHELLWGYKDEVL 187

QY 191 LNTYLPDMLPIKGKFGLVGMNNSGVFTVTCVQNFSLRIHLVDKNGLSKIDYWHSEQ 250
DB 188 VHIFRPDVPSP---NFGLFYERNGTNDGEYVFLTGEDNYLNTKIVEMNGKTSLDWMTTDT 244

QY 251 CNMINTSGQWAPFMTPESSLEFFSPSEACRSKMLTYNESRVFEGIPYTYFTAPDTL 310
DB 245 CNMINTGDSFPLISKDETLTYFSDFCRSVITYFSSFENVEGLPAFYKYKVAEILAN 304

QY 311 GSVYPPNEGFC----PCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLGLNPNPK 366
DB 305 SS---ENAGFCIPBGNMCDAGLVNLSICKNGAPIMSFPHFYQADEKFVSAIKGMRENKE 361

QY 367 EHSFLFDIHPVTGPMNCSVMQLSLYIKSVKGIGQTGKIEPPVLPLLWFEQSGMGCKP 426
DB 362 EHESFVDINELTGILGAKRFQINTVYVKGLDDFVETGNIRTWVPVYMLNES-VLIDKE 420

QY 427 LSTFYTYTLMPQVHLVYAOVLLGLGLLLVPIICQLRSQEKCFLFWSGSKSGSQDKEA 486
DB 421 TASQLKSVINTLLIVTNPITIALGVFFGLIFTWLACRQ-----GSTDEGTADERA 473

RESULT 6
JC5670
lysosomal membrane 85K glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5670
R;Tabuchi, N.; Akasaki, K.; Sasaki, T.; Kanda, N.; Tsuji, H.
J. Biochem. 122, 756-763, 1997
A;Title: Identification and characterization of a major lysosomal membrane glycoprotein.
A;Reference number: JC5670; MUID: 98060500; PMID: 9399579
A;Accession: JC5670
A;Molecule type: mRNA
A;Residues: 1-478 <TAB>
A;Cross-references: UNIPROT: O35114; UNIPARC: UPI00000231D6; GB: AB008553; NID: g2618485; PDB: 1WV7
C;Comment: This protein is involved in sequestration of particular cytoplasmic proteins
F;1-26/Domain: lysosomal integral membrane protein II
F;1-26/Domain: signal sequence #status predicted <SIG>
F;433-458/Domain: transmembrane #status predicted <TM>
F;474-475/Region: endosomal/lysosomal sorting signal

Query Match 27.3%; Score 732; DB 2; Length 478;
Best Local Similarity 32.1%; Pred. No. 6e-50;
Matches 154; Conservative 103; Mismatches 199; Indels 24; Gaps 9;

QY 15 GAGLLGFAALGVVMIL--WVPSLLKQVLKKNVRIDPSSLSFGMWKKEIPVPFYLVSVPFEV 72
DB 10 GTLSLLLVTSVLVARVFKQADVDTIEKNMWLQNGTKVFNSEKPEPLPVYIQIFYFN 69

QY 73 VNPNEVLNGQKPVVRERGPVYTYREFROKVNITFNDN-DTVSFVENRSLHFQPKSHGES 131
DB 70 TNPEEILQGEIPLLEEVPYTYRELNRKANVQFGENGTTISAVTNKAYVFNERNQSVGD 129

QY 132 -DIVLVPNIIVLGGSILMESKPSVSLKLMNTLALVTMGQRAFMRNTVGEIILWGYDDPPVHF 190
DB 130 VDLIRTNIPILL--TVVDLAQLTLLRELIEAMLKAYQQQLFVTHVHELLWGYKDEVL 187

A;Cross-references: UNIPARC:UPI0000174242
R;Catimel, B.; Parmentier, S.; Leung, L.L.; McGregor, J.L.
Biochem. J. 279, 419-425, 1991
A;Title: Separation of important new platelet glycoproteins (GPIa, GPIc, GPIIb and GPIIb/IIIa) and their relationship to the GPIIb/IIIa gene
A;Reference number: A56793; MUID:92061944; PMID:1953640
A;Accession: D56793
A;Molecule type: protein
A;Residues: 2, 'X', 4-6, 'X', 8-23 <CAT>
A;Cross-references: UNIPARC:UPI0000174243
A;Experimental source: platelet
R;Greenwalt, D.E.; Watt, K.W.K.; So, O.Y.; Jiwani, N.
Biochemistry 29, 7054-7059, 1990
A;Title: PAs IV, an integral membrane protein of mammary epithelial cells, is related to PAs I and II
A;Reference number: A35577; MUID:91027734; PMID:1699598
A;Accession: A35577
A;Molecule type: protein
A;Residues: 'XX', 4, 'X', 6, 'X', 8-30 <GRE>
A;Cross-references: UNIPARC:UPI0000174244
A;Experimental source: milk fat globule membrane, lactating mammary tissue epithelial cells
R;Wyller, B.; Daviet, L.; Borkiewicz, H.; Bordet, J.C.; McGregor, J.L.
Thromb. Haemost. 70, 500-505, 1993
A;Title: Cloning of the cDNA encoding human platelet CD36: comparison to PCR amplified cDNA
A;Reference number: 159613; MUID:94082337; PMID:7505064
A;Accession: 159613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-43, 'R', 45-237, 'D', 239-472 <RES>
A;Cross-references: UNIPARC:UPI0000168403; GB:S67532; NID:9456912; PID: AAD13993.1; PID: AAD13993.1
R;Tang, Y.; Taylor, K.T.; Sobiecki, D.A.; Medved, E.S.; Lipsky, R.H.
J. Biol. Chem. 269, 6011-6015, 1994
A;Title: Identification of a human CD36 isoform produced by exon skipping. Conservation of the cytoplasmic tail
A;Reference number: A53212; MUID:94164961; PMID:7509795
A;Accession: A53212
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-40, 144-169, 'ILNSLINKSSSM', 170-185 <TA3>
A;Cross-references: UNIPARC:UPI0000174245; GB:L06849
C;Comment: This protein mediates the interaction of platelets with collagen and thrombospondin
C;Genetics:
A;Gene: GDB:CD36
A;Cross-references: GDB:138800; OMIM:173510
A;Map position: 7q11.2-q11.2
A;Introns: 40/3; 94/2; 143/3; 185/2
C;Superfamily: lysosomal integral membrane protein II
C;Keywords: alternative splicing; blocked amino end; cell adhesion; glycoprotein; lipoprotein; receptor
F;2-472/Product: cell adhesion receptor CD36 #status predicted <MAT>
F;2-6/Domain: intracellular #status predicted <CYT>
F;7-30/Domain: transmembrane #status predicted <TM1>
F;31-439/Domain: extracellular #status predicted <EXT>
F;440-466/Domain: transmembrane #status predicted <TM2>
F;467-472/Domain: intracellular #status predicted <CYT2>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3, 7, 464, 466/Binding site: palmitate (Cys) (covalent) #status predicted
F;79, 102, 134, 163, 205, 220, 235, 247, 417/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 25.3%; Score 677; DB 1; Length 472;
Best Local Similarity 31.6%; Pred. No. 1.3e-45;
Matches 147; Conservative 104; Mismatches 190; Indels 24; Gaps 10;
QY 17 LGLLFAALGVVIMLVPSLIKQVVKVIRIDPSLSFGMKKEIPVPYLSVYFEVNP 76
DB 15 IGAVLAVFGGILMPVGDLLIKQVLEEGTAFKNVKTGTYYRQFVFDVQNP 74
QY 77 EV-LNGQKPVVRERGPVYR-EPRQKNITFN-DNDTVSFVENSLHFQDPKSHGSSDY 133
DB 75 DVAKNSKIKVQGRGPTTYRVLAKENITQDPEDHTVSFVQNGAIFEFSLSVGTEDN 134
QY 134 IVLPNILVGGSIIMESKPVSLKLMTMLALVTMGQRA-FMNRVTGEILWGYDDPFFVHFLN 192
DB 135 FTVNLNLAVAASHIQNFQVQ--MILNSLINKSSSMFQRTIRELLGWGRDFFLSLV- 190
QY 193 TYLPMMLPIKGFGLFVGMMNSGVFTVTFVQNFGRHLVDKWNGLSKIDYVHSSQCN 252
DB 191 -----PYPITSTTGVFPYNDYVDGYKVPNGKDNISKVAIIESYKGRNLSWPS-YCD 244
Query Match 25.3%; Score 677; DB 1; Length 472;
Best Local Similarity 31.6%; Pred. No. 1.3e-45;
Matches 147; Conservative 104; Mismatches 190; Indels 24; Gaps 10;
QY 17 LGLLFAALGVVIMLVPSLIKQVVKVIRIDPSLSFGMKKEIPVPYLSVYFEVNP 76
DB 15 IGAVLAVFGGILMPVGDLLIKQVLEEGTAFKNVKTGTYYRQFVFDVQNP 74
QY 77 EV-LNGQKPVVRERGPVYR-EPRQKNITFN-DNDTVSFVENSLHFQDPKSHGSSDY 133
DB 75 DVAKNSKIKVQGRGPTTYRVLAKENITQDPEDHTVSFVQNGAIFEFSLSVGTEDN 134
QY 134 IVLPNILVGGSIIMESKPVSLKLMTMLALVTMGQRA-FMNRVTGEILWGYDDPFFVHFLN 192
DB 135 FTVNLNLAVAASHIQNFQVQ--MILNSLINKSSSMFQRTIRELLGWGRDFFLSLV- 190
QY 193 TYLPMMLPIKGFGLFVGMMNSGVFTVTFVQNFGRHLVDKWNGLSKIDYVHSSQCN 252
DB 191 -----PYPITSTTGVFPYNDYVDGYKVPNGKDNISKVAIIESYKGRNLSWPS-YCD 244

DB 191 -----PYPITSTTGVFPYNDYVDGYKVPNGKDNISKVAIIESYKGRNLSWPS-YCD 244
QY 253 MINGTSQGMWAPMTPESSLEFFSPACRSKMLTYNESRVFEGIPTVYRFTAPDTLFANGS 312
DB 245 MINGTDAASFPFVFKSQVLOFFSSDICRSIYAVFBSDVNLKGIPIVYRFLPSKAFSPV 304
QY 313 VYPNBEFCF-----CRESGIQNSTCRFGAPLFLSHPHFYFNADPVLSEAVLGLNPNP 365
DB 305 ENPDNYCFCFTEKTIISKNCTSYGLVDISKCKEGRPVVITSLPHFLYASPDVSEPIGLHPNE 364
QY 366 KEHSLFDLHPVTGIPMNCVSKMQLSIYKSVKIGQGTGKIE-PVVLPLLWFFSQSGAMGG 424
DB 365 DEHRTYLDVEPITGFTLQFAKRLQVNLVAPSEKIQVLKMLKNYIVPILMLNETGTIGD 424
QY 425 KPLSTFTQLVLMPOVLHYAQVYLLGGLLLVPIT--COLRSQ 467
DB 425 EKAMFESQVTKINLLGLEMIILLSGVVFMVAFMISYACKSK 469
RESULT 8
CD36 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49590
R;Endemann, G.; Stanton, L.W.; Madden, K.S.; Bryant, C.M.; White, R.T.; Protter, A.A.
J. Biol. Chem. 268, 11811-11816, 1993
A;Title: CD36 is a receptor for oxidized low density lipoprotein.
A;Reference number: I49590; MUID:93280144; PMID:7685021
A;Accession: I49590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-472 <RES>
A;Cross-references: UNIPROT:Q08857; UNIPARC:UPI00000018D7; GB:L23108; NID:9567198; PID:N-
C;Superfamily: lysosomal integral membrane protein II
Query Match 24.7%; Score 662; DB 2; Length 472;
Best Local Similarity 30.5%; Pred. No. 2e-44;
Matches 142; Conservative 104; Mismatches 195; Indels 24; Gaps 10;
QY 17 LGLLFAALGVVIMLVPSLIKQVVKVIRIDPSLSFGMKKEIPVPYLSVYFEVNP 76
DB 15 IGAVLAVFGGILMPVGDLLIKQVLEEGTAFKNVKTGTYYRQFVFDVQNP 74
QY 77 EV-LNGQKPVVRERGPVYR-EPRQKNITFN-DNDTVSFVENSLHFQDPKSHGSSDY 133
DB 75 DVAKNSKIKVQGRGPTTYRVLAKENITQDPEDHTVSFVQNGAIFEFSLSVGTEDN 134
QY 134 IVLPNILVGGSIIMESKPVSLKLMTMLALVTMGQRA-FMNRVTGEILWGYDDPFFVHFLN 192
DB 135 FTVNLNLAVAASHIQNFQVQ--SLIKKSSSMFQRTSLKELLWGYKDPFLSLV- 190
QY 193 TYLPMMLPIKGFGLFVGMMNSGVFTVTFVQNFGRHLVDKWNGLSKIDYVHSSQCN 252
DB 191 -----PYPITSTTGVFPYNDYVDGYKVPNGKDNISKVAIIESYKGRNLSWPS-YCD 244
QY 253 MINGTSQGMWAPMTPESSLEFFSPACRSKMLTYNESRVFEGIPTVYRFTAPDTLFANGS 312
DB 245 MINGTDAASFPFVFKSQVLOFFSSDICRSIYAVFBSDVNLKGIPIVYRFLPSKAFSPV 304
QY 313 VYPNBEFCF-----CRESGIQNSTCRFGAPLFLSHPHFYFNADPVLSEAVLGLNPNP 365
DB 305 ENPDNYCFCFTEKTIISKNCTSYGLVDISKCKEGRPVVITSLPHFLYASPDVSEPIGLHPNE 364
QY 366 KEHSLFDLHPVTGIPMNCVSKMQLSIYKSVKIGQGTGKIE-PVVLPLLWFFSQSGAMGG 424
DB 365 DEHRTYLDVEPITGFTLQFAKRLQVNLVAPSEKIQVLKMLKNYIVPILMLNETGTIGD 424
QY 425 KPLSTFTQLVLMPOVLHYAQVYLLGGLLLVPIT--COLRSQ 467
DB 425 EKAMFESQVTKINLLGLEMIILLSGVVFMVAFMISYACKSK 469

RESULT 9

A47402
fatty acid binding/transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-May-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: A47402
R:Abumrad, N.A.; El-Maghrabi, M.R.; Amri, E.Z.; Lopez, E.; Grimaldi, P.A.
J. Biol. Chem. 268, 17665-17668, 1993
A:Title: Cloning of a rat adipocyte membrane protein implicated in binding or transport
A:Reference number: A47402; MUID:93352566; PMID:7688729

A:Accession: A47402
A:Molecule type: mRNA
A:Residues: 1-472 <ABU>

A:Cross-references: UNIPROT:Q07969; UNIPARC:UPI000015568; GB:L19658; NID:g310112; PIDN:

C:Superfamily: lysosomal integral membrane protein II
C:Keywords: glycoprotein; transmembrane protein
F:2-6/Domain: intracellular #status predicted <CYT1>
F:7-30/Domain: transmembrane #status predicted <TM1>
F:31-439/Domain: extracellular #status predicted <EXT>
F:440-466/Domain: transmembrane #status predicted <TM2>
F:467-472/Domain: intracellular #status predicted <CYT2>
F:79,102,134,205,220,235,247,417/Binding site: carboxydrate (Asn) (covalent) #status pre

Query Match 24.1%; Score 645; DB 1; Length 472;
Best Local Similarity 30.3%; Pred. No. 4.4e-43;
Matches 145; Conservative 91; Mismatches 192; Indels 50; Gaps 10;

Qy 17 LGLFAALGVVMIPLVSLIKQVLKVRIDPSLSFGMMKEIPVPYLSVYFEVNP 76

Db 15 IGAVLAVFGGILMPGVGLLEKTIKREVLLEBGTIAFKNWKVGTITVYRQFWVFDVQNP 74

Qy 77 EVL-NGQKPVVRGPPYR-BFRQKNITFNDND-TVSFVNRSLHFQDKHSGESDY 133

Db 75 EVAKNSSKIKVIQRPYTYRVYLAKENITQDPKDSVSVFQPNCAIFEPESLSVGTENDN 134

Qy 134 IVLNLIIVLG-----GSTLMESKPVSLKMLMTLALVTMGQRAFMNRTVGEI 179

Db 135 FTVNLAVAAAPHYIYNSFVGVNLNLIKKK-----SSMFQTRSLKEL 178

Qy 180 LMGYDDPFVHPLNTYLPDLPIKGLFVGMNNSGVFTFTGVQNFRIHLVDKWN 239

Db 179 LMGYKDPFLSLV-----PYEISTTVGVFPYNNVGVKVSNGKDNISKVAIIDTYK 232

Qy 240 LSKIDYHSEOCNMGTSQGMWAPFMTPESSLEFPSPACRSKMLYNSRVFEGIPY 299

Db 233 KRNLISYVES-YCDMINGTDAASFPLGKSRTLFFSFDICRSIYAVFSEVNLKGPVY 291

Qy 300 RFTAPDTLFGNSVYVPNEGFCP-----CRESGIQNVSTCRFGAPLFLSHPHFYNADP 352

Db 292 RFVLPAFASPLQNPNDNHCFTBKVISNNCTSYGVLDIGKCKGKVPYNSLPFLHASP 351

Qy 353 VLSAVLGLNPNKHESLFLDIHPTVGTIPMNCVSMQQLSLYIKSVKIGIGTGKIE-PVVL 411

Db 352 DVSEPIEGLNPTDEHRYLDVEPIGTFTLQFSKRLQVNLVLPARKIEALKNLKRPVIV 411

Qy 412 PLLWFEGSGANGKPLSTFTYTLVLMQVTLHYAQLVILGIGGLLLVPIL--COLRSQ 467

Db 412 PILMLNETGTIGDEKAEMFRNQRTGKIKLLGLVENVLLGVGVFMVAFMISYACRSK 469

RESULT 10

S38957
epithelial membrane protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: S38957

R:Hart, K.; Wilcox, M.
J. Mol. Biol. 234, 249-253, 1993

A:Title: A Drosophila gene encoding an epithelial membrane protein with homology to CD36

A:Reference number: S38957; MUID:94047068; PMID:7693949

A:Accession: S38957

A:Molecule type: mRNA

A:Residues: 1-519 <HAR>

A:Cross-references: UNIPROT:Q24336; UNIPARC:UPI00000774AD; EMBL:X73332; NID:g429163; PIDN:

C:Genetics:

A:Gene: FlyBase:emp

A:Cross-references: FlyBase:FBgn0010435

C:Superfamily: lysosomal integral membrane protein II

C:Keywords: transmembrane protein

F:2-19/Domain: intracellular #status predicted <CYT1>

F:20-39/Domain: transmembrane #status predicted <TM1>

F:460-482/Domain: transmembrane #status predicted <TM2>

F:483-519/Domain: intracellular #status predicted <CYT2>

Query Match 23.6%; Score 633; DB 1; Length 519;
Best Local Similarity 31.5%; Pred. No. 4.5e-42;
Matches 161; Conservative 92; Mismatches 214; Indels 44; Gaps 14;

Qy 6 RARWALGALGALLFAAL----GVVMILMVPSLIKQVLKVRIDPSSLSFGMMKEIPVP 62

Db 18 RKWWTI-----VVAALIIGGIIVVACEFTVLIDAVVDRMVVALREGAKTFGWAAPVPE 71

Qy 63 FYLSVYFPEVVPNEVL-NGQKPVVRGPPYR-BFRQKNITFNDND-TVSFVNRSLHF 121

Db 72 PRISLYIYNVTNADDFLSNGSKAIVDEVPYVYSETWEKVNIVENDNGHLSYNLRKIYSF 131

Qy 122 QPDKSHGSESDYIVLPNLIIVLGSIILMESKPVSLKMLMTLALVTMGQRAFMNRTVGEILW 181

Db 132 REDLSVGPEDDVIVVENIPMLSATSSQSKHAARFLRLAMASIMDLIKIKPFOVSVQQLLW 191

Qy 182 GYDDPPVHPLNTYLP--DMLPIKGLFVGMNNSGVFTFTGVQNFRIHLVDKWN 239

Db 192 GYEDPILKLAKDVVPKEQKLPYE-BEGLLYGKNGTSQGMWAPFMTPESSLEFPSPACRSKMLTY-NESRVFEGIPT 298

Qy 240 LSKIDYHSEOCNMGTSQGMWAPFMTPESSLEFPSPACRSKMLTY-NESRVFEGIPT 298

Db 251 RTHLPHTWTADACNTLAGTDSIFPPHIDHRIHLVYDKOLCRLLPLVFEKEVMTSEVPG 310

Qy 299 YRFTAPDTLFGNSVYVPNE-----GFCPCRESGIONVSTCRFGAPLFLSHPHFYNADP 352

Db 311 YRFTVGVFRCCQ--PPGQHVLSRGKSPCSNGLFNVLSCQYDSPIMLSPPHFLADE 368

Qy 353 VLSAVLGLNPNKPE-HSLFLDIHPTVGTIPMNCVSMQQLSLYIKSVKIGIGTGKIEPVVL 411

Db 369 SLRTQVEGISPPMKKEKHQFFDQPKMGTTLRVARIQINLAVSQVFDIKQVANFPDIIIF 428

Qy 412 PLLWFEGSGANGKPLSTFTYTLV--LMPQVLHYAQLV--LLGLGGLLLVPIICOLR- 465

Db 429 PILWFEE-----GIDNLPDEVTLMRFAEQPPKIRVALIVGLCALGVILLLLTFLCLRN 484

Qy 466 SQEKCFLFMWSG-----KKGSDQKE 485

Db 485 SHRQSTLHLEGSNYLATAQVDNMKNKQNDQ 515

RESULT 11

S43137

D-CD36 protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S43137; S43136

R:Franc, N.; Dimarcq, J.; Hoffmann, J.; Laqueux, M.

submitted to the EMBL Data Library, March 1994

A:Description: d-CD36 : a second Drosophila gene related to the CD36 family of cell adhe

A:Reference number: S43136

A:Accession: S43137

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-457 <FRA>

A:Cross-references: UNIPROT:Q27367; UNIPARC:UPI000016BB39; EMBL:Z31583; NID:g468537; PIDN:

C:Genetics:

A:Gene: FlyBase:croquemort

A:Reference number: S43137

C:Superfamily: lysosomal integral membrane protein II

Query Match 21.9%; Score 587; .DB 1; Length 457;

Query Match	18.3%	Score 490.5;	DB 2;	Length 534;
Best Local Similarity	27.0%;	Pred.No. 8.3e-31;		
Matches 147; Conservative 109; Mismatches 193; Indels 95; Gaps 24;				
QY	17	LGLLFAALGVVMTLMVP--SLIKOOVLKNVRIDPSSLSF-----GMWKEIPVPF	63	
Db	15	LGLLLAAGVILLIGPIDRINRVQ-----IQQFLGYTRDENGTVPNAMTWSWKLP	69	
QY	64	Y---LSVFPEVVNPNEVL--NGOKPVVRGRGPVYREFROKVNITFNDDNTSVENRSL	119	
Db	70	YAMQLNIWMFNVTNVDGILKRHEKPNLHGEPFVDEVEQKVYHRPADNTRVFPYKNQKL	129	
QY	120	-HFQPKS-----HGSSESDYIVLNILVLGGSIIMESKPVS-----LKMMTLALVTMGQR	169	
Db	130	YHFNKNASCPETHDKM--VTIIINVSP---QKLIDRADVTIFGVRIKFATESVLKWVSEA	184	

QY	71	EVVNPNVNLGQKPVVRERGPPVYRFRQKVN1 - TFNDNDTVGSFVENRSLHFQDPKSHG-	128
Db	67	NTYNDVEIQKGAKEPIVKEIGPPYFEEWKEKVEVEDHEENDITTYKRLDVHFHRFDLSGP	126
QY	129	-SES DYIVLPNTILVLCGSSILMESKPSVSLKMLMTLALVTMCQRPAMRTVGEILMGYDDPF	187
Db	127	LTAGEEVIINPHILFILA-----NVATINREKPSMLNVVEKSGINGIFDNPK	170
QY	188	VHFLNTYLPDML-----PIKG-----KFGLEFVGNN	213
Db	171	DFVFLRVKAMDIIMFPGIIINCRTDEPAPKAACVTKMKDQAVTGVIEYEPNNQFRFSLEGTNN	230
QY	214	S-NSGVFTVFTGVQNFPSRHLVDKNGLSKIDYWHSEQCNNMGTSQMMAPFTPESSL	272
Db	231	TWNPDVVTVKRGKGTIMDVGOVVALNGKPOIDTW- DHCNEFOCTDCTGVPPPTTYKDL	289

K; Rogers, M.B.; Sun, M.; Lerner, M.R.; Vogt, R.G.
J. Biol. Chem. 272, 14792-14799, 1997

A;Ritte, Snmp-1, a novel membrane protein of olfactory neurons of the silk moth *Antheraea*
A;Reference number: A59259; MUID:97313452; PMID:9169446

A;Accession: A59259
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 1525 <RQ>

A;Cross-references: UNIPROT:O02351; UNIPARC:UPI000007PD51; GB:U95026; NID:G2149911; PIDN:
A;Experimental source: strain wild

C;Genetics:
C;Superfamily: lysosomal integral membrane protein II

A;Gene: SNMP1

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 23, 2006, 12:35:04 ; Search time 147.5 Seconds
 (without alignments)
 2434.671 Million cell updates/sec
 Title: US-08-765-108-8
 Perfect score: 2681
 Sequence: 1 MGSSRRARWALGALGALL.....YSESLMSPAAGTGVLEAKL 509

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	1	SCRBI_MOUSE
2	2681	100.0	509	2	Q4FK30 mus musculus
3	2504	93.4	509	1	SCRBI_MOUSE
4	2484	92.7	509	2	Q6SR83 rattus norv
5	2479	92.5	509	2	Q6SR83 rattus norv
6	2447	91.3	509	1	SCRBI_MOUSE
7	2275.5	84.9	506	2	Q6B417 rattus norv
8	2215	82.6	509	1	SCRBI_MOUSE
9	2212	82.5	509	2	Q6T8F1 tupia glis
10	2200	82.1	509	2	Q52L25 homo sapien
11	2180	81.3	509	1	SCRBI_MOUSE
12	2148	80.1	509	2	Q6WIW8 RABIT
13	2022.5	75.4	552	1	SCRBI_MOUSE
14	2022.5	75.4	581	2	Q59FM4 HUMAN
15	1970	73.5	501	2	Q6WIW8 RABIT
16	1401.5	52.3	460	2	Q4S1T9 tetradon n
17	1311	48.9	457	2	Q7ZYX0 BRARE
18	768	28.6	2096	2	Q4S3J3 TETNG
19	746	27.8	532	2	Q64HW6 ONCMY
20	741.5	27.7	477	1	SCRBI_MOUSE
21	741.5	27.7	478	2	Q53Y63 HUMAN
22	734	27.4	477	1	SCRBI_MOUSE
23	732	27.3	477	1	SCRBI_MOUSE
24	729	27.2	483	2	Q5XH33 XENLA
25	727.5	27.1	531	2	Q8JG88 BRARE
26	722.5	26.9	484	2	Q7ZTL6 XENLA
27	721	26.9	522	2	Q7Q950 ANOGA
28	709	26.4	465	2	Q6DHC7 BRARE
29	695	25.9	460	2	Q4SAC1 TETNG
30	687	25.6	472	2	Q5BKES RAT
31	684.5	25.5	601	2	Q8IGY0 DROME

32	682.5	25.5	520	2	Q7KVF1 DROME
33	682.5	25.5	551	2	Q9W0X0 DROSOPHILA
34	678	25.3	471	1	CD36 MEGAU
35	678	25.3	472	2	Q925W0 RAT
36	677.5	25.3	471	2	Q5ZL18 CHICK
37	677	25.3	471	1	CD36 HUMAN
38	677	25.3	472	2	Q6IMX5 RAT
39	675	25.2	472	2	Q6J512 MACACA MULA
40	675	25.2	472	2	Q4R6B4 MACACA FASC
41	668	24.9	469	2	Q8SZV3 DROME
42	663	24.7	472	2	Q35754 RAT
43	662	24.7	471	1	CD36 MOUSE
44	659	24.6	472	2	Q8C6Z4 MOUSE
45	645	24.1	471	1	CD36 RAT

ALIGNMENTS

RESULT 1

SCRBI_MOUSE STANDARD; PRT; 509 AA.
 AC Q61003; O9CWJ7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
 GN Name=Scarb1; Synonyms=Srb1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96152374; PubMed=8560269;
 RA Acton S., Rigotti A., Landschulz K.T., Xu S., Hobbs H.H., Krieger M.;
 RT "Identification of scavenger receptor SR-BI as a high density
 lipoprotein receptor.";
 RL Science 271:518-520(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.R., Cousins S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmond S., Gustincich S., Hirokawa N., Jackson J., Jarvis E.D.,
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wynehaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).

RT vector (pDONR201);
 DR Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 SQ EMBL; CTO10222; CAJ18430.1; -; mRNA.
 Query Match 100.0%; Score: 2681; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 3.8e-195;
 Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MGSSRRARWALGALGALLFAALGVNMLVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
 1 MGSSRRARWALGALGALLFAALGVNMLVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
 61 VPFLSVYFFVVPVNPVNEVNGQKPVVRERGYPVYREFRQKVNITFNDNDTVSFVENSRLH 120
 61 VPFLSVYFFVVPVNPVNEVNGQKPVVRERGYPVYREFRQKVNITFNDNDTVSFVENSRLH 120
 121 FQPKSHGSESDYIVLPNVLVGSILMESKPVSLKMLMTLALVTMGORAFMNRVTGGEIL 180
 121 FQPKSHGSESDYIVLPNVLVGSILMESKPVSLKMLMTLALVTMGORAFMNRVTGGEIL 180
 181 WGYDDPFFVHFLNTLTPDMLPIKXGFLGVGNMNSNGVFTVFTGVQNPFSRIHLVDKNWGL 240
 181 WGYDDPFFVHFLNTLTPDMLPIKXGFLGVGNMNSNGVFTVFTGVQNPFSRIHLVDKNWGL 240
 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
 361 LNPFPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQTKIBPVVPLPLWFQSG 420
 361 LNPFPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQTKIBPVVPLPLWFQSG 420
 421 AMGKPLSTFTQVLVMPQVLYHYAQYVLLGGLLLVPIICQLRSQEKCFLPWGSKKG 480
 421 AMGKPLSTFTQVLVMPQVLYHYAQYVLLGGLLLVPIICQLRSQEKCFLPWGSKKG 480
 481 SODKEATQAYSESLSMPAAKTVLQEAKL 509
 481 SODKEATQAYSESLSMPAAKTVLQEAKL 509

RESULT 3
 SCRB1 RAT
 ID SCRB1 RAT STANDARD; PRT; 509 AA.
 AC P97943;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
 GN Name=Scarb1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RA Johnson S.C.M., Svensson P.A., Carlson B.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Ovary;
 RX PubMed=9177301; DOI=10.1006/bbr.1997.6646;
 RA Mizutani T., Sonoda Y., Minegishi T., Wakabayashi K., Miyamoto K.;
 FT "Cloning, characterization, and cellular distribution of rat scavenger
 receptor class B type 1 (SRB1) in the ovary."
 RL Biochem. Biophys. Res. Commun. 234:499-505(1997).

RN NUCLEOTIDE SEQUENCE, AND GLYCOSYLATION.
 RP STRAIN=Donryu; TISSUE=Testis;
 RC MEDLINE=22128898; PubMed=12016218; DOI=10.1074/jbc.M202879200;
 RA Kawasaki Y., Nakagawa A., Nagao K., Shiratsuchi A., Nakanishi Y.;
 RT "Phosphatidylserine binding of class B scavenger receptor type I, a
 phagocytosis receptor of testicular Sertoli cells."
 RL J. Biol. Chem. 277:27559-27566(2002).
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Lung;
 RC NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN INTERACTION WITH PDZK1.
 RP STRAIN=Wistar; TISSUE=Liver;
 RC MEDLINE=2030936; PubMed=10829064; DOI=10.1073/pnas.100114397;
 RA Ikemoto M., Arai H., Feng D., Tanaka K., Aoki J., Dohmae N., Takio K.,
 RA Adachi H., Tsujimoto M., Inoue K.;
 RT "Identification of a PDZ-domain-containing protein that interacts with
 the scavenger receptor class B type I."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:6538-6543(2000).
 CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
 cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
 cells. Probable receptor for HDL, located in particular region of
 the plasma membrane, called caveolae. Facilitates the flux of free
 and esterified cholesterol between the cell surface and
 extracellular donors and acceptors, such as HDL and to a lesser
 extent, apoB-containing lipoproteins and modified lipoproteins.
 Probably involved in the phagocytosis of apoptotic cells, via its
 phosphatidylserine binding activity (By similarity).
 CC -1- SUBUNIT: The C-terminal region binds to PDZK1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
 localized to cholesterol and sphingomyelin-enriched domains within
 the plasma membrane, called caveolae (By similarity).
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the CD36 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 EMBL; U76205; AAB19203.1; -; mRNA.
 EMBL; D89655; BAA14004.1; -; mRNA.
 EMBL; AB002151; BAA74541.1; -; mRNA.
 EMBL; BC076504; AAH76504.1; -; mRNA.
 PIR; JC5533; JC5533.
 Ensembl; ENSRNOG0000000981; Rattus norvegicus.
 InterPro; IPR002159; CD36
 InterPro; IPR05428; CD36_antigen.
 PANTHER; PTHR11923; CD36; 1.
 Pfam; PF01130; CD36; 1.
 PRINTS; PR01610; CD36FAMILY.
 PRINTS; PR01609; CD36FAMILY.
 Glycoprotein; Receptor; Transmembrane.
 TOPO_DOM 1 11 Cytoplasmic (Potential).
 TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 440 Extracellular (Potential).
 FT TRANSMEM 441 461 Potential.
 FT TOPO_DOM 462 509 Cytoplasmic (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 509 AA; 56957 MW; 792A0BB8D11A105 CRC64;


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Query Match          93.4%; Score 2504; DB 1; Length 509;
Best Local Similarity 92.3%; Pred. No. 1.1e-181;
Matches 470; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVIMILWPSLIKQVVKVNRIDPSSLSFGMKKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVIMILWPSLIKQVVKVNRIDPSSLSFGMKKEIP 60

Qy 61 VPYLSYVFFVNVNPEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLH 120
Db 61 VPYLSYVFFVNVNPEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLR 120

Qy 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMNTLALVTMGQAFMNRITVGEIL 180
Db 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMNTLALVTMGQAFMNRITVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTFTGVQNFSLHLVDKXNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTFTGVQNFSLHLVDKXNGL 240

Qy 241 SKIDYHSEQCNNINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300
Db 241 SEVNYHSEQCNNINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300

Qy 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360

Qy 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYIKSVKGVGQTKIEPVVPLLLWFRQSG 420
Db 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYIKSVKGVGQTKIEPVVPLLLWFRQSG 420

Qy 421 AMGGKPLSTFTYQLVLMQVHYAQVYLLGLGGLLLVPIICOLRSQEKCFLWMSGKKG 480
Db 421 MMGKTLNTFTYQLVLMQVHYAQVYLLGLGGLLLVPIIYQLRSQEKCFLWMSGKKG 480

Qy 481 SODKEAIAQYSESIMSPAAGTGLQEA 509
Db 481 SODKEAIAQYSESIMSPAAGTGLQEA 509

RESULT 4
Q6SR89 RAT PRELIMINARY; PRT; 509 AA.
ID Q6SR89 RAT PRELIMINARY; PRT; 509 AA.
AC Q6SR89;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scavenger receptor class B type 1.
GN Name=Scarb1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RX MEDLINE=9236778; PubMed=10221589; DOI=10.1385/ENDO.9.3.243;
RA McLean M.P., Sandhoff T.W.;
RT "Expression and hormonal regulation of the high-density lipoprotein
RT (HDL) receptor scavenger receptor class B type I messenger ribonucleic
RT acid in the rat ovary."
RL Endocrine 9:243-252(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RX MEDLINE=20043932; PubMed=10579331; DOI=10.1210/en.140.12.5669;
RA Lopez D., McLean M.P.;
RT "Sterol regulatory element-binding protein-1a binds to cis elements in
RT the promoter of the rat high density lipoprotein receptor SR-BI
RT gene.";
```

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RL Endocrinology 140:5669-5681(1999).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Steroidogenic tissues;
RA McLean M.P., Sandhoff T.W., Lopez D.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV451993; AAR18387.1; -; mRNA.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR GO; GO:0007155; P.cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 56859 MW; EA0A76ECD207706C CRC64;

Query Match          92.7%; Score 2484; DB 2; Length 509;
Best Local Similarity 91.7%; Pred. No. 3.6e-180;
Matches 467; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVIMILWPSLIKQVVKVNRIDPSSLSFGMKKEIP 60
Db 1 MGSSRRARWALGALGALLFAALGVVIMILWPSLIKQVVKVNRIDPSSLSFGMKKEIP 60

Qy 61 VPYLSYVFFVNVNPEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLH 120
Db 61 VPYLSYVFFVNVNPEVLNGQKPVVRERGPVYVREFRQKVNITFNDNDTVSVENRSLR 120

Qy 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMNTLALVTMGQAFMNRITVGEIL 180
Db 121 FQDKSHGSESDYIVLPNIIIVLGGSLMESKPVSLKLMNTLALVTMGQAFMNRITVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTFTGVQNFSLHLVDKXNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTFTGVQNFSLHLVDKXNGL 240

Qy 241 SKIDYHSEQCNNINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300
Db 241 SEVNYHSEQCNNINGTAGQWAPFMTPESSLEFFSPACRSKMLTYQESRVFEGIPTYR 300

Qy 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGCPRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360

Qy 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYIKSVKGVGQTKIEPVVPLLLWFRQSG 420
Db 361 LNPDPKHSFLDHPVTGIPMNCVKMQLSLYIKSVKGVGQTKIEPVVPLLLWFRQSG 420

Qy 421 AMGGKPLSTFTYQLVLMQVHYAQVYLLGLGGLLLVPIICOLRSQEKCFLWMSGKKG 480
Db 421 MMGKTLNTFTYQLVLMQVHYAQVYLLGLGGLLLVPIIYQLRSQEKCFLWMSGKKG 480

Qy 481 SODKEAIAQYSESIMSPAAGTGLQEA 509
Db 481 SODKEAIAQYSESIMSPAAGTGLQEA 509

RESULT 5
O88548 RAT PRELIMINARY; PRT; 509 AA.
ID O88548 RAT PRELIMINARY; PRT; 509 AA.
AC O88548;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type II pneumocyte CD36-related class B scavenger receptor.
GN Name=SRB1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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RN NUCLEOTIDE SEQUENCE.
RP STRAIN-Wistar;
RA Kolleck I., Schlame M., Fechner H., Looman A.C., Wisseel H.,
RA Ruestow B.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF071495; AAC33892.1; -, mRNA.
DR Ensemble; ENSRNOG0000000981; Rattus norvegicus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 57152 MW; 1272E4FE824AD7F8 CRC64;

Query Match 92.5%; Score 2479; DB 2; Length 509;
Best Local Similarity 91.2%; Pred. No. 8.6e-180;
Matches 464; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGGSSRARWVALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGGSSRARWVALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIVLPNIIIVLGGSIILMESKPSVLKIMMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGGSIILMESKPSVLKIMMTLALVTMGQAFMNRVTGEIL 180
Qy 121 FQPKSHGSESDYIVLPNIIIVLGGSIILMESKPSVLKIMMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGGSIILMESKPSVLKIMMTLALVTMGQAFMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGNMNSGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGNMNSGVFTVFTGVQNFRIHLVDKWNGL 240
Qy 241 SKIDYHSEQCWMINGTSGQWMAFMTPESSLEFPSPACRSMKLTYNESRVPESGIPYR 300
Db 241 SEVKYHSEQCWMINGTAGQWMAFMTPESSLEFPSPACRSMKLTVOESVFGIPYR 300
Qy 301 FTPADTLFANGSVYPNPGFCPCRESGIQNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTPADTLFANGSVYPNPGFCPCRESGIQNVSTCRFGAPFLSQPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKESLFLDHPVTGIPMNCVSKMQLSLYKSVKIGIQGTGKIIEPVVLPILWPFQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVSKMQLSLYKSVKVGQGTGKIIEPVVLPILWPFQSG 420
Qy 421 AMGCKPLSTFTQLVMPQVLYHQAQYVLLGGLLLVPIICQLRSQEKCFLFWGSKKG 480
Db 421 MMGKTLNTFTQLVMPQVLYHQAQYVLLGGLLLVPIIYQURSQEKCFLFWGSKKG 480
Qy 481 SODKEATQAYSESLSMPAAKCTVLEAKL 509
Db 481 SODKEAQAYSESLSMPAAKCTVQAEKL 509

RESULT 6
SCRB1_CRIGR STANDARD; PRT; 509 AA.
AC Q60417;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI) (HaSR-BI).
GN Name=SCARB1;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Cricetidae; Cricetinae; Cricetulus.

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NCBI_TaxID=10029;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovarian carcinoma;
RX MEDLINE=94342261; PubMed=7520436;
RA Acton S.L., Scherer P.E., Lodish H.F., Krieger M.;
RT "Expression cloning of SR-BI, a CD36-related class B scavenger receptor.";
RL J. Biol. Chem. 269:21003-21009(1994).
CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
CC cells. Probable receptor for HDL, located in particular region of
CC the plasma membrane, called caveolae. Facilitates the flux of free
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apoB-containing lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae (By similarity).
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the CD36 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U11453; AAA61572.1; -, mRNA.
CC PIR; A53920; A53920.
CC InterPro; IPR002159; CD36.
CC InterPro; IPR005428; CD36_antigen.
CC PANTHER; PTHR11923; CD36; 1.
CC Pfam; PF01130; CD36; 1.
CC PRINTS; PR01610; CD36ANTIGEN.
CC PRINTS; PR01609; CD36FAMILY.
CC Glycoprotein; Receptor; Transmembrane.
CC TOPO_DOM 1 11 Cytoplasmic (Potential).
CC TRANSHEM 12 32 Potential.
CC TOPO_DOM 33 440 Extracellular (Potential).
CC TRANSHEM 441 461 Potential.
CC TOPO_DOM 462 509 Cytoplasmic (Potential).
CC CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 509 AA; 56735 MW; 1A7C0F5F6CB61A17 CRC64;

Query Match 91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 2.3e-177;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGGSSRARWVALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGGSSRARWVALGALGALLFAALGVVMIIVPSLIKQVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENSRLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFNDNDTVSFVENSRLH 120
Qy 121 FQPKSHGSESDYIVLPNIIIVLGGSIILMESKPSVLKIMMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIIVLGGSIILMESKPSVLKIMMTLALVTMGQAFMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGNMNSGVFTVFTGVQNFRIHLVDKWNGL 240

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Db 181 WGEDPFWNFINKVLPDMFKPKGKGLFVEMNNSDGLFTVFTGVQNFQSKIHLDVRWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNDSRVFEGIPTYR 300
Db 241 SKVNYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPDPTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDPTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDIDHPVTGIPMNCVKMQLSLYKSVKGIQGTGKIEPVVPLPILWFEQSG 420
Db 361 LNPDPKHSFLDIDHPVTGIPMNCVKMQLSLYKSVKGIQGTGKIEPVVPLPILWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Db 421 AMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Qy 481 SODKEATQAYSESLSMSPAAGTIVLQEA 509
Db 481 SODKEATQAYSESLSMSPAAGTIVLQEA 509

RESULT 7
Q6B417 RAT PRELIMINARY; PRT; 506 AA.
AC Q6B417;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Scavenger receptor class B type 2.
GN Name=Scarb2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Lopez D., Rubin D., McLean M.P.;
RT "Regulation of the Rat SR-B Isoforms.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY682847; AAT85567.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 506 AA; 56342 MW; 6FDE625301320E2E CRC64;

Query Match 84.9%; Score 2275.5; DB 2; Length 506;
Best Local Similarity 86.4%; Pred. No. 2.5e-164;
Matches 432; Conservative 27; Mismatches 26; Indels 15; Gaps 2;

Qy 1 MCGSRARWALGICGALGILFANLGVNMLVPSLIKKOVLKNVIRDPSSLSFGWKKEIP 60
Db 1 MGVSSRARWALGLGVLLGILCAALGVIMLMVPSLIKKOVLKNVIRDPSSLSFGWKKEIP 60
Qy 61 VPFYLSVVFVFNNEVLNGKPVVRERGPVYVREFRQKNVITDNDNDTYSFVNRSILH 120
Db 61 VPFYLSVVFVFNNEVLNGKPVVRERGPVYVREFRQKNVITDNDNDTYPYIENRSLR 120
Qy 121 FQPKSHGSESDYIVLPNIIVLGSGILMESKPVSLKLMNTLALVTGQRAFPMNRTVGIL 180
Db 121 FQPKSHGSESDYIVLPNIIVLGSGILMESKPVSLKLMNTLALVTGQRAFPMNRTVGIL 180
Qy 181 WGEDPFWNFINKVLPDMFKPKGKGLFVEMNNSDGLFTVFTGVQNFQSKIHLDVRWNGL 240
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Db 181 WGEDPFWNFINKVLPDMFKPKGKGLFVGMNDSGSGVFTFTGVQNFQSKIHLDVRWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNDSRVFEGIPTYR 300
Db 241 SEVNYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYQSRVFEGIPTYR 300
Qy 301 FTAPDPTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDPTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDIDHPVTGIPMNCVKMQLSLYKSVKGIQGTGKIEPVVPLPILWFEQSG 420
Db 361 LNPDPKHSFLDIDHPVTGIPMNCVKMQLSLYKSVKGIQGTGKIEPVVPLPILWFEQSG 420
Qy 421 AMGGKPLSTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIICQLRSQKCFPLFWSGSKG 480
Db 421 MMGGKLTNTFTYQLVLMPOVLYHQAQVYLLGLGLLLVPIIYQLRSQ-----G 468
Qy 481 SODKEA---IQAYSESLSMSP 497
Db 469 PEDTSPPNLIAMSDQPPSP 488

RESULT 8
SCRBI_PIG
ID SCRBI_PIG STANDARD; PRT; 509 AA.
AC Q8SQCL;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SR-B1) (SR-B1) (High density lipoprotein receptor SR-B1).
GN Name=SCRBI;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim J.G., Vallet J.L., Christenson R.K.;
RT "Characterization of porcine high density lipoprotein (HDL) receptor SR-B1.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for different ligands such as phospholipids, cholesterol ester, lipoproteins, phosphatidylserine and apoptotic cells. Probable receptor for HDL, located in particular region of the plasma membrane, called caveolae. Facilitates the flux of free and esterified cholesterol between the cell surface and extracellular donors and acceptors, such as HDL and to a lesser extent, apob-containing lipoproteins and modified lipoproteins. Probably involved in the phagocytosis of apoptotic cells, via its phosphatidylserine binding activity (By similarity).
CC -!- SUBUNIT: The C-terminal region binds to PDZK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly localized to cholesterol and sphingomyelin-enriched domains within the plasma membrane, called caveolae (By similarity).
CC -!- PTM: N-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the CD36 family.

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EMBL; AF467889; AAL75567.1; -; mRNA.
InterPro; IPR002159; CD36.
InterPro; IPR005428; CD36_antigen.
PANTHER; PTHR11923; CD36; 1.
Pfam; PF01130; CD36; 1.
PRINTS; PR01610; CD36ANTIGEN.
PRINTS; PR01609; CD36FAMILY.
```

Glycoprotein; Receptor; Transmembrane.
 FT TOPO DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO DOM 33 439 Extracellular (Potential).
 FT TRANSMEM 440 460 Potential.
 FT TOPO DOM 461 509 Cytoplasmic (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc).
 FT CARBOHYD 108 108 N-linked (GlcNAc).
 FT CARBOHYD 173 173 N-linked (GlcNAc).
 FT CARBOHYD 212 212 N-linked (GlcNAc).
 FT CARBOHYD 255 255 N-linked (GlcNAc).
 FT CARBOHYD 310 310 N-linked (GlcNAc).
 FT CARBOHYD 330 330 N-linked (GlcNAc).
 FT CARBOHYD 383 383 N-linked (GlcNAc).
 SQ SEQUENCE 509 AA; 57514 MW; F7421796C391C4C1 CRC64;

Query Match 82.6%; Score 2215; DB 1; Length 509;
 Best Local Similarity 80.2%; Pred. No. 1e-159;
 Matches 408; Conservative 48; Mismatches 53; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Qy 61 VPFYLSVYFPEVVPNEVLNGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPFYLSVYFPEVVPNEVLNGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
 Qy 121 FQPKSHGSESDYIVLPNIIIVLGSLIMESKPSVLKMMTALVTMGORAFMNRVTGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIIVLGSLIMESKPSVLKMMTALVTMGORAFMNRVTGEIL 180
 Qy 181 WGYDDPFFVHINTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPFFVHINTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Qy 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
 Db 241 SKVNFHSDQCNMNGTSGQWAPFMTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
 Qy 301 FTAPDTLIFANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Db 301 FVAENTLIFANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPMPKESLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIEPVLPLLPFQSG 420
 Db 361 LHPNTEHSLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIEPVLPLLPFQSG 420
 Qy 421 AMGKPLSTFTYTLVMPQVLYHYAQVYLLGLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
 Db 421 AMEGETLQTFTYTLVMPQVLYHYAQVYLLGLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
 Qy 481 SODKEATQAYSESLSMSPAAGTGLQEARL 509
 Db 481 SODKEATQAYSESLSMSPAAGTGLQEARL 509

RESULT 9
 Q678F1_TUPGB
 ID Q678F1_TUPGB PRELIMINARY; PRT; 509 AA.
 AC Q678F1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Scavenger receptor class B member 1.
 GN Name=SCARB1;
 OS Tupia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupia.
 NCBI_TaxID=37347;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Barth H., Cerino R., Arcuri M., Hoffmann M., Schurmann P., Adah M.I.,

Gissler B., Zhao X., Chisetti V., Lavezzo B., Blum H.E.,
 von Weizsacker F., Vicelli A., Scarcelli E., Baumert T.F.;
 RT "Scavenger Receptor Class B Type I and Hepatitis C Virus Infection of
 Primary Tupaia Hepatocytes.";
 J. Virol. 79:5774-5785(2005).
 RL EMBL; AY428553; AAR12144.1; -; mRNA.
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004872; F:receptor activity; IEA.
 DR GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR002159; CD36.
 DR InterPro: IPR005428; CD36_antigen.
 DR Pfam: PF01130; CD36; 1.
 DR PRINTS; PRO1610; CD36ANTIGEN.
 DR PRINTS; PRO1609; CD36FAMILY.
 KW Receptor.
 SQ SEQUENCE 509 AA; 57369 MW; F0A3PBB1431PFB18 CRC64;

Query Match 82.5%; Score 2212; DB 2; Length 509;
 Best Local Similarity 80.0%; Pred. No. 1.7e-159;
 Matches 407; Conservative 49; Mismatches 53; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Db 1 MGSSRRARWALGALGLLFAALGVVMILMVPSLIKQVLKVRIDPSSLSFGMWKEIP 60
 Qy 61 VPFYLSVYFPEVVPNEVLNGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
 Db 61 VPFYLSVYFPEVVPNEVLNGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
 Qy 121 FQPKSHGSESDYIVLPNIIIVLGSLIMESKPSVLKMMTALVTMGORAFMNRVTGEIL 180
 Db 121 FQPKSHGSESDYIVLPNIIIVLGSLIMESKPSVLKMMTALVTMGORAFMNRVTGEIL 180
 Qy 181 WGYDDPFFVHINTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Db 181 WGYDDPFFVHINTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFRIHLVDKWNGL 240
 Qy 241 SKIDYHSEQCNMNGTSGQWAPFMTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
 Db 241 SKVNFHSDQCNMNGTSGQWAPFMTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
 Qy 301 FTAPDTLIFANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Db 301 FVAENTLIFANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
 Qy 361 LNPMPKESLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIEPVLPLLPFQSG 420
 Db 361 LHPNTEHSLFLDIHPVTGIPMNCVKQLSLYIKSVKGIQGTGKIEPVLPLLPFQSG 420
 Qy 421 AMGKPLSTFTYTLVMPQVLYHYAQVYLLGLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
 Db 421 AMEGETLQTFTYTLVMPQVLYHYAQVYLLGLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
 Qy 481 SODKEATQAYSESLSMSPAAGTGLQEARL 509
 Db 481 SODKEATQAYSESLSMSPAAGTGLQEARL 509

RESULT 10
 Q52LZ5_HUMAN
 ID Q52LZ5_HUMAN PRELIMINARY; PRT; 509 AA.
 AC Q52LZ5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Scavenger receptor class B, member 1.
 GN Name=SCARB1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC093732; AAH93732.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 509 AA; 56973 MW; 0184AE9CEC595374 CRC64;

Query Match 82.1%; Score 2200; DB 2; Length 509;
Best Local Similarity 79.6%; Pred. No. 1.4e-158;
Matches 405; Conservative 49; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVWILMPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Db 1 MGCSAKARWAGALGVGLLCAVLGAVMIVMPSLIKQVVKVNRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYVFFVWVNPVNLGQKPVWRERGVYVREFRQKNITFDNDITVSVFVENSLSH 120
Db 61 IPFLSVYVFFVWVNPVNLGQKPVWRERGVYVREFRQKNITFDNDITVSVFVENSLSH 120
Qy 121 FQPKSHGSESDYIVLPNLYLGGSLMESKPSVSLKMTLALVTMGQAPMNRVTGEIL 180
Db 121 FQPKSHGSESDYIVMPSNLYLGGSLMESKPSVSLKMTLALVTMGQAPMNRVTGEIM 180
Qy 181 WGYDDPFVHFLNTVLPDMLPTKGFGLVGNNGNSGVFTVGTQVQPSRTHLVKNGKL 240
Db 181 WGYDDPLVNLINKYPPGMPFPDQKPLFAELNNSDGLFTVGTQVQPSRTHLVKNGKL 240
Qy 241 SKIDYWHSEQCWNMGTSQMWAPMPTPESSILEFFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKVDFHSDQCNMGTSQMWAPMPTPESSILEFFSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFGANGVYPNPGFCPCRESGIQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FVAPKTLFGANGVYPNPGFCPCRESGIQNVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Qy 361 LNPKEHSLFLDHPVTGIPMNCSSVKMOLSIYTKSVKIGOTGKIEPVLPLWFEQSG 420
Db 361 LHPNQEASLSFLDHPVTGIPMNCSSVKMOLSIYTKSVKIGOTGKIEPVLPLWFEQSG 420
Qy 421 AMGQKPLSTFTYQLVLMQVLYHAQVLLGLGLLVLPIICQLRSQSKCFLWFGSKGK 480
Db 421 AMEGTILHTFTYQLVLMQVLYHAQVLLGLGLLVLPIICQLRSQSKCFLWFGSKGK 480
Qy 481 SODKEAIQAYSLSLMSPAKGTVLOEAKL 509
Db 481 SKDKEAIQAYSLSLMSPAKGTVLOEAKL 509

RESULT 11

SCRB1_BOVIN STANDARD; PRT; 509 AA.
ID SCRB1_BOVIN
AC O18824;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-BI).
DE Name=SCARB1;
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Corpus luteum;
RX MEDLINE=98068685; PubMed=9406850; DOI=10.1016/S0303-7207(97)00173-1;
RA Rajapaksha W.R.A.K.J.S., McBride M., Robertson L., O'Shaughnessy P.J.;
RT "Sequence of the bovine HDL-receptor (SR-BI) cDNA and changes in
receptor mRNA expression during granulosa cell luteinization in vivo
and in vitro.";
RL Mol. Cell. Endocrinol. 134:59-67(1997).
CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
cells. Probable receptor for HDL, located in particular region of
the plasma membrane, called caveolae. Facilitates the flux of free
and esterified cholesterol between the cell surface and
extracellular donors and acceptors, such as HDL and to a lesser
extent, apoB-containing lipoproteins and modified lipoproteins.
Probably involved in the phagocytosis of apoptotic cells, via its
phosphatidylserine binding activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
localized to cholesterol and sphingomyelin-enriched domains within
the plasma membrane, called caveolae (By similarity).
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the CD36 family.
CC -----
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between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; AF019384; AA870920.1; -, mRNA.
DR InterPro; IPR002159; CD36.
DR InterPro; IPR005428; CD36_antigen.
DR PANTHER; PTHR11923; CD36; 1.
DR Pfam; PF011130; CD36; 1.
DR PRINTS; PR01610; CD36ANTIGEN.
DR PRINTS; PR01609; CD36FAMILY.
DR Glycoprotein; Receptor; Transmembrane.
KW TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TOPO_DOM 12 32 Potential.
FT TRANSMEM 33 440 Extracellular (Potential).
FT TRANSMEM 441 461 Potential.
FT TOPO_DOM 462 509 Cytoplasmic (Potential).
FT CARBOHYD 102 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 509 AA; 57610 MW; B3B7FD368C2C12F CRC64;

Query Match 81.3%; Score 2180; DB 1; Length 509;
Best Local Similarity 78.6%; Pred. No. 4.6e-157;
Matches 400; Conservative 50; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGLLFAALGVVWILMPSLIKQVVKVNRIDPSSLSFGMWKEIP 60

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Db 1 MGNLRARVTAALGICLLFAVLGIMVWPSLIKQOVLKNVRIDPNSLSPFNWKEIP 60
Qy 61 VPFYLSVYFEVNVNEVNGOKPVYRERGYPVYRERQKVNITFNDNDTFSFVENRSLH 120
Db 61 VPFYLSVYFEVNVNEVNGOKPVYRERGYPVYRERQKVNITFNDNDTFSFVENRSLH 120
Qy 121 FQPKSHSGESDYVLPNHLVGGSLMESKPSVSLKMLMTLALVTMGORAFMNRVTGAIL 180
Db 121 FQPKSHSGESDYVLPNHLVGGSLMESKPSVSLKMLMTLALVTMGORAFMNRVTGAIL 180
Qy 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVONFSRIHLVDKNGVL 240
Db 181 WGYDDPLHILNQFPNSLPKGFGLFAELNNSDGLFTVFTGVONFSRIHLVDKNGVL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPMPTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKVNYWHSDQCNMINTSGQWAPMPTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FVAPSTLTFANGSVYPPNEGFCPCRESGIONVSTCRFNAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYKSVKGIGQTKIEPVVLPPLMFWESQ 420
Db 361 LHPNEBEHALFDHPVTGIPMNCVSKMQLSLYKSVKGIGQTKIEPVVLPPLMFWESQ 420
Qy 421 AMGGKPLSTFTYQLVLMQVHLHYAQVLLGGLLVLPIICQLRSQEKCFLFWSGSKKG 480
Db 421 AMEGTLETFTYQLVLMQVHLHYAQVLLGGLLVLPIICQLRSQEKCFLFWSGSKKG 480
Qy 481 SODKEATQAYSESLSMPAAKGTVLQEAEL 509
Db 481 SKDKEAVQAYSEFLMTSAPKGTVLQEARL 509

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RESULT 12

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Q6WIW9 RABIT PRELIMINARY; PRT; 509 AA.
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AC Q6WIW9;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Scavenger receptor class B type I.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
RA Ritsch A., Tancevski I., Schgoer W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Fatsch J.R.;
RT "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RL J. Lipid Res. 45:214-222(2004).
DR ENBL: AY283277; AAP40266.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR002159; CD36.
DR InterPro: IPR005428; CD36_antigen.
DR Pfam: PF01130; CD36.1.
DR PRINTS: PR01610; CD36ANTIGEN.
DR PRINTS: PR01609; CD36FAMILY.
KW Receptor.
SQ SEQUENCE 509 AA; 57052 MW; 00DD47F1AF2DB4E0 CRC64;

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Query Match 80.1%; Score 2148; DB 2; Length 509;
 Best Local Similarity 77.6%; Pred. No. 1.2e-154;
 Matches 395; Conservative 55; Mismatches 59; Indels 0; Gaps 0;

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Qy 1 MGSSRARWVALGIGALGLLFAALGVVMILWVPSLIKQOVLKNVRIDPNSLSPFNWKEIP 60
Db 1 MGRRARARAAAGLGVVGLLCAVGVAVLIAAAPPILRQVVLKNVRIDPNSLSPFNWKEIP 60
Qy 61 VPFYLSVYFEVNVNEVNGOKPVYRERGYPVYRERQKVNITFNDNDTFSFVENRSLH 120
Db 61 APFYLSVYFFDVVNPBILKGEKQVREPGYVYRERQKVNITFNDNDTFSFLEHRSFQ 120
Qy 121 FQPKSHSGESDYVLPNHLVGGSLMESKPSVSLKMLMTLALVTMGORAFMNRVTGAIL 180
Db 121 FQPKSRGSDYIVMPNHLVLSASMMENRPLGLKMLMTLAFSLGORAFMNRVTGIM 180
Qy 181 WGYDDPPVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVONFSRIHLVDKNGVL 240
Db 181 WGYDDPLHILNQFPNSLPKGFGLFAELNNSDGLFTVFTGVONFSRIHLVDKNGVL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPMPTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKVNYWHSDQCNMINTSGQWAPMPTPESSLEFSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FVAPSTLTFANGSVYPPNEGFCPCRESGIONVSTCRFNAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYKSVKGIGQTKIEPVVLPPLMFWESQ 420
Db 361 LHPNEBEHALFDHPVTGIPMNCVSKMQLSLYKSVKGIGQTKIEPVVLPPLMFWESQ 420
Qy 421 AMGGKPLSTFTYQLVLMQVHLHYAQVLLGGLLVLPIICQLRSQEKCFLFWSGSKKG 480
Db 421 AMEGTLETFTYQLVLMQVHLHYAQVLLGGLLVLPIICQLRSQEKCFLFWSGSKKG 480
Qy 481 SODKEATQAYSESLSMPAAKGTVLQEAEL 509
Db 481 SKDKEAVQAYSEFLMTSAPKGTVLQEARL 509

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RESULT 13

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SCRBI HUMAN STANDARD; PRT; 552 AA.
ID SCRBI HUMAN STANDARD; PRT; 552 AA.
AC Q8WT0; Q14016; Q6RFK4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scavenger receptor class B member 1 (SRB1) (SR-B1) (CD36 antigen-like
DE 1) (CD36 and LIMP-II analogous 1) (CLA-1) (Collagen type I receptor,
DE Thrombospondin receptor-like 1).
GN Name=SCARB1; Synonyms=CD36L1, CLA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Promyelocyte;
RX MEDLINE=9336811; PubMed=7689561;
RA Calvo D.; Vega M.;
RT "Identification, primary structure and distribution of CLA-1, a novel
RT member of the CD36/LIMP-II gene family.";
J. Biol. Chem. 268:18929-18935(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RA Hirano K.-I., Yamashita S., Matsuzawa Y.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3).
RX TISSUE=Prostate, and Rhabdomyosarcoma;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

```

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[4]
RX FUNCTION.
RX MEDLINE=22244044; PubMed=12356718; DOI=10.1093/emboj/cdf529;
RA Scarselli E., Anselmi H., Cerino R., Roccasecca R.M., Accali S.,
RA Filocamo G., Traboni C., Nicosia A., Cortese R., Vitelli A.;
RT "The human scavenger receptor class B type I is a novel candidate
RT receptor for the hepatitis C virus."
RL EMBO J. 21:5017-5025 (2002).
[5]
RX GLYCOSYLATION.
RX MEDLINE=22128898; PubMed=12016218; DOI=10.1074/jbc.M202879200;
RA Kawasaki Y., Nakagawa A., Nagosa K., Shiratsuchi A., Nakanishi Y.;
RT "Phosphatidylserine binding of class B scavenger receptor type I, a
RT phagocytosis receptor of testicular Sertoli cells."
RL J. Biol. Chem. 277:27559-27566 (2002).
[6]
RX INTERACTION WITH HCV E1/E2 ENVELOPE HETERODIMER.
RX MEDLINE=22928135; PubMed=12913001; DOI=10.1074/jbc.M305289200;
RA Bartosch B., Vitelli A., Granier C., Goujon C., Dubuisson J.,
RA Pascale S., Scarselli E., Cortese R., Nicosia A., Cosset F.-L.;
RT "Cell entry of hepatitis C virus requires a set of co-receptors that
RT include the CD81 tetraspanin and the SR-B1 scavenger receptor."
RL J. Biol. Chem. 278:41624-41630 (2003).
[7]
RX VARIANT SER-2.
RX MEDLINE=22407477; PubMed=12519372;
RX DOI=10.1034/j.1399-0004.2003.630108.x;
RA Tai E.S., Adiconis X., Ordovas J.M., Carmena-Ramon R., Real J.,
RA Corella D., Ascaso J., Carmena R.;
RT "Polymorphisms at the SRB1 locus are associated with lipoprotein
RT levels in subjects with heterozygous familial hypercholesterolemia."
RL Clin. Genet. 63:53-58 (2003).
[8]
RX VARIANTS SER-2; ILE-135 AND SER-167.
RX PubMed=12966036; DOI=10.1093/hmg/ddg314;
RA Morabia A., Cayanis E., Costanza M.C., Ross B.M., Flaherty M.S.,
RA Alvin G.B., Das K., Gilliam T.C.;
RT "Association of extreme blood lipid profile phenotypic variation with
RT cardiovascular disease risk factors."
RL Hum. Mol. Genet. 12:2733-2743 (2003).
CC -1- FUNCTION: Receptor for different ligands such as phospholipids,
CC cholesterol ester, lipoproteins, phosphatidylserine and apoptotic
CC cells. Probable receptor for HDL located in particular region of
CC and esterified cholesterol between the cell surface and
CC extracellular donors and acceptors, such as HDL and to a lesser
CC extent, apoB-containing lipoproteins and modified lipoproteins.
CC Probably involved in the phagocytosis of apoptotic cells, via its
CC phosphatidylserine binding activity. Receptor for hepatitis C
CC virus glycoprotein E2. Binding between SCARB1 and E2 was found to
CC be independent of the genotype of the viral isolate.
CC -1- SUBUNIT: Plays a critical role in HCV attachment and/or cell entry
CC by interacting with HCV E1/E2 glycoproteins heterodimer. The C-
CC terminal region binds to PDZK1 (By similarity).
CC -1- INTERACTION:

CC P55345;HRMTLL1; NDExp=1; IntAct=EBI-78657, EBI-78458;
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Predominantly
CC localized to cholesterol and sphingomyelin-enriched domains within
CC the plasma membrane, called caveolae.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=3;
CC IsoId=Q8WTV0-1; Sequence=Displayed;
CC Note=May be due to a competing donor splice site. No
CC experimental confirmation available;
CC Name=1; Synonyms=SR-B1;
CC IsoId=Q8WTV0-2; Sequence=VSP_008554;
CC Name=2; Synonyms=SR-BII;
CC IsoId=Q8WTV0-3; Sequence=VSP_008553, VSP_008554;
CC Name=4; Synonyms=SR-BIII;
CC IsoId=Q8WTV0-4; Sequence=VSP_011037, VSP_008554;
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- PTM: N-glycosylated.
CC -1- POLYMORPHISM: The Ser-2 variant is associated with higher plasma
CC triglyceride concentration in subjects with heterozygous familial
CC hypercholesterolemia.
CC -1- SIMILARITY: Belongs to the CD36 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; Z22555; CAA80277.1; -; mRNA.
CC EMBL; AF515445; AAQ08185.1; -; mRNA.
CC EMBL; BC022087; -; NOT ANNOTATED CDS; mRNA.
CC EMBL; BC080647; AAH80647.1; -; mRNA.
CC PIR; S36656; A48528.
CC IntAct; Q8WTV0; -;
CC Ensembl; ENSG00000073060; Homo sapiens.
CC HGNC; HGNC:1664; SCARB1.
CC MIM; 601040; -; C:plasma membrane; TAS.
CC GO; GO:0005886; -; Receptor activity; TAS.
CC GO; GO:0004872; F:transporter activity; TAS.
CC GO; GO:0005215; F:cholesterol metabolism; TAS.
CC GO; GO:0008203; P:cholesterol metabolism; TAS.
CC GO; GO:0006810; P:transport; TAS.
CC InterPro; IPR002159; CD36.
CC InterPro; IPR005428; CD36_antigen.
CC PANTHER; PTHR11923; CD36; 1.
CC Pfam; PF01130; CD36; 1.
CC PRINTS; PR01610; CD36ANTIGEN.
CC PRINTS; PR01609; CD36FAMILY.
KW Alternative splicing; Glycoprotein; Polymorphism; Receptor;
KW Transmembrane.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 44 Extracellular (Potential).
FT TRANSMEM 44 46 Potential.
FT TOPO_DOM 46 52 Cytoplasmic (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 42 MGSAKARWAAGALGVAGLCVAGVAVMVVPSLIKQOVL
FT K -> MALQPSW (in isoform 4).
FT /FTID=VSP_011037.
FT VARSPLIC 43 142 Missing (in isoform 2).
FT /FTID=VSP_008553.
FT VARSPLIC 468 552 VGQARARADSHSLACWGKASDRITLWPTAWSPPPAAVL
FT RLCSGSGCHWGLSTLAFACRVATTLPLVLEGLPSLGGG
FT TGS -> EKCYLFWSSSKGSKDKEAIQAYSESLMTAPKG


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SVLQRAKL (in isoform 1, isoform 2 and
isoform 4).
/FTID=VSP_008554.
G -> S (in dbSNP:4238001).
/FTID=VAR_017098.
V -> I.
/FTID=VAR_017099.
G -> S.
/FTID=VAR_017100.
S -> G (in dbSNP:10396213).
/FTID=VAR_019507.
C -> R (in dbSNP:2293440).
/FTID=VAR_017101.
F -> L (in Ref. 2).
F -> S (in Ref. 1).
SEQUENCE 552 AA; 60878 MW; 0680BD771FEA284F CRC64;

Query Match      75.4%; Score 2022.5; DB 1; Length 552;
Best Local Similarity 74.6%; Pred. No. 4.8e-145;
Matches 375; Conservative 52; Mismatches 67; Indels 9; Gaps 2;

QY 1 MGSSRARARWALGALGALLFAALGVVMILMVPVSLIKQOVLKNVRIIDPSSLSFGMWKEIP 60
Db 1 MGCSAKARWAAGALGVAGLLCAVLGAVMIVMVPVSLIKQOVLKNVRIIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVTFEVPVNEVLNGQKPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 120
Db 61 IPPYLSVTFEVPVNEVLNGQKPVVRERGYPVYRFRQKVNITPNDNDTVSFLEYRTFQ 120
QY 121 FQPKSHGSSDYIVLPNVLVGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSSDYIVLPNVLVGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIM 180
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Db 241 SKVDFWHSQDNMNGTSGQWMPPTPESSLEFPSPACRSMKLMYKESGVFEGIPYR 300
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Db 301 FVAPKTLTFANGSVYPPNPGFCPCRESGIONVSTCRFSAPLFLSHPHFNADPVLSEAVTG 360
QY 361 LNPMPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGOTGKIIEPVVPLLWFQSG 420
Db 361 LHPNQEAHSLFDLHPVTGIPMNCVKLQSLYKSVAGIGOTGKIIEPVVPLLWFQESG 420
QY 421 AMGKPLSTFTYQLVLMPOVLYAQQYVLLGLGGLLLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMEGETLHTFTYQLVLMPOVLYAQQYVLLGLGGLLLVPIICQLRSQKCFLFWGSKKG 480
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Db 476 RADSHSLACWKGASDRTLWPTA 498

RESULT 14
Q59FM4 HUMAN PRELIMINARY; PRT; 581 AA.
AC Q59FM4;
DT 10-MAY-2005 (TremBLrel. 30, Created)
DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
DE Scavenger receptor class B member 1 variant (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

SVLQRAKL (in isoform 1, isoform 2 and
isoform 4).
/FTID=VSP_008554.
G -> S (in dbSNP:4238001).
/FTID=VAR_017098.
V -> I.
/FTID=VAR_017099.
G -> S.
/FTID=VAR_017100.
S -> G (in dbSNP:10396213).
/FTID=VAR_019507.
C -> R (in dbSNP:2293440).
/FTID=VAR_017101.
F -> L (in Ref. 2).
F -> S (in Ref. 1).
SEQUENCE 552 AA; 60878 MW; 0680BD771FEA284F CRC64;

Query Match      75.4%; Score 2022.5; DB 1; Length 552;
Best Local Similarity 74.6%; Pred. No. 4.8e-145;
Matches 375; Conservative 52; Mismatches 67; Indels 9; Gaps 2;

QY 1 MGSSRARARWALGALGALLFAALGVVMILMVPVSLIKQOVLKNVRIIDPSSLSFGMWKEIP 60
Db 1 MGCSAKARWAAGALGVAGLLCAVLGAVMIVMVPVSLIKQOVLKNVRIIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVTFEVPVNEVLNGQKPVVRERGYPVYRFRQKVNITPNDNDTVSFVENRSLH 120
Db 61 IPPYLSVTFEVPVNEVLNGQKPVVRERGYPVYRFRQKVNITPNDNDTVSFLEYRTFQ 120
QY 121 FQPKSHGSSDYIVLPNVLVGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSSDYIVLPNVLVGGILMESKPVSLKLMNTLALVTMGORAFMNRVTGEIM 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
Db 181 WGYKDPVLNLINKYPPGMPFKDFGLFAELNNSDGLFTVFTGVQNFSRHLVDKWNGL 240
QY 241 SKIDYHSEQCNMINGTSGQWAPMPTPESSLEFPSPACRSMKLTYNESRVFEGIPYR 300
Db 241 SKVDFWHSQDNMNGTSGQWMPPTPESSLEFPSPACRSMKLMYKESGVFEGIPYR 300
QY 301 FTAPDTLTFANGSVYPPNPGFCPCRESGIONVSTCRFSAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FVAPKTLTFANGSVYPPNPGFCPCRESGIONVSTCRFSAPLFLSHPHFNADPVLSEAVTG 360
QY 361 LNPMPKHSFLDHPVTGIPMNCVKMQLSLYKSVKGIGOTGKIIEPVVPLLWFQSG 420
Db 361 LHPNQEAHSLFDLHPVTGIPMNCVKLQSLYKSVAGIGOTGKIIEPVVPLLWFQESG 420
QY 421 AMGKPLSTFTYQLVLMPOVLYAQQYVLLGLGGLLLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMEGETLHTFTYQLVLMPOVLYAQQYVLLGLGGLLLVPIICQLRSQKCFLFWGSKKG 480
QY 481 SQDKEATQAY-----SESLSMPAA 499
Db 476 RADSHSLACWKGASDRTLWPTA 498

RESULT 15
Q6TW8_RABIT PRELIMINARY; PRT; 501 AA.
AC Q6TW8;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Scavenger receptor class B type II.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
RA Ritsch A., Tancevski I., Schgoer W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Patech J.R.;
RT "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RL J. Lipid Res. 45:214-222(2004).

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RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209436; BAD92673.1; -, mRNA.
KW Receptor.
FT NON TER
SQ SEQUENCE 581 AA; 64186 MW; 795810C1C2PA75A3 CRC64;

Query Match      75.4%; Score 2022.5; DB 2; Length 581;
Best Local Similarity 74.6%; Pred. No. 5.1e-145;
Matches 375; Conservative 52; Mismatches 67; Indels 9; Gaps 2;

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AC Q6TW8;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Scavenger receptor class B type II.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14595001; DOI=10.1194/jlr.M300353-JLR200;
RA Ritsch A., Tancevski I., Schgoer W., Pfeifhofer C., Gander R.,
RA Eller P., Foeger B., Stanzl U., Patech J.R.;
RT "Molecular characterization of rabbit scavenger receptor class B types
RT I and II: portal to central vein gradient of expression in the
RT liver.";
RL J. Lipid Res. 45:214-222(2004).

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DR EMBL; AY283278; AAP40267.1; -: mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
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DR InterPro; IPR005428; CD36_antigen.
DR Pfam; PF01130; CD36; 1.
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Best Local Similarity 77.3%; Pred. No. 4.2e-141;
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Qy 241 SKIDYHSEQNMINGTSGQWAPFMTPESSLEFPSPSEACRSMKLTYNESRVPEGIPTYR 300
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Qy 301 FTA PDTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNDADPVLSEAVLG 360
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Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMOLSLYIKSVKGIGQTKIBPVVLPVLPVLPVLPV 420
Db 361 LHPNEEEHALFDHPVTGIPMNCVSKLQLSLYKKAIRGIGQTKIEPVVLPVLPVLPV 420

Qy 421 AMGKPLSTFTYQLVLPQVILHYAQYVLLGLGGLLLVPIICQLRSQ 467
Db 421 AMEGETLSTFTYQLVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 467

Search completed: February 23, 2006, 12:45:06
Job time : 148.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:45:24 ; Search time 34 Seconds
(without alignments)
1237.704 Million cell updates/sec

Title: US-08-765-108-8

Perfect score: 2681

Sequence: 1 MGSRRARWALGLGALL.....YSESLMSPAKGTVLQEAFL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5 COMB.pcp.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2681	100.0	509	1 US-08-559-505-4	Sequence 4, Appli
2	2681	100.0	509	1 US-08-749-907-4	Sequence 4, Appli
3	2681	100.0	509	2 US-09-241-581B-8	Sequence 8, Appli
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6	2447	91.3	509	1 US-08-559-505-2	Sequence 2, Appli
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27	568	21.2	412	2 US-09-949-016-11488	Sequence 11488, A

28 436 16.3 458 2 US-09-270-767-43768 Sequence 43768, A
29 431 16.1 310 2 US-09-270-542-90 Sequence 90, Appli
30 346 12.9 332 2 US-09-270-767-46306 Sequence 46306, A
31 295 11.0 462 2 US-09-270-767-45262 Sequence 45262, A
32 267 10.0 158 2 US-09-270-767-61875 Sequence 61875, A
33 230 8.6 301 2 US-09-270-767-33112 Sequence 33112, A
34 229 8.5 301 2 US-09-270-767-48329 Sequence 48329, A
35 229 8.5 248 2 US-09-270-767-59167 Sequence 59167, A
36 189 7.0 74 2 US-09-513-999C-6528 Sequence 6528, Ap
37 181 6.8 181 2 US-09-270-767-42865 Sequence 42865, A
38 106 4.0 172 2 US-09-270-767-60022 Sequence 60022, A
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41 99 3.7 320 2 US-09-134-000C-4950 Sequence 4950, Ap
42 98.5 3.7 414 2 US-10-104-047-2031 Sequence 2031, Ap
43 97.5 3.6 45 2 US-09-161-939A-21 Sequence 21, Appli
44 97.5 3.6 924 2 US-09-583-110-3216 Sequence 3216, Ap
45 97.5 3.6 928 2 US-09-107-433-2917 Sequence 2917, Ap

ALIGNMENTS

RESULT 1

US-08-559-505-4
; Sequence 4, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/559,505
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; OTHER INFORMATION: murine Scavenger Receptor Class BI."

US-08-559-505-4

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-08-749-907-4
; Sequence 4, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; OTHER INFORMATION: murine Scavenger Receptor Class B1."
US-08-749-907-4

Query Match 100.0%; Score 2681; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGSSRRARWALGALGALLFAALGVVMIWVPSLIKQVVKVNRIDPSSLSFGWKEIP 60
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DB 61 VPFYLSVYFFVVPNEVNLGKQVVRERGYPVYFRQKVNITFNDNDTVSFVNRSLH 120
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DB 121 POPDKSHGSESDYIVLPNIIIVLGGSIIMESKPVSLKMMTLALVTMGQAFMNRVTGEIL 180
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RESULT 3

US-09-241-581B-8
; Sequence 8, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B

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; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for
; the murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-241-581B-8

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60

Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTYSFVENRSLH 120
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RESULT 4
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; Sequence 4, Application US/09385799
; Patent No. 6962688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385.799
; FILING DATE: 30-Aug-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-385-799-4

Query Match 100.0%; Score 2681; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Db 1 MGGSSRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60

Qy 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTYSFVENRSLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYRFRQKVNITFDNDTYSFVENRSLH 120

Qy 121 PQPKSHGSESDYIVLPNIIILVGGSIILMESKPVSLKLMNTLALVTMGORAFMNRVTGSEIL 180
Db 121 PQPKSHGSESDYIVLPNIIILVGGSIILMESKPVSLKLMNTLALVTMGORAFMNRVTGSEIL 180

Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFSTRHLVDKKNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFSTRHLVDKKNGL 240

Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPEACRSMLKLTYNESRVFEGIPYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPEACRSMLKLTYNESRVFEGIPYR 300

Qy 301 FTAPDTLPANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFTNADPVLSEAVLG 360
Db 301 FTAPDTLPANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFTNADPVLSEAVLG 360

Qy 361 LNPMPKHSFLDHPVTGIPMNCVVKMOLSLYTKSVKGIGOTGKIEBPVVLPLLWFEOG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVVKMOLSLYTKSVKGIGOTGKIEBPVVLPLLWFEOG 420

Qy 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGLGGLLLVPIICQLRSQEKCFLWSSGSKG 480

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Db 421 AMGGKPLSTFTQVLVLPQVLAHYAQVLLGLGGLLLVPIICQLRSQKCFLEWGSCKG 480
QY 481 SODKEAIOAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIOAYSESLSMPAAKGTVLQEA 509
RESULT 5
PCT-US95-07721-8
; Sequence 8, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for
; OTHER INFORMATION: the murine Scavenger Receptor Class BI."
PCT-US95-07721-8
Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 1,7e-284;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGGSSRAKVAALGALGALLFAALGVNMLVPSLIQQOVLKVRIDPSSLSFGWKKEIP 60
Db 1 MGGSSRAKVAALGALGALLFAALGVNMLVPSLIQQOVLKVRIDPSSLSFGWKKEIP 60
QY 61 VPFLSVVFFVFNPNVNLNGQKPVVRERGYPVYVREFRQKVNITFDNDVTSFVENSRLH 120
Db 61 VPFLSVVFFVFNPNVNLNGQKPVVRERGYPVYVREFRQKVNITFDNDVTSFVENSRLH 120
QY 121 FQPKSHGSESDYVLPNVLGGSILMESKPSVSLKMTLALVTMGORAPMNTVGEIL 180
Db 121 FQPKSHGSESDYVLPNVLGGSILMESKPSVSLKMTLALVTMGORAPMNTVGEIL 180
QY 181 WGYDDPFVHFLNTLVPDMLPIKGKGLFVGNMNSGVFTVFTGVQNFRIHLVDKNGL 240
Db 181 WGYDDPFVHFLNTLVPDMLPIKGKGLFVGNMNSGVFTVFTGVQNFRIHLVDKNGL 240
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Db 241 SKIDYWHSEQCNGMINTSGQMWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
QY 301 FTAPDITLFANGSVYPNEGFCPCRESGIQNVSTCRGAPLFLSHPHFYNNADPVLSEAVLG 360
Db 301 FTAPDITLFANGSVYPNEGFCPCRESGIQNVSTCRGAPLFLSHPHFYNNADPVLSEAVLG 360
QY 361 LNPNPKEHSLFLDIHPVTGIPMNCVSKMOLSLYIKSVKGIGQTKIEPVVLPPLLWFEQSG 420
Db 361 LNPNPKEHSLFLDIHPVTGIPMNCVSKMOLSLYIKSVKGIGQTKIEPVVLPPLLWFEQSG 420
QY 421 AMGGKPLSTFTQVLVLPQVLAHYAQVLLGLGGLLLVPIICQLRSQKCFLEWGSCKG 480
Db 421 AMGGKPLSTFTQVLVLPQVLAHYAQVLLGLGGLLLVPIICQLRSQKCFLEWGSCKG 480
QY 481 SODKEAIOAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIOAYSESLSMPAAKGTVLQEA 509
RESULT 6
US-08-559-505-2
; Sequence 2, Application US/08559505
; Patent No. 5925333
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Susan L. Acton, Attilio Rigotti, Helen H.
; APPLICANT: Hobbs and Kathy Landshulz
; TITLE OF INVENTION: METHODS FOR MODULATION OF LIPID UPTAKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,505
; FILING DATE: 29-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464

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; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175,
; OTHER INFORMATION: 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 repre
; OTHER INFORMATION: N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21, 251,
; OTHER INFORMATION: 280, 321, 323, 334, 384 and 470 represent potential disulfide
US-08-559-505-2

Query Match          91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVWILMPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRARWAVAGLVGVLCAVLGVWVILMPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFVWVNPNEVNGKPVWRERGPVYVREPRQKVNITFDNDTVSFVENSRLH 120
Db 61 VPVYLSVYFFVWVNPSEILKEKPVWRERGPVYVREPRHKANITFDNDTVSFVHRSRLH 120
Qy 121 FQPKSHGSESDYILVLPNLIIVLGGSIILMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIILPNILVILGAVNMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKNWGL 240
Db 181 WGYDDPFVFNKYLDPDMPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDNRWGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEPSPSACSMKLTYNESRVFEGIPTYR 300
Db 241 SKVNYHSEQCNMINGTSGQWAPFMTPOSSLFSPSACSMKLTTHDSGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCFCRESGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTA PKTLFANGSVYPPNEGFCFCLESIGIONVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPMPKSHSLDHPVTGIPMNCVSKQLSIYKSVKIGQTKIEPVLPILLWFQSG 420
Db 361 LNPDPREHSLFDHPVTGIPMNCVSKQLSIYKAVKIGQTKIEPVLPILLWFQSG 420
Qy 421 AMGCKPLSTFTQVLMPQVLYAQVLLGLGILLVPIICOLRSQEKCLFWSGSKG 480
Db 421 AMGGEPLNTFTQVLMPQVLYQVYVLLGLGILLVPIYQLRSQEKCLFWSGSKG 480
Qy 481 SODKEATQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEATQAYSESLSMPAAKGTVLQEAKL 509

RESULT 7
US-08-749-907-2
; Sequence 2, Application US/08749907
; Patent No. 5962322
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; OTHER INFORMATION: Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-3
; OTHER INFORMATION: potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; OTHER INFORMATION: 251, 280, 321, 323, 334, 384 and 470 represent potential disul
US-08-749-907-2

Query Match          91.3%; Score 2447; DB 1; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVWILMPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRARWAVAGLVGVLCAVLGVWVILMPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFVWVNPNEVNGKPVWRERGPVYVREPRQKVNITFDNDTVSFVENSRLH 120
Db 61 VPVYLSVYFFVWVNPSEILKEKPVWRERGPVYVREPRHKANITFDNDTVSFVHRSRLH 120
Qy 121 FQPKSHGSESDYILVLPNLIIVLGGSIILMESKPSVLKLMNTLALVTMGORAFMNRVTGEIL 180
Db 121 FQPKSHGSESDYIILPNILVILGAVNMESKAGLKLMTLGLATLQORAFMNRVTGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFRIHLVDKNWGL 240
Db 181 WGYDDPFVFNKYLDPDMPFIKGFGLFVEMNNSDGLFTVFTGVQNFSKIHLVDNRWGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEPSPSACSMKLTYNESRVFEGIPTYR 300
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Qy 61 VPYLSVYFVFNPNVNLGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPYLSVYFVFNPNVNLGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIIVLPNVLGGSILMESKPVSLKAMMTLALVTMGORAFNRTVGBIL 180
Db 121 FQPKSHGSESDYIIVLPNVLGGSILMESKPVSLKAMMTLALVTMGORAFNRTVGBIL 180
Qy 181 WGYDDPFVHFNLTYPDLPIKGFGLFVGNMNSGVFTVFTGVQNFSRHLVDKNGNL 240
Db 181 WGYDDPFVHFNLTYPDLPIKGFGLFVGNMNSGVFTVFTGVQNFSRHLVDKNGNL 240
Qy 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 421 AMGKPLSTFTQVLVMPQVLYHAYVLLGLGILLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMGKPLSTFTQVLVMPQVLYHAYVLLGLGILLVPIICQLRSQKCFLFWGSKKG 480
Qy 481 SODKEAIOAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIOAYSESLSMPAAKGTVLQEAKL 509

RESULT 10

US-09-032-894-4
; Sequence 4, Application US/09032894
; Patent No. 6130041

; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human

US-09-032-894-4

Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVMIWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRARWALGALGALLFAALGVVMIWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPYLSVYFVFNPNVNLGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPYLSVYFVFNPNVNLGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIIVLPNVLGGSILMESKPVSLKAMMTLALVTMGORAFNRTVGBIL 180
Db 121 FQPKSHGSESDYIIVLPNVLGGSILMESKPVSLKAMMTLALVTMGORAFNRTVGBIL 180
Qy 181 WGYDDPFVHFNLTYPDLPIKGFGLFVGNMNSGVFTVFTGVQNFSRHLVDKNGNL 240
Db 181 WGYDDPFVHFNLTYPDLPIKGFGLFVGNMNSGVFTVFTGVQNFSRHLVDKNGNL 240
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Db 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300

Qy 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDKHSLFLDIHPVTGIPMNCVSKVQLSIYIKAVKGIGQTKIEBPVVLPLWFQSG 420
Db 361 LNPDKHSLFLDIHPVTGIPMNCVSKVQLSIYIKAVKGIGQTKIEBPVVLPLWFQSG 420
Qy 421 AMGKPLSTFTQVLVMPQVLYHAYVLLGLGILLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMGKPLSTFTQVLVMPQVLYHAYVLLGLGILLVPIICQLRSQKCFLFWGSKKG 480
Qy 481 SODKEAIOAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIOAYSESLSMPAAKGTVLQEAKL 509

RESULT 11

US-09-031-626-4
; Sequence 4, Application US/09031626
; Patent No. 6228581

; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human

US-09-031-626-4

Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRARWALGALGALLFAALGVVMIWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRARWALGALGALLFAALGVVMIWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPYLSVYFVFNPNVNLGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPYLSVYFVFNPNVNLGOKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIIVLPNVLGGSILMESKPVSLKAMMTLALVTMGORAFNRTVGBIL 180
Db 121 FQPKSHGSESDYIIVLPNVLGGSILMESKPVSLKAMMTLALVTMGORAFNRTVGBIL 180
Qy 181 WGYDDPFVHFNLTYPDLPIKGFGLFVGNMNSGVFTVFTGVQNFSRHLVDKNGNL 240
Db 181 WGYDDPFVHFNLTYPDLPIKGFGLFVGNMNSGVFTVFTGVQNFSRHLVDKNGNL 240
Qy 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMNGTSGOWWAPFMTPESSLEFPSPACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPDKHSLFLDIHPVTGIPMNCVSKVQLSIYIKAVKGIGQTKIEBPVVLPLWFQSG 420
Db 361 LNPDKHSLFLDIHPVTGIPMNCVSKVQLSIYIKAVKGIGQTKIEBPVVLPLWFQSG 420

Db 361 LNPPREHSLFLDHPVTGIPMNCVKLIQISLYIKAVKIGIGQTGKIBPVVLPVLLWFFQSG 420
Qy 421 AMGKPLSTFTYQLVLPMPVLYHYAQVYLLGGLLLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMGGEPLNTFTYQLVLPMPVLYHYAQVYLLGGLLLVPIICQLRSQKCFLFWGSKKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 12
US-09-241-581B-4
; Sequence 4, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-1."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane
; domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane
; domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257,
; 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."

; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions
; 21, 251, 280, 321, 323, 334, 384 and
; 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-241-581B-4
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGGSSRARWALGIGLGLLFAALGVVMILMPSLTKQVLKNVRIDPSSLSFCMWKEIP 60
Db 1 MGGSSRARWAVAGLVGVVGLLCAVLGVVMILMPSLTKQVLKNVRIDPSSLSFCMWKEIP 60
Qy 61 VPFLSVYFPEVVPNEVLNGKQPVVRERGPYVYRFRQKVNITFNDNDTVSFVNEHSLH 120
Db 61 VPFLSVYFPEVVPNEVLNGKQPVVRERGPYVYRFRQKVNITFNDNDTVSFVNEHSLH 120
Qy 121 FQPKSHGSESDYIVLPNLIIVLGGSLIMESKPVSLKLMMTLALVTMGQRAFMRNRTVGEIL 180
Db 121 FQPKSHGSESDYIILPNLIIVLGGAVNMESKAGLKLMMTLGLATLQRAFMNRTVGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGCVFTFTGVQNFSLHLVDKWNGL 240
Db 181 WGYDDPFVFNKYLPMFPFKGFLFVEMNNSDGLFTVFTGVQNFSLHLVDKWNGL 240
Qy 241 SKIDYHSEQCNNINGTSGOMWAPFMTPESSLSFFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKYNYHSEQCNNINGTSGOMWAPFMTPESSLSFFSPACRSMKLTVDHSGVFGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESIGNVSTCRFGAPLFLSHPHYPNADPVLSEAVLG 360
Db 301 FTAPKTLTFANGSVYPPNEGFCPCRESIGNVSTCRFGAPLFLSHPHYPNADPVLSEAVLG 360
Qy 361 LNPNKHEHSLFLDIHPVTGIPMNCVKMQLSLYIKSVKGIGQTKIEPVVLPVLLWFFQSG 420
Db 361 LNPPREHSLFLDIHPVTGIPMNCVKLIQISLYIKAVKIGIGQTKIEPVVLPVLLWFFQSG 420
Qy 421 AMGKPLSTFTYQLVLPMPVLYHYAQVYLLGGLLLVPIICQLRSQKCFLFWGSKKG 480
Db 421 AMGGEPLNTFTYQLVLPMPVLYHYAQVYLLGGLLLVPIICQLRSQKCFLFWGSKKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEAKL 509

RESULT 13
US-08-265-428-4
; Sequence 4, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428

;; FILING DATE: 530
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: MIT6620
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 815-6508
;; TELEFAX: (404) 815-6555
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 509 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..509
;; OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger
;; FEATURE:
;; NAME/KEY: Domain
;; LOCATION: 9..32
;; OTHER INFORMATION: /note= "Putative transmembrane
;; OTHER INFORMATION: domain."
;; FEATURE:
;; NAME/KEY: Domain
;; LOCATION: 440..464
;; OTHER INFORMATION: /note= "Putative transmembrane
;; OTHER INFORMATION: domain."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1..385
;; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
;; OTHER INFORMATION: 173-175, 212-214, 227-229, 255-257, 310-312,
;; OTHER INFORMATION: 330-332 and 383-385 represent potential N-linked glycosylation
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 21..470
;; OTHER INFORMATION: /note= "The cysteines at positions
;; OTHER INFORMATION: 21, 251, 280, 321, 323, 334, 384 and 470 represent
;; OTHER INFORMATION: potential disulfide linkages."
US-08-265-428-4
Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
Qy 1 MGSRRARWALGALGALLPAALGVVNMILWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWAVAGLVGVGELLCAVLGVVILWPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPFLSVYFFVNVNPNVNLQKPVVRERGYPVTRFRQKVNITFNNDTVSFVENSLH 120
Db 61 VPFLSVYFFVNVNPNVNLQKPVVRERGYPVTRFRQKVNITFNNDTVSFVENSLH 120
Qy 121 FQPKSHGSDYIVLPNVLGSGILMESVPVSLKMTLALVTMGORAFMNTVGEIL 180
Db 121 FQPKSHGSDYIILPNVLGSAVMESKAGLKLMTLGLTGLORAFMNTVGEIL 180
Qy 181 WGYDDPPFVHLYLTPDMLPIKGFGLFVGNMNSGVFTVFTGVQNFPSRIHLVDKNGL 240
Db 181 WGYDDPPFVNFINKYLPDMFPIKGFGLFVENNSDGLFTVFTGVQNFPSRIHLVDKNGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPWPTPESSILEFFSPACRSMKLTYNESRVFGIPTYR 300
Db 241 SKVNYHSEQCNMINGTSGQWAPWPTPESSILEFFSPACRSMKLTVDSDGVFGIPTYR 300
Qy 301 FTAPDTLPANGSVVPPNEGFCFCEGSIONYVTCFGLPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVVPPNEGFCFCEGSIONYVTCFGLPFLSHPHFYNADPVLSEAVLG 360

Qy 361 LNPMPKHSFLDHPVTVGTPMNCVVMQSLYIKSVKGIGQTKIBPVVPLPLWFQSG 420
Db 361 LNPDPREHSFLDHPVTVGTPMNCVVKLQISLYIKAVKIGIGQTKIBPVVPLPLWFQSG 420
Qy 421 AMGKPLSTFTVLVMPQVLYHAQYVLLGLGGLLAVPIICQLRSQEKCFLWSSGSKKG 480
Db 421 AMGGEPLNTFTQLVMPQVLYVQYVLLGLGGLLAVPIVYQURSQEKCFLWSSGSKKG 480
Qy 481 SQDKEALQAYSESLSMSPAAGTGVLEAKL 509
Db 481 SQDKEALQAYSESLSMSPAAGTGVLEAKL 509
RESULT 14
US-09-385-799-2
; Sequence 2, Application US/09385799
; Patent No. 6962688
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385,799
; FILING DATE: 30-Aug-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,

173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
potential N-linked glycosylation sites."

FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..470
OTHER INFORMATION: /note= "The cysteines at positions 21,
251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
linkages."

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-385-799-2

Query Match 91.3%; Score 2447; DB 2; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIILVPSLIKQVLRIDPSSLSFGMWKEIP 60
Db 1 MGSSARARWAVAGLVGVVLLCAVLGVVMIILVPSLIKQVLRIDPSSLSFGMWKEIP 60

Qy 61 VPFLSVYFFVVPNEVLGQKPVRRGPGVYVRRGQKVNITFNDNDTVSFVNRSLH 120
Db 61 VPFLSVYFFVVPNEVLGQKPVRRGPGVYVRRGQKVNITFNDNDTVSFVNRSLH 120

Qy 121 FQPKSHGSESDYILPNILVGLGSIILMESKPVSLKMTLALVTMGQAFPMNRTVGEIL 180
Db 121 FQPKSHGSESDYILPNILVGLGSIILMESKPVSLKMTLALVTMGQAFPMNRTVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKNGL 240

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKNGL 240

Qy 241 SKIDYWHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACSMKLTYNESRVFEGITPYR 300
Db 241 SKIDYWHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACSMKLTYNESRVFEGITPYR 300

Qy 301 FTAPDTLFPANGSVYPPNPGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPDTLFPANGSVYPPNPGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360

Qy 361 LNPDPKSHSLFDHPVTGIPMNCVSMOLSLYKSVKIGQOTGKIIEPVVPLLWFQSG 420
Db 361 LNPDPKSHSLFDHPVTGIPMNCVSMOLSLYKSVKIGQOTGKIIEPVVPLLWFQSG 420

Qy 421 AMGKPLSTFTQVLMPQVLYAQVLLGLGILLVPIICQLRSQEKCFLWSGSKG 480
Db 421 AMGKPLSTFTQVLMPQVLYAQVLLGLGILLVPIICQLRSQEKCFLWSGSKG 480

Qy 481 SODKEAIOAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIOAYSESLSMPAAKGTVLQEA 509

RESULT 15
PCT-US95-07721-4
; Sequence 4, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07721
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..509
OTHER INFORMATION: /function= "Amino acid sequence for the
Hamster Scavenger Receptor Class B-I."
FEATURE:
NAME/KEY: Domain
LOCATION: 9..32
OTHER INFORMATION: /note= "Putative transmembrane
domain."
FEATURE:
NAME/KEY: Domain
LOCATION: 440..464
OTHER INFORMATION: /note= "Putative transmembrane
domain."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..385
OTHER INFORMATION: /note= "Positions 102-104, 108-110,
173-175, 212-214, 227-229, 255-257,
310-312, 330-332 and 383-385 represent
potential N-linked glycosylation sites."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21..470
OTHER INFORMATION: /note= "The cysteines at positions
21, 251, 280, 321, 323, 334, 384 and
470 represent potential disulfide
linkages."
PCT-US95-07721-4

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 7.4e-259;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSSRRARWALGALGALLFAALGVVMIILVPSLIKQVLRIDPSSLSFGMWKEIP 60
Db 1 MGSSARARWAVAGLVGVVLLCAVLGVVMIILVPSLIKQVLRIDPSSLSFGMWKEIP 60

Qy 61 VPFLSVYFFVVPNEVLGQKPVRRGPGVYVRRGQKVNITFNDNDTVSFVNRSLH 120
Db 61 VPFLSVYFFVVPNEVLGQKPVRRGPGVYVRRGQKVNITFNDNDTVSFVNRSLH 120

Qy 121 FQPKSHGSESDYILPNILVGLGSIILMESKPVSLKMTLALVTMGQAFPMNRTVGEIL 180
Db 121 FQPKSHGSESDYILPNILVGLGSIILMESKPVSLKMTLALVTMGQAFPMNRTVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGWNNNSGVFTVFTGVQNFRIHLVDKNGL 240

Qy 241 SKIDYWHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACSMKLTYNESRVFEGITPYR 300
Db 241 SKIDYWHSEQCNMNGTSGQWAPFMTPESSLEFSPSEACSMKLTYNESRVFEGITPYR 300

Search completed: February 23, 2006, 12:47:16
Job time : 35 secs

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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:46:19 ; Search time 121 Seconds
(without alignments)
1757.646 Million cell updates/sec

Title: US-08-765-108-8

Perfect score: 2881

Sequence: 1 MGSRRARWALGALGALL.....YSELSMPAAKGTVLQBAKL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2681	100.0	509	3	US-09-148-012-4
2	2681	100.0	509	4	US-10-178-611-4
3	2681	100.0	509	4	US-10-164-863-4
4	2681	100.0	509	4	US-10-706-073-4
5	2681	100.0	509	5	US-10-933-037-4
6	2605	97.2	513	4	US-10-322-281-565
7	2447	91.3	509	3	US-09-148-012-2
8	2447	91.3	509	3	US-09-779-152-4
9	2447	91.3	509	4	US-10-023-610-4
10	2447	91.3	509	4	US-10-178-611-2
11	2447	91.3	509	4	US-10-164-863-2
12	2447	91.3	509	4	US-10-212-848-4
13	2447	91.3	509	4	US-10-706-073-2
14	2447	91.3	509	5	US-10-933-037-2
15	2200	82.1	509	3	US-09-779-152-2
16	2200	82.1	509	4	US-10-023-610-2
17	2200	82.1	509	4	US-10-212-848-2
18	2200	82.1	509	5	US-10-494-555-1
19	2193	81.8	532	4	US-10-276-774-2382
20	2192	81.8	509	4	US-10-648-593-219
21	2192	81.8	509	5	US-10-794-198A-12
22	2160	80.6	509	4	US-10-210-172-116
23	2068.5	77.2	537	5	US-10-450-763-52676
24	2022.5	75.4	552	4	US-10-313-641-12
25	2022.5	75.4	552	4	US-10-428-551-12
26	1976	73.7	458	4	US-10-322-281-568
27	1844	68.8	416	4	US-10-210-172-118

28 741.5 27.7 478 4 US-10-408-765A-657 Sequence 657, Appl
29 741.5 27.7 478 4 US-10-794-899-90 Sequence 90, Appl
30 727.5 27.1 531 4 US-10-403-571-158 Sequence 158, Appl
31 682.5 25.5 520 6 US-11-097-143-4890 Sequence 4890, Appl
32 677 25.3 471 4 US-10-048-917-1 Sequence 1, Appl
33 677 25.3 472 3 US-09-836-544-21 Sequence 21, Appl
34 677 25.3 472 4 US-10-372-683-45 Sequence 45, Appl
35 677 25.3 472 4 US-10-398-593-2 Sequence 2, Appl
36 645 24.1 472 4 US-10-196-703-44 Sequence 44, Appl
37 642.5 24.0 471 4 US-10-408-765A-3022 Sequence 3022, Appl
38 585 21.8 491 6 US-11-097-143-8385 Sequence 8385, Appl
39 572 21.3 534 6 US-11-097-143-24735 Sequence 24735, A
40 537 20.0 861 6 US-11-097-143-12084 Sequence 12084, A
41 530.5 19.8 513 6 US-11-097-143-2697 Sequence 2697, Appl
42 518.5 19.3 553 6 US-11-097-143-16122 Sequence 16122, A
43 518.5 19.3 589 4 US-10-108-605-355 Sequence 355, Appl
44 518.5 19.3 589 6 US-11-013-314-6 Sequence 6, Appl
45 510 19.0 589 6 US-11-097-143-7293 Sequence 7293, Appl

ALIGNMENTS

RESULT 1

US-09-148-012-4
; Sequence 4, Application US/09148012
; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: In The Treatment Of Steroidal Overproduction
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: 60/057,943
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-09-148-012-4

Query Match 100.0%; Score 2681; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.1e-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWALGALGALLFAALGVVMIILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60

Qy 61 VPFYLSVYFVFNPNVNGQKQVVRGYPVYVREFRQKVNITFNDNDTYSFVENRSLH 120
Db 61 VPFYLSVYFVFNPNVNGQKQVVRGYPVYVREFRQKVNITFNDNDTYSFVENRSLH 120

Qy 121 FQPKSHGSSDYLVLPNLIIVLGGSIILMESKPSVLKLMMTLALVTMGORAPMNTVGBIL 180
Db 121 FQPKSHGSSDYLVLPNLIIVLGGSIILMESKPSVLKLMMTLALVTMGORAPMNTVGBIL 180

Qy 181 WGYDDPFPVHFLNTYLPDKLPKKGFLGVGNMNSNSGVFTVFTGVQNFPSRIHLVDKWNGL 240
Db 181 WGYDDPFPVHFLNTYLPDKLPKKGFLGVGNMNSNSGVFTVFTGVQNFPSRIHLVDKWNGL 240

Qy 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFSPSEACRSMKLTYNESRVFEGIPYR 300
Db 241 SKIDYWHSEQCNMINGTSGQWAPFMTPESSLEFSPSEACRSMKLTYNESRVFEGIPYR 300

Qy 301 FTAPDTTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTAPDTTLFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360

Qy 361 LNPMPKSHSLFLDTHPVGTGIPMNCVSRMQLSLYIKSVKIGTGTGKIEPVLPLLWFQSG 420

Db 361 LNPKEHSLFDLHPVTGIPMNCVKMQLSLYKSVKIGQTKIEPVLPLLMFQSG 420
Qy 421 AMGKPLSTFTQVLMPQVHLHYAQVLLGLGGLLLVPIICQURSQEKCFLFWGSKKG 480
Db 421 AMGKPLSTFTQVLMPQVHLHYAQVLLGLGGLLLVPIICQURSQEKCFLFWGSKKG 480
Qy 481 SODKEATQAYSESLMSPAAGTGLVQEA 509
Db 481 SODKEATQAYSESLMSPAAGTGLVQEA 509

RESULT 2

US-10-178-611-4
; Sequence 4, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/178.611
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/749,907
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER:

MIT7538

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794

TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 509 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: misc. feature

LOCATION: 1..509

OTHER INFORMATION: /Function = "Amino acid sequence for the

marine Scavenger Receptor Class B1."

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-178-611-4

Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.1e-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSSRRARWALGALGLLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFGMWKEIP 60
Db 1 MGGSSRRARWALGALGLLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFGMWKEIP 60

Qy 61 VPVLSVYFFVVPVNPNEVLNGQKPVVRERGPVYVREPROKVNITFNDNDTVSFVENSRLH 120
Db 61 VPVLSVYFFVVPVNPNEVLNGQKPVVRERGPVYVREPROKVNITFNDNDTVSFVENSRLH 120

Qy 121 FQPKDGHGSSDYIVLPNIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Db 121 FQPKDGHGSSDYIVLPNIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFSSIHILVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFSSIHILVDKWNGL 240
Qy 241 SKIDYWHSEQCNNINGTSGQMWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKIDYWHSEQCNNINGTSGQMWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLIFANGSVYPPNEGFCPCREGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLIFANGSVYPPNEGFCPCREGIQNVSTCRFGAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPKEHSLFDLHPVTGIPMNCVKMQLSLYKSVKIGQTKIEPVLPLLMFQSG 420
Db 361 LNPKEHSLFDLHPVTGIPMNCVKMQLSLYKSVKIGQTKIEPVLPLLMFQSG 420
Qy 421 AMGKPLSTFTQVLMPQVHLHYAQVLLGLGGLLLVPIICQURSQEKCFLFWGSKKG 480
Db 421 AMGKPLSTFTQVLMPQVHLHYAQVLLGLGGLLLVPIICQURSQEKCFLFWGSKKG 480
Qy 481 SODKEATQAYSESLMSPAAGTGLVQEA 509
Db 481 SODKEATQAYSESLMSPAAGTGLVQEA 509

RESULT 3

US-10-164-863-4

; Sequence 4, Application US/10164863

; Publication No. US20030232879A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Monty

; APPLICANT: Miettinen, Helena

; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY

; FILE REFERENCE: MIT 9094

; CURRENT APPLICATION NUMBER: US/10/164,863

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: US 09/148,012

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 60/057,943

; PRIOR FILING DATE: 1997-09-05

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 509

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-164-863-4

Query Match 100.0%; Score 2681; DB 4; Length 509;

Best Local Similarity 100.0%; Pred. No. 7.1e-255;

Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGGSSRRARWALGALGLLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFGMWKEIP 60
Db 1 MGGSSRRARWALGALGLLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFGMWKEIP 60

Qy 61 VPVLSVYFFVVPVNPNEVLNGQKPVVRERGPVYVREPROKVNITFNDNDTVSFVENSRLH 120
Db 61 VPVLSVYFFVVPVNPNEVLNGQKPVVRERGPVYVREPROKVNITFNDNDTVSFVENSRLH 120

Qy 121 FQPKDGHGSSDYIVLPNIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180
Db 121 FQPKDGHGSSDYIVLPNIIVLGSSILMESKPVSLKLMMTLALVTMGQRAFMRNTVGEIL 180

Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFSSIHILVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSNGVFTVFTGVQNFSSIHILVDKWNGL 240

Qy 241 SKIDYWHSEQCNNINGTSGQMWAPFMTPESSLEFFSPACRSMKLTYNESRVFEGIPTYR 300

Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420
Qy 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLWSSGSKG 480
Db 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLWSSGSKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
RESULT 4
US-10-706-073-4
; Sequence 4, Application US/10706073
; Publication No. US20040077526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: In The Treatment Of Steroidal Overproduction
; FILE REFERENCE: M178299
; CURRENT APPLICATION NUMBER: US/10706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mouse
US-10-706-073-4
Query Match 100.0%; Score 2681; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.le-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFEVVNPNEVLNGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENRSLH 120
Db 61 VPVYLSVYFFEVVNPNEVLNGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKKGFLFVGWNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKKGFLFVGWNNNSGVFTVFTGVQNFRIHLVDKWNGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420

Db 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQTKIEBPVVLPLLWFQSG 420
Qy 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLWSSGSKG 480
Db 421 AMGCKPLSTFTQVLMPQVLAHYVLLGLGGLLLVPIICOLRSQEKCFLWSSGSKG 480
Qy 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
Db 481 SODKEAIQAYSESLSMPAAKGTVLQEA 509
RESULT 5
US-10-933-037-4
; Sequence 4, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10933,037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..509
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; murine Scavenger Receptor Class B1."
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-933-037-4
Query Match 100.0%; Score 2681; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 7.le-255;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSSRRARWALGALGALLPAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFEVVNPNEVLNGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENRSLH 120
Db 61 VPVYLSVYFFEVVNPNEVLNGQKPVVRERGPVYVREFRQKNITFNNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNVLGGSILMESKPVSLKLMMTLALVTMQRAPMNTVGEIL 180


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Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLLWFEQSG 420
Db 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLLWFEQSG 420
Qy 421 AMGGKPLSTFTYQVLMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
Db 421 AMGGKPLSTFTYQVLMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
Qy 481 SODKEAIQAYSESLSMSPAAGTGLVQEA 509
Db 481 SODKEAIQAYSESLSMSPAAGTGLVQEA 509

RESULT 6
US-10-322-281-565
; Sequence 565, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-565

Query Match 97.2%; Score 2605; DB 4; Length 513;
Best Local Similarity 98.4%; Pred. No. 2.2e-247;
Matches 501; Conservative 0; Mismatches 2; Indels 6; Gaps 3;

Qy 1 MGSSRRARWV--GLGALGLLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFGMWKEIP 60
Db 11 MGSSRRARWV--GLGALGLLFAALGVVMIWVPSLIKQVVKVRIIDPSSLSFGMWKEIP 68
Qy 61 VPFYLSVYFVFNPNNEVLNQKPVVRERGPVYVREPRQKNITFDNDNTVSFVENRSLH 120
Db 69 VPFYLSVYFVFNPNNEVLNQKPVVRERGPVYVREPRQKNITFDNDNTVSFVENRSLH 128
Qy 121 FQPKSHGSSDYLVLPNVLGSLIMESKPSLKMMTLALVTMGQAFMRTVGEIL 180
Db 129 FQPKSHGSSDYLVLPNVLGSLIMESKPSLKMMTLALVTMGQAFMRTVGEIL 188
Qy 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 240
Db 189 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFSLHLVDKWNGL 248
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIPTYR 300
Db 249 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFPSPACRSMKLTYNESRVFEGIP--Y 306
Qy 301 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFYNADPVLSEAVLG 360
Db 307 FTAPDTLFANGSVYPNNEGFCPCRESGIONVSTCRFCGAPLFLSHPHFYNADPVLSEAV-- 364
Qy 361 LNPMPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLLWFEQSG 420
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Db 365 LQPNPKHSFLDHPVTGIPMNCVSKMQLSLYIKSVKIGQGTGKIEPVVPLLWFEQSG 424
Qy 421 AMGGKPLSTFTYQVLMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 480
Db 425 AMGGKPLSTFTYQVLMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQEKCFLFWSGSKG 484
Qy 481 SODKEAIQAYSESLSMSPAAGTGLVQEA 509
Db 485 SODKEAIQAYSESLSMSPAAGTGLVQEA 513

RESULT 7
US-09-148-012-2
; Sequence 2, Application US/09148012
; Patent No. US20020099040A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-B1 Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MTT7150CIP2
; CURRENT APPLICATION NUMBER: US/09/148,012
; CURRENT FILING DATE: 1998-09-04
; EARLIER FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (310)..(312)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
; LOCATION: (330)..(332)
; OTHER INFORMATION: Potential
; NAME/KEY: CARBOHYD
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LOCATION: (383)..(385)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (21)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (251)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (280)
OTHER INFORMATION: Potential
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NAME/KEY: DISULFID
LOCATION: (321)
OTHER INFORMATION: Potential
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NAME/KEY: DISULFID
LOCATION: (323)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (334)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (384)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (470)
OTHER INFORMATION: Potential
US-09-148-012-2

Query Match 91.3%; Score 2447; DB 3; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGGSSRARWALGALGLLFAALGVVMIWVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
DB 1 MGGSSRARWAVAGLVGVGLLCAVLGVVMIWVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFEVVNPNEVLNGQKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
DB 61 VPFLSYVFFEVVNPNEVLNGQKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
QY 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPVSLKMMTTLALVTMGQRAFMRNTVGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPVSLKMMTTLALVTMGQRAFMRNTVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTVGVQNFSLHLDVKNGL 240
DB 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTVGVQNFSLHLDVKNGL 240
QY 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVPFGIPTYR 300
DB 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVPFGIPTYR 300
QY 301 FTAPDTLFGANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPDTLFGANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPDKHSLFLDIHPVTGIPMNCVVKQISLYIKSVKIGIQTKIPVVLPLWPFQSG 420
DB 361 LNPDKHSLFLDIHPVTGIPMNCVVKQISLYIKSVKIGIQTKIPVVLPLWPFQSG 420
QY 421 AMGKPLSTFTQVLVMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
DB 421 AMGKPLSTFTQVLVMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
QY 481 SQDKEAIQAYSESIMSPAAGTGLQEA 509
DB 481 SQDKEAIQAYSESIMSPAAGTGLQEA 509

RESULT 9
US-10-023-610-4
Sequence 4, Application US/10023610
Publication No. US20030023059A1
GENERAL INFORMATION:

Db 481 SQDKEAIQAYSESIMSPAAGTGLQEA 509
RESULT 8
US-09-779-152-4
Sequence 4, Application US/09779152
Publication No. US20030044782A1
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Ordovas, Jose M.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
FILE REFERENCE: WNI-172CP2
CURRENT APPLICATION NUMBER: US/09/779,152
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 08/890,979
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 509
TYPE: PRI
ORGANISM: Human
US-09-779-152-4

Query Match 91.3%; Score 2447; DB 3; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGGSSRARWALGALGLLFAALGVVMIWVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
DB 1 MGGSSRARWAVAGLVGVGLLCAVLGVVMIWVPSLIIKQVVKVNRIDPSSLSFGMWKEIP 60
QY 61 VPFLSYVFFEVVNPNEVLNGQKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
DB 61 VPFLSYVFFEVVNPNEVLNGQKPVVRERGYPVYVREFRQKVNITFNDNDTVSFVENSRLH 120
QY 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPVSLKMMTTLALVTMGQRAFMRNTVGEIL 180
DB 121 FQPKSHGSESDYIVLPNIIIVLGSILMESKPVSLKMMTTLALVTMGQRAFMRNTVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTVGVQNFSLHLDVKNGL 240
DB 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVTFTVGVQNFSLHLDVKNGL 240
QY 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVPFGIPTYR 300
DB 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPACRSMKLTYNESRVPFGIPTYR 300
QY 301 FTAPDTLFGANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
DB 301 FTAPDTLFGANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPDKHSLFLDIHPVTGIPMNCVVKQISLYIKSVKIGIQTKIPVVLPLWPFQSG 420
DB 361 LNPDKHSLFLDIHPVTGIPMNCVVKQISLYIKSVKIGIQTKIPVVLPLWPFQSG 420
QY 421 AMGKPLSTFTQVLVMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
DB 421 AMGKPLSTFTQVLVMPQVLYHYAQVYLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
QY 481 SQDKEAIQAYSESIMSPAAGTGLQEA 509
DB 481 SQDKEAIQAYSESIMSPAAGTGLQEA 509

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; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/10/023.610
; CURRENT FILING DATE: 2001-12-17
; EARLIER APPLICATION NUMBER: 09/686,106
; EARLIER FILING DATE: 2000-10-10
; EARLIER APPLICATION NUMBER: 09/032,894
; EARLIER FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
; US-10-023-610-4

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWAVAGLVGVGLLCAVLGVVMIILVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFEVVNPNEVLNGKQPVVRERGYPVYRFRQKVNITFDNDTVSFVENRSLH 120
Db 61 VPVYLSVYFFEVVNPSEILKGEKPVVRERGYPVYRFRHKANITFDNDTVSFVEHRSLSH 120
Qy 121 FQDPKSHGSESDYIILPNILVLGSIILMESKPVSLKLMMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGSAVMESKAGLKLMTLGLATLQRAFMRNRTVGEIL 180
Qy 181 WGYDDPFVHFNLTLPDMLPIKKGFLFVGMNNSGVTFTVTCVQNPFSRIHLVDKNGSL 240
Db 181 WGYDDPFVFNKYLDPDMPFIKKGFLFVEMNNSDSGLFTVTCVQNFSKIHLVDNRNGL 240
Qy 241 SKIDYHSEQCNMINTSGQWAPFMTPESSLEFSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKVNYHSEQCNMINTSGQWAPFMTPESSLEFSPACRSKMLTYHDSGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVYPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFANGSVYPPNEGFCPCLESIGNVSTCRFGAPFLSHPHFYNADPVLSEAVLG 360
Qy 361 LNPMPKHSFLDTHPVGTGIPMNCVVMQSLYIKSVKGIGQGTGKIIPPVVLPLLWPFQSG 420
Db 361 LNPDPREHSLFLDTHPVGTGIPMNCVVKLQISLYIKAVKGIGQGTGKIIPPVVLPLLWPFQSG 420
Qy 421 AMGSKPLSTFTQVLVMPQVLYHAYQVLLGLGGLLLVPIICQSRQEKCFLFWGSGKKG 480
Db 421 AMGGEPLNTFTQVLVMPQVLYHAYQVLLGLGGLLLVPIIYQSRQEKCFLFWGSGKKG 480
Qy 481 SODKEATQAVSESLMSPAKGTVLQEAKL 509
Db 481 SODKEATQAVSESLMSPAKGTVLQEAKL 509

RESULT 10
US-10-178-611-2
; Sequence 2, Application US/10178611
; Publication No. US20030167475A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
```

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; STATE: Georgia.
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/178,611
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-178-611-2

Query Match          91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMIILVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGSRRARWAVAGLVGVGLLCAVLGVVMIILVPSLIKQVLLKNVRIDPSSLSFGMWKEIP 60
Qy 61 VPVYLSVYFFEVVNPNEVLNGKQPVVRERGYPVYRFRQKVNITFDNDTVSFVENRSLH 120
Db 61 VPVYLSVYFFEVVNPSEILKGEKPVVRERGYPVYRFRHKANITFDNDTVSFVEHRSLSH 120
Qy 121 FQDPKSHGSESDYIILPNILVLGSIILMESKPVSLKLMMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQDRSHGSESDYIILPNILVLGSAVMESKAGLKLMTLGLATLQRAFMRNRTVGEIL 180
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QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
QY 241 SKIDYHSEOCNMGNTSGQWAPMTPESSLEPSPACRSMKLTYNESRVFEGIPYR 300
Db 241 SKIDYHSEOCNMGNTSGQWAPMTPESSLEPSPACRSMKLTYNESRVFEGIPYR 300
QY 301 FTAPDTLFGANGSVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLFGANGSVPPNEGFCPCRESGIONVSTCRFGAPFLSHPHFYFNADPVLSEAVLG 360
QY 361 LNPMPKHSFLDHPVTGTPMNCVSMQSLYIKSVKGIQGTGKIEPVVPLPLWFEGSG 420
Db 361 LNPMPKHSFLDHPVTGTPMNCVSMQSLYIKSVKGIQGTGKIEPVVPLPLWFEGSG 420
QY 421 AMGGKPLSTFTVTLVMPQVLYHAYQVLLGLGGLLLVPIICOLRSQKCPFWGSKKG 480
Db 421 AMGGKPLSTFTVTLVMPQVLYHAYQVLLGLGGLLLVPIICOLRSQKCPFWGSKKG 480
QY 481 SODKEAIQAYSESLMSPAAGTIVLOEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLOEAKL 509

RESULT 11
US-10-164-863-2
; Sequence 2, Application US/10164863
; Publication No. US20030232879A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: LIPID-ALTERING COMPOSITIONS FOR THE TREATMENT OF INFERTILITY
; FILE REFERENCE: MIT 9094
; CURRENT APPLICATION NUMBER: US/10/164,863
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/148,012
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD

; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
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; NAME/KEY: CARBOHYD
; LOCATION: (330)..(332)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (383)..(385)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (21)..(21)
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; FEATURE:
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; LOCATION: (251)..(251)
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; NAME/KEY: DISULFID
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; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (321)..(321)
; OTHER INFORMATION: Potential
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; LOCATION: (323)..(323)
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; NAME/KEY: DISULFID
; LOCATION: (334)..(334)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (384)..(384)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (470)..(470)
; OTHER INFORMATION: Potential
US-10-164-863-2

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;
QY 1 MGSSRRARWVALGALGALLFAALGVVMIILVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
Db 1 MGSSRRARWVALGALGALLFAALGVVMIILVPSLIKQOVLKNVRIDPSSLSFGWKKEIP 60
QY 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYVREFRQKVNITFDNDTYSFVENRSLH 120
Db 61 VPFYLSVYFFEVVNPNEVLNGQKPVVRERGYPVYVREFRQKVNITFDNDTYSFVENRSLH 120
QY 121 FQPKSHGSESDYIILNVLVGLGSIILMESKPVSLKLMNTLALVTMGORAPMNTVGEIL 180
Db 121 FQPKSHGSESDYIILNVLVGLGSIILMESKPVSLKLMNTLALVTMGORAPMNTVGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
Db 181 WGYDDPFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSRHLVDKWNGL 240
QY 241 SKIDYHSEOCNMGNTSGQWAPMTPESSLEPSPACRSMKLTYNESRVFEGIPYR 300

Db 241 SKNYWHEQCNMNGTSGQWAPFMTPOSSLEFFSPEACRSMKLTVDHSGVFEGIPTYR 300
QY 301 FTAPDTLFPANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFPANGSVYPNNEGFCPCLESIGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPDPKHSFLDHPVTGIPMNCVKMOLSLYKSVKGIGOTGKIIEPVVLPVLLWPFQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGOTGKIIEPVVLPVLLWPFQSG 420
QY 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGIGGLLLVPIICQLRSQEKCFLEFWSGSKKG 480
Db 421 AMGGELNTFTYQLVLMPOVLHYQYVYVLLGIGGLLLVPIIYQLRSQEKCFLEFWSGSKKG 480
QY 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509

RESULT 12
US-10-212-848-4
; Sequence 4, Application US/10212848
; Publication No. US2004002325A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Jeanette
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RISK FACTORS
; TITLE OF INVENTION: FOR ABNORMAL LIPID LEVELS AND THE DISEASES AND DISORDERS
; TITLE OF INVENTION: ASSOCIATED THEREWITH
; FILE REFERENCE: MMI-012
; CURRENT APPLICATION NUMBER: US/10/212,848
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-848-4

Query Match 91.3%; Score 2447; DB 4; Length 509;
Best Local Similarity 89.0%; Pred. No. 8.3e-232;
Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGGSSRARWALGALGALLFAALGVVMIWVPSLIKQOVLKNYRIDPSSLSFGMWKEIP 60
Db 1 MGGSSARARWAVAGLVGVLLCAVLGVMIWVPSLIKQOVLKNYRIDPSSLSFGMWKEIP 60
QY 61 VPFYLSVYFVFNPNVNEVINGQKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFVFNPNVNEVINGQKPVVRERGYPVYRERQKVNITFNDNDTVSFVENRSLH 120
QY 121 POPKSHGESDYIILPNILVLGGSILMESKVLKMMTLALVTMGORAFMNRVTGEIL 180
Db 121 POPDRSHGESDYIILPNILVLGAVNMESKVLKMMTLGLATLGORAFMNRVTGEIL 180
QY 181 WGYDDPFVHFLNTYLPDMLPIKGEGFLVGVNNSGVTFTVGTQVNSRIHLVDKNGL 240
Db 181 WGYEDPFVFNKLYLPDMFPIKGRFGLFVGVNNSDGLFTFTVGTQVNSFKIHLVDKNGL 240
QY 241 SKIDYWHSEQCNMNGTSGQWAPFMTPESSLEFFSPEACRSMKLTYNESRVFEGIPTYR 300
Db 241 SKNYWHEQCNMNGTSGQWAPFMTPOSSLEFFSPEACRSMKLTVDHSGVFEGIPTYR 300
QY 301 FTAPDTLFPANGSVYPNNEGFCPCRESGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
Db 301 FTAPKTLFPANGSVYPNNEGFCPCLESIGIONVSTCRFGAPLFLSHPHFYNADPVLSEAVLG 360
QY 361 LNPDPKHSFLDHPVTGIPMNCVKMOLSLYKSVKGIGOTGKIIEPVVLPVLLWPFQSG 420
Db 361 LNPDPREHSLFLDHPVTGIPMNCVKLQISLYIKAVKGIGOTGKIIEPVVLPVLLWPFQSG 420
QY 421 AMGGKPLSTFTYQLVLMPOVLHYAQYVLLGIGGLLLVPIIYQLRSQEKCFLEFWSGSKKG 480

Db 421 AMGGELNTFTYQLVLMPOVLHYQYVYVLLGIGGLLLVPIIYQLRSQEKCFLEFWSGSKKG 480
QY 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509
Db 481 SODKEAIQAYSESLMSPAAGTIVLQEAKL 509

RESULT 13
US-10-706-073-2
; Sequence 2, Application US/10706073
; Publication No. US2004007526A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: SR-BI Antagonist And Use Thereof As Contraceptives And
; FILE REFERENCE: MIT8299
; CURRENT APPLICATION NUMBER: US/10/706,073
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/148,012
; PRIOR FILING DATE: 1998-10-04
; PRIOR APPLICATION NUMBER: 60/057,943
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Hamster
; NAME/KEY: TRANSMEM
; LOCATION: (9)..(32)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (440)..(464)
; OTHER INFORMATION: Putative
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (102)..(104)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (108)..(110)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (173)..(175)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (212)..(214)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (227)..(229)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (255)..(257)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (310)..(312)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (330)..(332)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (383)..(385)
; OTHER INFORMATION: Potential

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FEATURE:
NAME/KEY: DISULFID
LOCATION: (21)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (251)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (280)
OTHER INFORMATION: Potential
FEATURE:
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LOCATION: (321)
OTHER INFORMATION: Potential
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LOCATION: (323)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (334)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (384)
OTHER INFORMATION: Potential
FEATURE:
NAME/KEY: DISULFID
LOCATION: (470)
OTHER INFORMATION: Potential
US-10-706-073-2

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Query Match 91.3%; Score 2447; DB 4; Length 509;
 Best Local Similarity 89.0%; Pred. No. 8.3e-232; Indels 0; Gaps 0;
 Matches 453; Conservative 35; Mismatches 21;

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Qy 1 MGSSRAARWALGALGALLFAALGVNMLVPSLIKKOVLKNVRIDPSSLSFGWKEIP 60
Db 1 MGSSRAARWAVGLGVGLCAVLGVNMLVPSLIKKOVLKNVRIDPSSLSFGWKEIP 60
Qy 61 VPFYLSVYFFVFNPNVNGOKPVVRERGPVYRFRKQKVNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFVFNPNVNGOKPVVRERGPVYRFRKQKVNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGESDYVLPNVLGGILMESPVSLKAMTLALVTMGORAFNRTVGEIL 180
Db 121 FQPKSHGESDYVLPNVLGGILMESPVSLKAMTLALVTMGORAFNRTVGEIL 180
Qy 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGMNNSGVFTVTFVQNFSTRHLVDKNGNL 240
Db 181 WGYDDPFVHFLNTYLPDMLPTKGFGLFVGMNNSGVFTVTFVQNFSTRHLVDKNGNL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPWMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEQCNMINGTSGQWAPWMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTADTLFANGSVYPPNPGFCRESGTONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FTADTLFANGSVYPPNPGFCRESGTONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Qy 361 LNPDKHSLFDHPVTGIPMNCVKMOLSIYTKSVKIGQTKIEBPVLPVLLWFQSG 420
Db 361 LNPDKHSLFDHPVTGIPMNCVKMOLSIYTKSVKIGQTKIEBPVLPVLLWFQSG 420
Qy 421 AMGGKPLSTFTYQLVMPQVLYHAQYVLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
Db 421 AMGGKPLSTFTYQLVMPQVLYHAQYVLLGLGGLLLVPIICQLRSQKCFLFWSGSKG 480
Qy 481 SODKEAIOAYSSELSMSPAAGTGVLOEAKL 509
Db 481 SODKEAIOAYSSELSMSPAAGTGVLOEAKL 509

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RESULT 14
US-10-933-037-2
; Sequence 2, Application US/10933037
; Publication No. US20050136005A1
; GENERAL INFORMATION:
; APPLICANT: Monty Krieger, Attilio Rigotti, and Karen Kozarsky
; TITLE OF INVENTION: METHODS FOR MODULATION OF CHOLESTEROL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst, Arnall Golden & Gregory
; STREET: 2800 One Atlantic Center
; 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933.037
; FILING DATE: 02-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT7538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..509
; OTHER INFORMATION: /function= "Amino acid sequence for the
; Hamster Scavenger Receptor Class B-I."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 9..32
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..464
; OTHER INFORMATION: /note= "Putative transmembrane domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..385
; OTHER INFORMATION: /note= "Positions 102-104, 108-110,
; 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent
; potential N-linked glycosylation sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..470
; OTHER INFORMATION: /note= "The cysteines at positions 21,
; 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide
; linkages."
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-933-037-2

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Query Match 91.3%; Score 2447; DB 5; Length 509;
 Best Local Similarity 89.0%; Pred. No. 8.3e-232;
 Matches 453; Conservative 35; Mismatches 21; Indels 0; Gaps 0;

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Qy 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSISFGMWKEIP 60
Db 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSISFGMWKEIP 60
Qy 61 VPFYLSVYFFVFNPNNEVLNGQKVPVRERGYPVYRERFRQKNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFVFNPNNEVLNGQKVPVRERGYPVYRERFRQKNITFNDNDTVSFVENRSLH 120
Qy 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPSVSLKLMMTLALVTMQRAFNMRTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPSVSLKLMMTLALVTMQRAFNMRTVGEIL 180
Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSTRHLVDKWNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSTRHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLPILLWFEQSG 420
Db 361 LNPDPKHSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLPILLWFEQSG 420
Qy 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQKCFLFWSGSKKG 480
Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQKCFLFWSGSKKG 480
Qy 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
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RESULT 15
US-09-779-152-2
; Sequence 2, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779,152
; PRIOR APPLICATION NUMBER: 2001-02-08
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-779-152-2
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Query Match 82.1%; Score 2200; DB 3; Length 509;
Best Local Similarity 79.6%; Pred. No. 1.9e-207;
Matches 405; Conservative 49; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSISFGMWKEIP 60
Db 1 MGSRRARWALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSISFGMWKEIP 60
Qy 61 VPFYLSVYFFVFNPNNEVLNGQKVPVRERGYPVYRERFRQKNITFNDNDTVSFVENRSLH 120
Db 61 VPFYLSVYFFVFNPNNEVLNGQKVPVRERGYPVYRERFRQKNITFNDNDTVSFVENRSLH 120
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Qy 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPSVSLKLMMTLALVTMQRAFNMRTVGEIL 180
Db 121 FQPKSHGSESDYIVLPNIIVLGGSILMESKPSVSLKLMMTLALVTMQRAFNMRTVGEIL 180
Qy 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSTRHLVDKWNGL 240
Db 181 WGYDDPFFVHFLNTYLPDMLPIKGFGLFVGMNNSGVFTVFTGVQNFSTRHLVDKWNGL 240
Qy 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKIDYHSEOCNMINGTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYR 300
Qy 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYFNADPVLSEAVLG 360
Db 301 FTAPDTLFGANGSVYPNNEGFCPCRESGIONVSTCRFCAPLFLSHPHFYFNADPVLSEAVLG 360
Qy 361 LNPDPKHSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLPILLWFEQSG 420
Db 361 LNPDPKHSFLDIHPVTGIPMNCVSKMQLSLYIKSVKGIGQTKIEPVPVLPILLWFEQSG 420
Qy 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQKCFLFWSGSKKG 480
Db 421 AMGGKPLSTFTYTLVLMPOVLHYAQVYLLGLGILLVPIICQLRSQKCFLFWSGSKKG 480
Qy 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
Db 481 SODKEAIOAYSESLMSPAAGTIVLQEA 509
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Search completed: February 23, 2006, 12:51:25
Job time : 123 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:47:29 ; Search time 11.5 Seconds
(without alignments)
658.923 Million cell updates/sec

Title: US-08-765-108-8
Perfect score: 2681
Sequence: 1 MGSSRRARWALGALGALL.....YSELSMPAAKGTVLQEAFL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2192	81.8	509	7 US-11-055-309A-12	Sequence 12, Appl
2	2192	81.8	509	7 US-11-072-175-219	Sequence 219, App
3	2192	81.8	532	6 US-10-821-234-918	Sequence 918, App
4	98.5	3.7	414	7 US-11-072-512-2031	Sequence 2031, Ap
5	97	3.6	1075	7 US-11-098-686-10295	Sequence 10295, A
6	90	3.4	909	7 US-11-076-187-4	Sequence 4, Appli
7	88	3.3	890	7 US-11-072-512-2992	Sequence 2992, Ap
8	86.5	3.2	379	6 US-10-793-626-1512	Sequence 1512, Ap
9	85	3.2	320	7 US-11-142-700-6	Sequence 6, Appli
10	84.5	3.2	453	7 US-11-185-878-5	Sequence 5, Appli
11	84.5	3.2	455	7 US-11-182-946-3	Sequence 3, Appli
12	84	3.1	1130	7 US-11-086-482-1	Sequence 1, Appli
13	84	3.1	1130	7 US-11-192-341-23	Sequence 23, Appl
14	84	3.1	1735	7 US-11-040-472-13	Sequence 13, Appl
15	83.5	3.1	636	7 US-11-098-686-10289	Sequence 10289, A
16	82.5	3.1	687	6 US-10-055-877-200	Sequence 200, App
17	82	3.1	400	7 US-11-077-386-26	Sequence 26, Appl
18	82	3.1	610	7 US-11-142-700-16	Sequence 16, Appl
19	81	3.0	803	7 US-11-098-686-10461	Sequence 10461, A
20	81	3.0	1332	7 US-11-091-643-18	Sequence 18, Appl
21	81	3.0	3716	7 US-11-052-554A-141	Sequence 141, App
22	80.5	3.0	813	6 US-10-509-950-1	Sequence 1, Appli
23	80.5	3.0	1206	6 US-10-995-561-709	Sequence 709, App
24	80.5	3.0	1307	6 US-10-995-561-711	Sequence 711, App
25	80.5	3.0	2256	7 US-11-144-368-4	Sequence 4, Appli

26	80.5	3.0	2458	7 US-11-186-999-6	Sequence 6, Appli
27	80.5	3.0	2458	7 US-11-186-999-13	Sequence 13, Appl
28	80	3.0	420	6 US-10-935-494-3	Sequence 3, Appli
29	80	3.0	1394	6 US-10-935-494-31	Sequence 31, Appl
30	79.5	3.0	1167	6 US-10-942-072-6	Sequence 6, Appli
31	79.5	3.0	1167	6 US-10-942-072-13	Sequence 13, Appl
32	79.5	3.0	1168	6 US-10-942-072-11	Sequence 11, Appl
33	79.5	3.0	2455	7 US-11-186-999-4	Sequence 4, Appli
34	79.5	3.0	2515	7 US-11-113-424-53	Sequence 53, Appl
35	79	2.9	254	7 US-11-054-515-1259	Sequence 1259, Ap
36	79	2.9	857	7 US-11-052-554A-218	Sequence 218, App
37	79	2.9	1081	7 US-11-142-700-23	Sequence 23, Appl
38	79	2.9	1089	7 US-11-098-686-10150	Sequence 10150, A
39	78.5	2.9	555	7 US-11-072-512-2011	Sequence 2011, Ap
40	78.5	2.9	685	7 US-11-142-700-25	Sequence 25, Appl
41	78.5	2.9	952	7 US-11-207-626A-45	Sequence 45, Appl
42	78.5	2.9	1342	7 US-11-113-202-14	Sequence 14, Appl
43	78	2.9	304	7 US-11-142-700-2	Sequence 2, Appli
44	78	2.9	685	7 US-11-098-686-10574	Sequence 10574, A
45	78	2.9	1390	6 US-10-957-351-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-11-055-309A-12
; Sequence 12, Application US/11055309A
; Publication No. US20050282750A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: Treatment for Dark Adaptation
; FILE REFERENCE: HO-P0231US5
; CURRENT APPLICATION NUMBER: US/11/055,309A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 509
; TYPE: PRT
; ORGANISM: HUMAN
US-11-055-309A-12

Query Match	81.8%	Score	2192;	DB 7;	Length	509;
Best Local Similarity	79.4%	Pred. No.	4.5e-199;			
Matches	404;	Conservative	49;	Mismatches	56;	Indels 0; Gaps 0;
Qy	1	MGSSRRARWALGALGALLFAALGVNMI	LMVPSLIKQVQLKNVRIDPSSLSFGMWKEIP	60		
Db	1	MGCSAKARWAAGALGVAGLLCAVLGA	VMIWVPSLIKQVQLKNVRIDPSSLSFGMWKEIP	60		
Qy	61	VPFVLSYFVEVNVNPNVNGQKPVYR	PGVYVYRPGKVNITFNDNDTVSPVENS	SLH 120		
Db	61	IPFVLSYFDFVNMPSILKGEKQVYR	PGVYVYRPGKVNITFNDNDTVSPVENS	SLH 120		
Qy	121	FQPKSHGSSSDYLVLPNIILVGLSS	ILMKSPLSKLMTLALVTMGORAFMNTV	GEIL 180		
Db	121	FQPSKSHGSSSDYLVLPNIILVGLAA	VNMENKPMTLKIMTLAFTTLGERAFM	NTRVGEIM 180		
Qy	181	WGYYDDPFVHFINTYLPDMLPIKGF	GLFVGMMNSNGVFTVFTGVQNFRIH	LVDKWGL 240		
Db	181	WGYYDDPFVHFINTYLPDMLPIKGF	GLFVGMMNSNGVFTVFTGVQNFRIH	LVDKWGL 240		

Db 181 WGYKDPVLNLINKYFPGMFPKDFGLFAELNNSDSLFTVFTGVQVNSRIHLVDKWNGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKVDFWHSDDQCNMINGSQWMPFMTPESSLEFFSPACRSKMLTKESGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 301 FVAPKTLFANGSIYPPNEGFCPCLESIGIONVSTCRFSAPLFLSHPHFNADPVLAEAVTG 360
Qy 361 LNPMPKEHSLFLDIHPVTGIPMNCVKMQLSLYIKSVKGIGQTKIEPVVPLPLWFQSG 420
Db 361 LHPNQEAHSLFLDIHPVTGIPMNCVKLQLSLYMKSVAGIGQTKIEPVVPLPLWFAESG 420
Qy 421 AMGKPLSTFTYQLVLMPOVLYHAQVYLLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
Db 421 AMEGTLLHTFTYQLVLMPKVMHYAQVLLGCVLLLVVICQIRSQEKCYLEFWSSKKG 480
Qy 481 SQDKEAIOAYSESLSMSPAAGTGVLEAKL 509
Db 481 SKDKEAIOAYSESLSMTSAPKGSVLQEAKL 509

RESULT 2
US-11-072-175-219
; Sequence 219, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 219
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-219

Query Match 81.8%; Score 2192; DB 7; Length 509;
Best Local Similarity 79.4%; Pred. No. 4.5e-199;
Matches 404; Conservative 49; Mismatches 56; Indels 0; Gaps 0;

Qy 1 MGSRRARWVALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 1 MGCSAKARWAAAGALGAVGLCAVLGAVMIVMVPSLIKQOVLKNVRIDPSSLSFNMWKEIP 60
Qy 61 VPFYLSVYFVFNPNVNEVLNGKPVRRERGYPVYRERQKVNITFNDNDTVSFVENSLSH 120
Db 61 IPFYLVSVYFVFNPNVNEVLNGKPVRRERGYPVYRERQKVNITFNDNDTVSFLEYRTFQ 120
Qy 121 FQPKSHGSES DYI VLPN ILV LGSILMESKPVSLKMMTLALVTMGQAFMNRVTGEIL 180
Db 121 FQPKSHGSES DYI VLPN ILV LGSILMESKPVSLKMMTLALVTMGQAFMNRVTGEIM 180
Qy 181 WGYDDPFVHFLNTYLPDMLPIKKGKGLFVGMNNSGVFTVFTGVQVNSRIHLVDKWNGL 240
Db 181 WGYKDPVLNLINKYFPGMFPKDFGLFAELNNSDSLFTVFTGVQVNSRIHLVDKWNGL 240
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
Db 241 SKVDFWHSDDQCNMINGSQWMPFMTPESSLEFFSPACRSKMLTKESGVFEGIPTYR 300
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360

Db 301 FVAPKTLFANGSIYPPNEGFCPCLESIGIONVSTCRFSAPLFLSHPHFNADPVLAEAVTG 360
Qy 361 LNPMPKEHSLFLDIHPVTGIPMNCVKMQLSLYIKSVKGIGQTKIEPVVPLPLWFQSG 420
Db 361 LHPNQEAHSLFLDIHPVTGIPMNCVKLQLSLYMKSVAGIGQTKIEPVVPLPLWFAESG 420
Qy 421 AMGKPLSTFTYQLVLMPOVLYHAQVYLLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
Db 421 AMEGTLLHTFTYQLVLMPKVMHYAQVLLGCVLLLVVICQIRSQEKCYLEFWSSKKG 480
Qy 481 SQDKEAIOAYSESLSMSPAAGTGVLEAKL 509
Db 481 SKDKEAIOAYSESLSMTSAPKGSVLQEAKL 509

RESULT 3
US-10-821-234-918
; Sequence 918, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 918
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-918

Query Match 81.8%; Score 2192; DB 6; Length 532;
Best Local Similarity 79.4%; Pred. No. 4.8e-199;
Matches 404; Conservative 49; Mismatches 56; Indels 0; Gaps 0;

Qy 1 MGSRRARWVALGALGALLFAALGVVMILMVPSLIKQOVLKNVRIDPSSLSFGMWKEIP 60
Db 24 MGCSAKARWAAAGALGAVGLCAVLGAVMIVMVPSLIKQOVLKNVRIDPSSLSFNMWKEIP 83
Qy 61 VPFYLSVYFVFNPNVNEVLNGKPVRRERGYPVYRERQKVNITFNDNDTVSFVENSLSH 120
Db 84 IPFYLVSVYFVFNPNVNEVLNGKPVRRERGYPVYRERQKVNITFNDNDTVSFLEYRTFQ 143
Qy 121 FQPKSHGSES DYI VLPN ILV LGSILMESKPVSLKMMTLALVTMGQAFMNRVTGEIL 180
Db 144 FQPKSHGSES DYI VLPN ILV LGSILMESKPVSLKMMTLALVTMGQAFMNRVTGEIM 203
Qy 181 WGYDDPFVHFLNTYLPDMLPIKKGKGLFVGMNNSGVFTVFTGVQVNSRIHLVDKWNGL 240
Db 204 WGYKDPVLNLINKYFPGMFPKDFGLFAELNNSDSLFTVFTGVQVNSRIHLVDKWNGL 263
Qy 241 SKIDYHSEQCNMINGTSGQWAPFMTPESSLEFFSPACRSKMLTYNESRVFEGIPTYR 300
Db 264 SKVDFWHSDDQCNMINGSQWMPFMTPESSLEFFSPACRSKMLTKESGVFEGIPTYR 323
Qy 301 FTAPDTLTFANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSHPHFNADPVLSEAVLG 360
Db 324 FVAPKTLFANGSIYPPNEGFCPCLESIGIONVSTCRFSAPLFLSHPHFNADPVLAEAVTG 383
Qy 361 LNPMPKEHSLFLDIHPVTGIPMNCVKMQLSLYIKSVKGIGQTKIEPVVPLPLWFQSG 420
Db 384 LHPNQEAHSLFLDIHPVTGIPMNCVKLQLSLYMKSVAGIGQTKIEPVVPLPLWFAESG 443
Qy 421 AMGKPLSTFTYQLVLMPOVLYHAQVYLLGGLLLVPIICOLRSQEKCFLFWSSKKG 480
Db 444 AMEGTLLHTFTYQLVLMPKVMHYAQVLLGCVLLLVVICQIRSQEKCYLEFWSSKKG 503

Qy 481 SODKEAIOAYSESLSMPAAKGTVLQRAKL 509
Db 504 SKDKEAIOAYSESLSMTAPKGSVLQRAKL 532

RESULT 4

US-11-072-512-2031
; Sequence 2031, Application US/11072512
; Publication No. US2006002945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO

APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI

APPLICANT: WAKAMATSU, AI

APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU

APPLICANT: NAGAI, KEIICHI

APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKA, ICHIRO

APPLICANT: SEKI, NAOHICO

APPLICANT: YOSHIKAWA, TSUTOMU

APPLICANT: OTSUKA, MOTOTYUKI

APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: Novel full length cDNA

FILE REFERENCE: 084335-0191

CURRENT APPLICATION NUMBER: US/11/072,512

CURRENT FILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US 60/350,978

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: JP 2001-379298

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2031

LENGTH: 414

TYPE: PRT

ORGANISM: Homo sapiens

US-11-072-512-2031

Query Match 3.7%; Score 98.5; DB 7; Length 414;
Best Local Similarity 20.4%; Pred. No. 0.18;
Matches 88; Conservative 56; Mismatches 136; Indels 151; Gaps 26;

Qy 13 GLGALGLLFAALGVVMIWVPSLIKQ-VLKNVRIDPSSLSFGMWKEIPVPFYLVSVPFE 71
Db 81 GTGHVAYL--AGCVVILDPKENKQHI FNTARKSLALAFS-----PDGKIYVT----- 128
Qy 72 VVNEVLNGQKPVVR-----RGPVVYREFQKVNITFNDNTVSVFVNRSLHFPQDKSH 127
Db 129 ----GE--NGHRPAVRIMDVBEKNQVAEMLGHKYGVA-----CVAFSNNMKH 169
Qy 128 ----GSESDIYVLNVLGSGILMESKPSVSLKMM-----TLALVTMGORAFMNRVTG 177
Db 170 IVSMGYQHDVWL--NVWDWKDIDVVASNKVSCRVALSFSDSSYFVTVG-----NRHVR 222
Qy 178 BILGYDDPPFVHL-----NTYLPDMLPIKGFGLFVGNNNSGVFTVFTGVQNFPSRIHL 233
Db 223 --FW-----FLEVSTETKVTSTVPLVGRSGILGELHNN-----IFCGV----- 258
Qy 234 VDKWGLSKIDYHSEQCNMINGTSQGMWAPFMTPESSLEPFSPEACRSKMLTYNESRVF 293
Db 259 -----AC-----GRGRMAGSTFCVSYSGL-----LCQ-----FNEKEVL 287
Qy 294 EGIPYRFTAPDTLFPANGSVVPPNEGFCPCRESGIONVSTCRFGAPLFLSH----- 344
Db 288 EKWLNLKVSLSCLCVSQELI-----FCGCTDGIVR-----IFQASHLYLANLP 332

Qy 345 -PHEYNADPVLSEAVLGNP-----NPKHSLFLDIHPVTGIP-----MNCVSMQLSLYIK 395
Db 333 KPHYLGVYD-----VAQGLEPFLFHRKAEAVPYDTALTDPDTHQWLSCVYK-DHSIYIW 386
Qy 396 SVKGIGOTGKI 406
Db 387 DVKDINRVGKV 397

RESULT 5

US-11-098-686-10295

; Sequence 10295, Application US/11098686

; Publication No. US20060024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REFERENCE: 09531-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: PCT/US03/31318

PRIOR FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10295

LENGTH: 1075

TYPE: PRT

ORGANISM: Lawsonia intracellularis

US-11-098-686-10295

Query Match 3.6%; Score 97; DB 7; Length 1075;

Best Local Similarity 19.6%; Pred. No. 0.99;

Matches 84; Conservative 65; Mismatches 146; Indels 134; Gaps 22;

Qy 17 LGLL-FAALGVVMIWVPSLIKQV-----LKNVRIDPSSLSFGMWKEIPVP-FYL-- 65
Db 14 LGIIVFEGITFYFIKQHPQVITNKLSTISKQLKDTGISANSIGFHI---VPPPKLYLTN 70
Qy 66 -----SVYFEVVPNEVL-----NGOKPVVRERGPY 92
Db 71 VILQTKGDTIHKECLITPKITNLSGNISYISIEVIQPIASILQNEQKNSKTTGYA 130
Qy 93 VYREFQKVNITFNDNTVSVFVNRSLHFPQDKSHGSESDYVLPNVLVLGGSLMESKP 152
Db 131 IPKQVSHLQLI---TDSKLFIEGNSITFQ-----NNDYCP--KIINGKI-----G 173
Qy 153 VSLKMLMTALVTMGORAFMNRVTVEILWGYDDPFVHFLNT-----YL 195
Db 174 VSKLTSSKL-----TADLIW-----EIMTVSNNSSTAQKSIEKVQLHI 215
Qy 196 PDLPIKGFGLFVGNNNSGVFTVFTGVQNFPS-----RIHLVDKWNGL-----SKIDY 245
Db 216 EDM-PYK-----INTALLHDTSPLYDLFTNKTCTKTFKVSIGAIPTTNTANNITFDTTKLEK 270
Qy 246 WHSQCNW-----INGT--SQQ-----MWAPMTPEP-SLEFPSPACRSKMLTYNESR 291
Db 271 DNSDKLTMHQHLIEGLTPNGNTSIPILLSVPFTTSSDMDTHPPPLLIRKSKLLFDKTH 330
Qy 292 VFEGIPYRFTAPDTLFPANGSV-----YPPNEGFCPCRESGIONVSTCRFGAPLFLSHP 345
Db 331 IDLHGTTIKNVDLTSLNLFDFDGTMDVKNFSPFPWFTFAQLPNGIQLHALNQLSGBIKFTLSP 390
Qy 346 HFTNADPVL 354
Db 391 QQVNAQKII 399

RESULT 6

US-11-076-187-4

; Sequence 4, Application US/11076187

; Publication No. US20050244857A1

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-10-793-626-1512

Query Match	3.2%;	Score	86.5;	DB	6;	Length	379;
Best Local Similarity	21.8%;	Pred. No.	2.2;				
Matches	83;	Conservative	49;	Mismatches	153;	Indels	95;
Gaps	19;						
QY	113	FVENRSLH-FOPDKSHGESDYIVLPNILVLG-----GSILMESKPVSVS---	154				
Db	3	FSANAILNVFPLRGCHDLEANTVIG--IVMGAYMLTAMLPFWAQIILARVGPVKVLRI	60				
QY	115	LKLMTLALVTWGORAFMNRVTGSIILGYDDPWFH-LNTYLPDMLPIKKGFLGVGMNN	213				
Db	61	ILLINAMALVLYGTGLEGYLVARIMOGCVCTAFFMSLQLGIITDALPER-----YRS	112				
QY	214	SNSGVFTVFTGVQNFPSRIHLVDKWNGLSKIDYHSEQCNMINTGSCQWAPFWPTPESSLE	273				
Db	113	EGVSLYSLSFTIPNL-----LGPLIANGIHWVE--NNTFPAIWMIFIAVTITLIF	159				
QY	274	FPSPEACRSMKLTYNESGRVFGIPTYRTAPTDLFANGSVYPNEGFCPCRESG-IQNVS	332				
Db	160	GYYRTTFANTQEVAPKBEV---LPFNAMTVVGVFFKNAL-----FC---SGMIMILS	206				
QY	333	TCRFGA-----PLFLSHPHFNADPVLSEAVILGNPNPKHSILPLDIHPVTGIPMNCVSK	387				
Db	207	SIVFGAMSTFPLTYTVREGFANA-----GIFLTIQAITVV---IAR	244				
QY	388	MOLSIIYIKSVHGIQGTGKIEPVLPLLWFEG-SGAMGKGPLSTF-----YTVQLVM	437				
Db	245	FYLRYKVPVS-DGLMWH-HRFMMIVLTLMIASIIIVAGPQILSFVYISAIFGITQALVY	302				
QY	438	POVLHYAQYVLLIGGLLLL	457				
Db	303	PTLTATYSFVLFPKIGRNMLL	322				

```

RESULT 9
US-11-142-700-6
; Sequence 6, Application US/11142700
; Publication No. US20060026721A1
; GENERAL INFORMATION:
; APPLICANT: Stephen M. Allen
; APPLICANT: Gary M. Fader
; APPLICANT: Saverio Carl Falco
; APPLICANT: Anthony J. Kinney
; APPLICANT: Jonathan E. Lightner
; APPLICANT: Guo-Hua Miao
; APPLICANT: J. Antoni Rafalski
; APPLICANT: Catherine J. Thorpe
; TITLE OF INVENTION: Plant Cellulose Synthases
; FILE REFERENCE: BB-1170
; CURRENT APPLICATION NUMBER: US/11/142,700
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/09/720,383
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/092,844
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Zea mays
US-11-142-700-6

```

```

QY 195 -----LPDMLPIKGKGLFGVMNNSGVF--TVPTGQNFSRIHLVDKWNGLSKIDYHWS 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 LAYCTTIPAVCLLTGKF-IIPTLNNLASIWI FIALEFLSIATSVLSL--RWSGVSIEDWWRN 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 EQCNMINGTSGOMWAPMTPESSILEFFSPSEACRSMKLTYNESRVFEGIPTVRFETA---P 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 163 EQFWIGGVSAAHLFAVPQGLKVLGGVDTSFTVTISKAAGDEADAFGDLYLFKWTLLVPP 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 305 DTL 307
   |||
Db 223 TTL 225

```

RESULT 10
US-11-185-878-5
; Sequence 5, Application US/11185878
; Publication No. US20050282217A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
; FILE REFERENCE: EP379PD1
; CURRENT APPLICATION NUMBER: US/11/185,878
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/280,047
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 09/580,212
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/086,483
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/069,112
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/050,936
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 453
; TYPE: PRT
; ORGANISM: human
US-11-185-878-5

RESULT 11
US-11-182-946-3
; Sequence 3, Application US/11182946

QY	287	YNESRVFEGIPTYRF-TAPDTL	FANGSVYPPNEGFCPCRESGIGNVSTCRGAPLFLSHP	345
DB	167	Y-EGRVYH-----YRINTASD-----GKLYVSSSES-----	RFNTLAELVHH	201
QY	346	HFYNADPVL-----EAVLGLNPNPKHSLFLDHPVTGIPMNCVSKMQLSLYI	394	
DB	202	HSTVADGLITTLHYDPAPKRNKPTVYGVSPNDKWM-----	ERTDITM	244
QY	395	KSVKGIGQTKIEPVLPVLLWFEQSGAMGGKPL-----	STFTQLVLMPOVLHYAQYV	447
DB	245	KHKLGGQYGEYEGV-----WKYSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQ	300	
QY	448	LLGL 451		
DB	301	LLGV 304		
<p>RESULT 13</p> <p>US-11-192-341-23</p> <p>; Sequence 23, Application US/11192341</p> <p>; Publication No. US20060030583A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: SGX Pharmaceuticals, Inc.</p> <p>; APPLICANT: Arnold, William D.</p> <p>; APPLICANT: Bounaud, Pierre</p> <p>; APPLICANT: Gosberg, Andreas</p> <p>; APPLICANT: Li, Zhe</p> <p>; APPLICANT: McDonald, Ian W.</p> <p>; APPLICANT: Steensma, Ruo W.</p> <p>; APPLICANT: Wilson, Mark E.</p> <p>; TITLE OF INVENTION: Pyrrolo-Pyridine Kinase Modulators</p> <p>; FILE REFERENCE: 022132-004510US</p> <p>; CURRENT APPLICATION NUMBER: US/11/192,341</p> <p>; CURRENT FILING DATE: 2005-07-27</p> <p>; PRIOR APPLICATION NUMBER: 60/683,510</p> <p>; PRIOR FILING DATE: 2005-05-19</p> <p>; PRIOR APPLICATION NUMBER: 60/591,888</p> <p>; PRIOR FILING DATE: 2004-07-27</p> <p>; PRIOR APPLICATION NUMBER: 60/591,887</p> <p>; PRIOR FILING DATE: 2004-07-27</p> <p>; NUMBER OF SEQ ID NOS: 23</p> <p>; SOFTWARE: PatentIn version 3.1</p> <p>; SEQ ID NO 23</p> <p>; LENGTH: 1130</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Homo sapiens</p> <p>US-11-192-341-23</p>				
<p>Query Match 3.1%; Score 84; DB 7; Length 1130;</p> <p>Best Local Similarity 21.1%; Pred. No. 18;</p> <p>Matches 64; Conservative 36; Mismatches 98; Indels 106; Gaps 14;</p>				
QY	204	KFGLFVGMNNSGVFT-----VFTGVQNFRIHLVDKWNGLSKIDYWHSEQCMMNGTS	258	
DB	51	KENLLAGSPENDPNLFVLYDFVASGDNTLS-----ITKGEKLVLYGNHNGEWCEAQTKN	106	
QY	259	GQWAP--FWTPESLSE-----PF-----SPEACRSKMLT	286	
DB	107	GQGWVPSNYITPVNSLEKHSWYHGPVSRNAAYLLSSGINGSFLVRESSESPGORSISLR	166	
QY	287	YNESRVFEGIPTYRF-TAPDTL	FANGSVYPPNEGFCPCRESGIGNVSTCRGAPLFLSHP	345
DB	167	Y-EGRVYH-----YRINTASD-----GKLYVSSSES-----	RFNTLAELVHH	201
QY	346	HFYNADPVL-----EAVLGLNPNPKHSLFLDHPVTGIPMNCVSKMQLSLYI	394	
DB	202	HSTVADGLITTLHYDPAPKRNKPTVYGVSPNDKWM-----	ERTDITM	244
QY	395	KSVKGIGQTKIEPVLPVLLWFEQSGAMGGKPL-----	STFTQLVLMPOVLHYAQYV	447
DB	245	KHKLGGQYGEYEGV-----WKYSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQ	300	

Qy 448 LLGL 451
Db 301 LLGV 304

RESULT 14

US-11-040-472-13

; Sequence 13, Application US/11040472

; Publication No. US20050283857A1

; GENERAL INFORMATION:

; APPLICANT: Adang, Michael

; APPLICANT: Hua, Gang

; APPLICANT: Chen, Jiang

; APPLICANT: Abdullah, Mohd

; TITLE OF INVENTION: Peptides for Inhibiting Insects

; FILE REFERENCE: UGR-105CP

; CURRENT APPLICATION NUMBER: US/11/040,472

; CURRENT FILING DATE: 2005-01-21

; PRIOR APPLICATION NUMBER: US 60/538,715

; PRIOR FILING DATE: 2004-01-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 1735

; TYPE: PRT

; ORGANISM: Anopheles gambiae

US-11-040-472-13

Query Match 3.1%; Score 84; DB 7; Length 1735;

Best Local Similarity 20.8%; Pred. No. 33;

Matches 100; Conservative 54; Mismatches 147; Indels 180; Gaps 27;

Qy 32 VPSLIKQVKNVRIDPSSLSFGMWK--EI-----PVFPVLSVYFVFNPN 76

Db 829 IPPIDK--VLQNVII--SDMKSNWHVFEIVLMDTNKKQPVHDPFNDGQVYQEKIPSN 884

Qy 77 EVLNGQKPVVRERG-----PY-----VYREFROKVNITFNDNDTVSEV--ENRSLHP 121

Db 885 TA-----IVRVEGKDQDRDPVYHTVSVEINRDPFQQLQRYFEVDSTGRATYKENNDL-- 936

Qy 122 QPKSHGSESDYIVLPNLTVL--GSSILMESKPVSLKMMTLALVTMQRQAFMRTVGEI 179

Db 937 -LDRDAGLES-----IMINIVLMDNAGGYDIQNR--VSTNINLTLL----- 974

Qy 180 LMWYDDPFVHPHLPDMLPIKFGFLVGMNNSGCVFTVFTGVQNFPSRIHLVDKWNQ 239

Db 975 -----DINDHTP--KLPELADELKVS--ENAKQG--YIVKT--PFAALDLDKRT 1018

Qy 240 LSKIDYHSEQCNNINGTSGQWAPFMTPESSLEFFGPE---ACRSKMLTYNESRVFEGI 296

Db 1019 NAKINYIEE-----MTPEPETPLFSLNIDENAVPRVAQDLKGFVGT 1062

Qy 297 PTYFTAPDTLFPANGSVYPPNEGCPCEBSIQNVISICRP-----G 337

Db 1063 WTLKIKACD-----RGSEYEP---IPLTEPKNCETRDYELTVEPFNNTPTSPSR 1115

Qy 338 APLFLSHPHFYNADPVLS-----EAV-----LGLNPNKEHSLF--- 371

Db 1116 AOLRLKYESLQNGRLVETNGSPLPKPEAIDDDGGIYGDVTFPSLTSTNDGEQDHEVFRVD 1175

Qy 372 -----LDIHPVTGIPMNCV-----KMLSLYIKSVKGIQGTGKIE 407

Db 1176 KVDNKTGLLVLENSLAVQP---FPKNYSITVIARDGGDRQSEAAIHVVFINMTGEPAPLE 1232

Qy 408 P 408

Db 1233 P 1233

RESULT 15

US-11-098-686-10289

; Sequence 10289, Application US/11098686

; Publication No. US20060024696A1

; GENERAL INFORMATION:

; APPLICANT: Kapur, Vivek and Gebhart, Connie J.

; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

; FILE REFERENCE: 09531-128001

; CURRENT APPLICATION NUMBER: US/11/098,686

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: PCT/US03/31318

; PRIOR FILING DATE: 2003-10-01

; PRIOR APPLICATION NUMBER: US 60/416,395

; PRIOR FILING DATE: 2002-10-04

; NUMBER OF SEQ ID NOS: 11433

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 10289

; LENGTH: 636

; TYPE: PRT

; ORGANISM: Lawsonia intracellullaris

US-11-098-686-10289

Query Match 3.1%; Score 83.5; DB 7; Length 636;

Best Local Similarity 18.8%; Pred. No. 8.9;

Matches 74; Conservative 54; Mismatches 145; Indels 121; Gaps 16;

Qy 17 LGLLFAALGVVMILMVPSLIKQVKNVRIDPSSLSFGMWKEIIPVPFVLSVY----- 68

Db 142 IGIILCSLGVSWILLRPIAKK---INNIPVSVRWFFSVW--IILASITTIYSPPTFSNN 196

Qy 69 -----PFEVVNPNNEVLNGO--KPVVRERGPV--VYREFROKVNITENDNDTVS 112

Db 197 ALSQELSKNGIWSLFSFRNNQDYOQFYVIDKKLAFELHHELIENPSVFFNDN---S 253

Qy 113 FVENRSLHPQPKSHGSESDYIVLPNLTVLGSSILMESKPVSLKMMTLALVTMQRQAFM 172

Db 254 MEWRRIYH-----SNSPEKHLNVTIIVVESLGSVSLGDRTPHLNDLSKKCLYFTNMKATG 308

Qy 173 NRTV-----GEIL--WGYYDDPFVHPHLPDMLP 200

Db 309 TRTVRGLEAILSLPPTPGASIVRRPNHNLFTGTGLFRQGYDTVIY----- 357

Qy 201 IKGKFGFLVGMNNSNG-----VFTVFTGVQNFPSRIHLVDKWNGLSKIDYWH 247

Db 358 --GGYGFDMNNEFFSGNGFRIIDRSTIPDEYKFTTNWAGICDEDLFDVAVREADIATYS 415

Qy 248 SEQCNMINTSGQWAPFMTPESSLEFFSPEACRSKMLTYNESRVFEGIPTYRFTA----- 303

Db 416 NKPPYHVALTTSN--HRPFTYDGRVDVPSGTS--RTGAIKYTDVAI-----HRFLKEAKK 467

Qy 304 -----PDTLF-----ANGSVYPPNEGFCPC 323

Db 468 KPWFSDTIFITIVADHTAGSAGKTVLPDPNDYDIPC 501

Search completed: February 23, 2006, 12:51:54

Job time : 13.5 secs

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